

645										650					655				
Asp	Ala	Arg	Ala	Glu	Gln	Leu	Ala	Ala	Met	Pro	Leu	Phe	Glu	Arg	Leu				
			660					665					670						
Ala	Gln	Arg	Ile	Ile	Asp	Gly	Asp	Lys	Asn	Gly	Leu	Glu	Asp	Asp	Leu				
		675				680						685							
Glu	Ala	Gly	Met	Lys	Glu	Lys	Ser	Pro	Ile	Ala	Ile	Ile	Asn	Glu	Asp				
	690					695					700								
Leu	Leu	Asn	Gly	Met	Lys	Thr	Val	Gly	Glu	Leu	Phe	Gly	Ser	Gly	Gln				
705					710					715					720				
Met	Gln	Leu	Pro	Phe	Val	Leu	Gln	Ser	Ala	Glu	Thr	Met	Lys	Thr	Ala				
				725					730					735					
Val	Ala	Tyr	Leu	Glu	Pro	Phe	Met	Glu	Glu	Glu	Ala	Glu	Ala	Thr	Gly				
			740					745					750						
Ser	Ala	Gln	Ala	Glu	Gly	Lys	Gly	Lys	Ile	Val	Val	Ala	Thr	Val	Lys				
		755					760					765							
Gly	Asp	Val	His	Asp	Ile	Gly	Lys	Asn	Leu	Val	Asp	Ile	Ile	Leu	Ser				
	770					775					780								
Asn	Asn	Gly	Tyr	Asp	Val	Val	Asn	Leu	Gly	Ile	Lys	Gln	Pro	Leu	Ser				
785					790					795					800				
Ala	Met	Leu	Glu	Ala	Ala	Glu	Glu	His	Lys	Ala	Asp	Val	Ile	Gly	Met				
				805					810					815					
Ser	Gly	Leu	Leu	Val	Lys	Ser	Thr	Val	Val										
			820					825											

<210> 215

<211> 621

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> RXN03074

<400> 215

tttgtgggca atctgggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60

tagcaggaca	agcatactgt	tttagtttcta	tgctgtgggc	atg	act	caa	agt	gct	115
				Met	Thr	Gln	Ser	Ala	
				1				5	

cca	gaa	ttc	att	gcc	acc	gca	gac	ctc	gta	gac	atc	atc	ggc	gac	aac	163
Pro	Glu	Phe	Ile	Ala	Thr	Ala	Asp	Leu	Val	Asp	Ile	Ile	Gly	Asp	Asn	
				10				15					20			

gcg	caa	tca	tgc	gac	act	cag	ttt	caa	aac	ctt	gga	ggt	gcc	aca	gaa	211
Ala	Gln	Ser	Cys	Asp	Thr	Gln	Phe	Gln	Asn	Leu	Gly	Gly	Ala	Thr	Glu	
			25					30					35			

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

 cag taatttgttt tgacgacgca gta 621
 Gln

<210> 216

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15

 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 217
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> FRXA02906

<400> 217
 tttgtgggca atctgggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60

tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

 cag taatttggtt tgacgacgca gta 621
 Gln

<210> 218

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 218

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15

 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

 Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

 Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

 Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

 Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

 Glu Ala Pro Ile Lys Gln
 165

<210> 219

<211> 1557

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1534)

<223> RXN00132

<400> 219

aacagcttca atcaattcgg tgtccactcc aacatgtaga gtgggtgcgcg ttaaaaaagt 60

tttcctaatt	ttcattttct	taaaaggagc	tcgccaggac	atg	gca	cag	gtt	atg	115
				Met	Ala	Gln	Val	Met	
				1				5	

gac	ttc	aag	gtt	gcc	gat	ctt	tca	cta	gca	gag	gca	gga	cgt	cac	cag	163
Asp	Phe	Lys	Val	Ala	Asp	Leu	Ser	Leu	Ala	Glu	Ala	Gly	Arg	His	Gln	
			10						15				20			

att	cgt	ctt	gca	gag	tat	gag	atg	cca	ggg	ctc	atg	cag	ttg	cgc	aag	211
Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys	
			25					30					35			

gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggg	tct	259
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser	
		40					45					50				

atc	cac	atg	acg	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	act	gct	307
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala	
	55					60					65					

ttg	ggc	gct	gag	gtt	cgt	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag	355
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln	
70					75					80					85	

gat	gag	gct	gca	gcg	gct	atc	gtt	gtc	ggc	tcc	ggc	acc	gtc	gaa	gag	403
Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu	
				90					95					100		

cca	gct	ggg	gtt	cca	gta	ttc	gcg	tgg	aag	ggg	gag	tca	ctg	gag	gag	451
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu	
			105					110					115			

tac	tgg	tgg	tgc	atc	aac	cag	atc	ttc	agc	tgg	ggc	gat	gag	ctg	cca	499
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro	
		120					125					130				

aac	atg	atc	ctc	gac	gac	ggc	ggg	gac	gcc	acc	atg	gct	gtt	att	cgc	547
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg	
	135					140					145					

ggg	cgc	gaa	tac	gag	cag	gct	ggg	ctg	gtt	cca	cca	gca	gag	gcc	aac	595
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn	
150					155					160				165		

gat	tcc	gat	gag	tac	atc	gca	ttc	ttg	ggc	atg	ctg	cgt	gag	gtt	ctt	643
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu	
			170					175						180		

gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggg	691
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly	
			185					190					195			

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct 739
 Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala
 200 205 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc 787
 Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val
 215 220 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc 835
 Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile
 230 235 240 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg 883
 Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val
 250 255 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag
 1027
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac
 1075
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg
 1123
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg
 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag
 1219
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc
 1267
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc
 1315
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac
 1363

Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac
 1411

Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
 425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc
 1459

Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
 440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc
 1507

Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
 455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag
 1554

Pro Phe Lys Pro Glu His Tyr Arg Tyr
 470 475

gga
 1557

<210> 220

<211> 478

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 220

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
 1 5 10 15

Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
 35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro

145		150		155		160
Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met						
		165		170		175
Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala						
		180		185		190
Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg						
		195		200		205
Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn						
		210		215		220
Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr						
		225		230		240
Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met						
		245		250		255
Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly						
		260		265		270
Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu						
		275		280		285
Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val						
		290		295		300
Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala						
		305		310		320
Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys						
		325		330		335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp						
		340		345		350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys						
		355		360		365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val						
		370		375		380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro						
		385		390		400
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile						
		405		410		415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu						
		420		425		430
Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu						
		435		440		445
Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly						
		450		455		460
Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr						
		465		470		475

<210> 221
 <211> 128
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(105)
 <223> FRXA00132

<400> 221
 cac gtt gag gct ctc ggc ggt cag ctc acc gaa ctg acc aag gag cag 48
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15

 gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

 tac cgc tac taatgattgt cagcattgag gga 128
 Tyr Arg Tyr
 35

<210> 222
 <211> 35
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 222
 His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
 1 5 10 15

 Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
 20 25 30

 Tyr Arg Tyr
 35

<210> 223
 <211> 1396
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1396)
 <223> FRXA01371

<400> 223
 aacagcttca atcaattcgg tgtccactcc aacatgtaga gtggtgcgcg ttaaaaaagt 60

 tttcctaatt ttcattttct taaaaggagc tgcgcaggac atg gca cag gtt atg 115
 Met Ala Gln Val Met
 1 5

 gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
 Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln

10						15						20						
att	cgt	ctt	gca	gag	tat	gag	atg	cca	ggc	ctc	atg	cag	ttg	cgc	aag	211		
Ile	Arg	Leu	Ala	Glu	Tyr	Glu	Met	Pro	Gly	Leu	Met	Gln	Leu	Arg	Lys			
			25					30					35					
gaa	ttc	gca	gac	gag	cag	cct	ttg	aag	ggc	gcc	cga	att	gct	ggc	tct	259		
Glu	Phe	Ala	Asp	Glu	Gln	Pro	Leu	Lys	Gly	Ala	Arg	Ile	Ala	Gly	Ser			
		40					45					50						
atc	cac	atg	acg	gtc	cag	acc	gcc	gtg	ctt	att	gag	acc	ctc	act	gct	307		
Ile	His	Met	Thr	Val	Gln	Thr	Ala	Val	Leu	Ile	Glu	Thr	Leu	Thr	Ala			
	55					60					65							
ttg	ggc	gct	gag	gtt	cgt	tgg	gct	tcc	tgc	aac	att	ttc	tcc	acc	cag	355		
Leu	Gly	Ala	Glu	Val	Arg	Trp	Ala	Ser	Cys	Asn	Ile	Phe	Ser	Thr	Gln			
	70				75					80					85			
gat	gag	gct	gca	gcg	gct	atc	gtt	gtc	ggc	tcc	ggc	acc	gtc	gaa	gag	403		
Asp	Glu	Ala	Ala	Ala	Ala	Ile	Val	Val	Gly	Ser	Gly	Thr	Val	Glu	Glu			
				90					95					100				
cca	gct	ggc	gtt	cca	gta	ttc	gcg	tgg	aag	ggc	gag	tca	ctg	gag	gag	451		
Pro	Ala	Gly	Val	Pro	Val	Phe	Ala	Trp	Lys	Gly	Glu	Ser	Leu	Glu	Glu			
			105					110					115					
tac	tgg	tgg	tgc	atc	aac	cag	atc	ttc	agc	tgg	ggc	gat	gag	ctg	cca	499		
Tyr	Trp	Trp	Cys	Ile	Asn	Gln	Ile	Phe	Ser	Trp	Gly	Asp	Glu	Leu	Pro			
		120					125					130						
aac	atg	atc	ctc	gac	gac	ggc	ggc	gac	gcc	acc	atg	gct	gtt	att	cgc	547		
Asn	Met	Ile	Leu	Asp	Asp	Gly	Gly	Asp	Ala	Thr	Met	Ala	Val	Ile	Arg			
	135					140					145							
ggc	cgc	gaa	tac	gag	cag	gct	ggc	ctg	gtt	cca	cca	gca	gag	gcc	aac	595		
Gly	Arg	Glu	Tyr	Glu	Gln	Ala	Gly	Leu	Val	Pro	Pro	Ala	Glu	Ala	Asn			
	150				155					160					165			
gat	tcc	gat	gag	tac	atc	gca	ttc	ttg	ggc	atg	ctg	cgt	gag	gtt	ctt	643		
Asp	Ser	Asp	Glu	Tyr	Ile	Ala	Phe	Leu	Gly	Met	Leu	Arg	Glu	Val	Leu			
				170					175					180				
gct	gca	gag	cct	ggc	aag	tgg	ggc	aag	atc	gct	gag	gcc	gtt	aag	ggc	691		
Ala	Ala	Glu	Pro	Gly	Lys	Trp	Gly	Lys	Ile	Ala	Glu	Ala	Val	Lys	Gly			
			185					190					195					
gtc	acc	gag	gaa	acc	acc	acc	ggc	gtg	cac	cgc	ctg	tac	cac	ttc	gct	739		
Val	Thr	Glu	Glu	Thr	Thr	Thr	Gly	Val	His	Arg	Leu	Tyr	His	Phe	Ala			
		200					205					210						
gaa	gaa	ggc	gtg	ctg	cct	ttc	cca	gcg	atg	aac	gtc	aac	gac	gct	gtc	787		
Glu	Glu	Gly	Val	Leu	Pro	Phe	Pro	Ala	Met	Asn	Val	Asn	Asp	Ala	Val			
	215					220					225							
acc	aag	tcc	aag	ttt	gat	aac	aag	tac	ggc	acc	cgc	cac	tcc	ctg	atc	835		
Thr	Lys	Ser	Lys	Phe	Asp	Asn	Lys	Tyr	Gly	Thr	Arg	His	Ser	Leu	Ile			
	230				235					240					245			
gac	ggc	atc	aac	cgc	gcc	act	gac	atg	ctc	atg	ggc	ggc	aag	aac	gtg	883		
Asp	Gly	Ile	Asn	Arg	Ala	Thr	Asp	Met	Leu	Met	Gly	Gly	Lys	Asn	Val			
			250						255					260				

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc 931
 Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
 265 270 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac 979
 Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
 280 285 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag
 1027
 Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
 295 300 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac
 1075
 Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
 310 315 320 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg
 1123
 Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
 330 335 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg
 1171
 Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
 345 350 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag
 1219
 His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
 360 365 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc
 1267
 Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
 375 380 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc
 1315
 Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
 390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac
 1363
 Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
 410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg
 1396
 Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
 425 430

<210> 224

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
 1 5 10 15
 Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
 20 25 30
 Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
 35 40 45
 Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
 50 55 60
 Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
 65 70 75 80
 Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
 85 90 95
 Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
 100 105 110
 Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
 115 120 125
 Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
 130 135 140
 Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
 145 150 155 160
 Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
 165 170 175
 Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
 180 185 190
 Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
 195 200 205
 Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
 210 215 220
 Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
 225 230 235 240
 Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
 245 250 255
 Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
 260 265 270
 Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
 275 280 285
 Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
 290 295 300
 Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
 305 310 315 320
 Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys

325	330	335
Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp 340	345	350
Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys 355	360	365
Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val 370	375	380
Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro 385	390	395
Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile 405	410	415
Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu 420	425	430

<210> 225
 <211> 2358
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2335)
 <223> RXN02085

<400> 225
 caccgcgtga tttcgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60
 gatccgcacg ttcggctcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
 Met Thr Ser Asn Phe
 1 5
 tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
 Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
 10 15 20
 aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
 Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
 25 30 35
 ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259
 Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
 40 45 50
 tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
 Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
 55 60 65
 atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
 Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
 70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc	403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg	
90 95 100	
tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg	451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met	
105 110 115	
acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct	499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser	
120 125 130	
gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc	547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu	
135 140 145	
cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt	595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly	
150 155 160 165	
cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct	643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro	
170 175 180	
ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag	691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys	
185 190 195	
tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc	739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr	
200 205 210	
gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act	787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr	
215 220 225	
ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc	835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly	
230 235 240 245	
gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc	883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly	
250 255 260	
gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt	931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly	
265 270 275	
gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc	979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg	
280 285 290	
acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc	
1027	
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg	
295 300 305	
ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac	
1075	
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr	
310 315 320 325	

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507
 Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555
 Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603
 Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651
 Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699
 Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747
 His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795
 Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843
 Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga
 1891
 Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg
 585 590 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc
 1939
 Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg
 600 605 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg
 1987
 Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met
 615 620 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat
 2035
 Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
 630 635 640 645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc
 2083
 Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
 650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg
 2131
 Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
 665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt
 2179
 Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
 680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc
 2227
 Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
 695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct
2275

Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc
2323

Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac
2358

Gly Ala Thr Ile
745

<210> 226

<211> 745

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
130 135 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145 150 155 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
165 170 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
180 185 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
195 200 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Phe Asp Ala
 355 360 365
 Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
 370 375 380
 Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
 385 390 395 400
 Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
 405 410 415
 Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
 420 425 430
 Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
 435 440 445
 Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
 450 455 460
 Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
 465 470 475 480
 Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
 485 490 495
 Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
 500 505 510
 Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
 515 520 525
 Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr

530				535				540							
Ile 545	Leu	Ala	Trp	Ser	Phe 550	Val	Arg	Asp	Asp	Gln 555	Pro	Leu	Ala	Thr	Thr 560
Ala	Asp	Gln	Val	Ala 565	Leu	Ala	Leu	Arg	Asp 570	Glu	Ile	Asn	Asp	Leu 575	Ile
Glu	Ala	Gly	Ala 580	Lys	Ile	Ile	Gln	Val 585	Asp	Glu	Pro	Ala	Ile 590	Arg	Glu
Leu	Leu	Pro 595	Leu	Arg	Asp	Val	Asp 600	Lys	Pro	Ala	Tyr	Leu 605	Gln	Trp	Ser
Val 610	Asp	Ser	Phe	Arg	Leu	Ala 615	Thr	Ala	Gly	Ala 620	Pro	Asp	Asp	Val	Gln
Ile 625	His	Thr	His	Met	Cys 630	Tyr	Ser	Glu	Phe	Asn 635	Glu	Val	Ile	Ser	Ser 640
Val	Ile	Ala	Leu	Asp 645	Ala	Asp	Val	Thr	Thr 650	Ile	Glu	Ala	Ala	Arg 655	Ser
Asp	Met	Gln	Val 660	Leu	Ala	Ala	Leu	Lys 665	Ser	Ser	Gly	Phe	Glu 670	Leu	Gly
Val	Gly	Pro 675	Gly	Val	Trp	Asp	Ile 680	His	Ser	Pro	Arg	Val 685	Pro	Ser	Ala
Gln	Lys 690	Val	Asp	Gly	Leu	Leu 695	Glu	Ala	Ala	Leu	Gln 700	Ser	Val	Asp	Pro
Arg 705	Gln	Leu	Trp	Val	Asn 710	Pro	Asp	Cys	Gly	Leu 715	Lys	Thr	Arg	Gly	Trp 720
Pro	Glu	Val	Glu	Ala 725	Ser	Leu	Lys	Val	Leu 730	Val	Glu	Ser	Ala	Lys 735	Gln
Ala	Arg	Glu	Lys 740	Ile	Gly	Ala	Thr	Ile 745							

```
<210> 227
<211> 1923
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1900)
<223> FRXA02085
```

<400> 227
caccgggtga ttctgcgaac cttgaaacat cgtcagaaga ttgccgtgcg tcctagccgg 60

gatccgcacg ttcgggtcaa gcagaaagtc tttaactcac atg act tcc aac ttt 115
Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu

10								15					20					
aag	ttc	gcg	ctc	gaa	ggc	tac	tgg	aat	gga	tca	att	gaa	ggt	cgc	gaa	211		
Lys	Phe	Ala	Leu	Glu	Gly	Tyr	Trp	Asn	Gly	Ser	Ile	Glu	Gly	Arg	Glu			
			25					30					35					
ctt	gcg	cag	acc	gcc	cgc	caa	ttg	gtc	aac	act	gca	tcg	gat	tct	ttg	259		
Leu	Ala	Gln	Thr	Ala	Arg	Gln	Leu	Val	Asn	Thr	Ala	Ser	Asp	Ser	Leu			
			40				45					50						
tct	gga	ttg	gat	tcc	gtt	ccg	ttt	gca	gga	cgt	tcc	tac	tac	gac	gca	307		
Ser	Gly	Leu	Asp	Ser	Val	Pro	Phe	Ala	Gly	Arg	Ser	Tyr	Tyr	Asp	Ala			
		55				60					65							
atg	ctc	gat	acc	gcc	gct	att	ttg	ggg	gtg	ctg	ccg	gag	cgt	ttt	gat	355		
Met	Leu	Asp	Thr	Ala	Ala	Ile	Leu	Gly	Val	Leu	Pro	Glu	Arg	Phe	Asp			
		70			75					80					85			
gac	atc	gct	gat	cat	gaa	aac	gat	ggg	ctc	cca	ctg	tgg	att	gac	cgc	403		
Asp	Ile	Ala	Asp	His	Glu	Asn	Asp	Gly	Leu	Pro	Leu	Trp	Ile	Asp	Arg			
				90				95						100				
tac	ttt	ggc	gct	gct	cgc	ggg	act	gag	acc	ctg	cct	gca	cag	gca	atg	451		
Tyr	Phe	Gly	Ala	Ala	Arg	Gly	Thr	Glu	Thr	Leu	Pro	Ala	Gln	Ala	Met			
			105					110					115					
acc	aag	tgg	ttt	gat	acc	aac	tac	cac	tac	ctc	gtg	ccg	gag	ttg	tct	499		
Thr	Lys	Trp	Phe	Asp	Thr	Asn	Tyr	His	Tyr	Leu	Val	Pro	Glu	Leu	Ser			
		120				125						130						
gcg	gat	aca	cgt	ttc	gtt	ttg	gat	gcg	tcc	gcg	ctg	att	gag	gat	ctc	547		
Ala	Asp	Thr	Arg	Phe	Val	Leu	Asp	Ala	Ser	Ala	Leu	Ile	Glu	Asp	Leu			
		135				140					145							
cgt	tgc	cag	cag	gtt	cgt	ggc	gtt	aat	gcc	cgc	cct	gtt	ctg	gtt	ggg	595		
Arg	Cys	Gln	Gln	Val	Arg	Gly	Val	Asn	Ala	Arg	Pro	Val	Leu	Val	Gly			
					155					160					165			
cca	ctg	act	ttc	ctt	tcc	ctt	gct	cgc	acc	act	gat	ggg	tcc	aat	cct	643		
Pro	Leu	Thr	Phe	Leu	Ser	Leu	Ala	Arg	Thr	Thr	Asp	Gly	Ser	Asn	Pro			
				170				175						180				
ttg	gat	cac	ctg	cct	gca	ctg	ttt	gag	gtc	tac	gag	cgc	ctc	atc	aag	691		
Leu	Asp	His	Leu	Pro	Ala	Leu	Phe	Glu	Val	Tyr	Glu	Arg	Leu	Ile	Lys			
			185					190					195					
tct	ttc	gat	act	gag	tgg	gtt	cag	atc	gat	gag	cct	gcg	ttg	gtc	acc	739		
Ser	Phe	Asp	Thr	Glu	Trp	Val	Gln	Ile	Asp	Glu	Pro	Ala	Leu	Val	Thr			
		200				205						210						
gat	gtt	gct	cct	gag	gtt	ttg	gag	cag	gtc	cgc	gct	ggg	tac	acc	act	787		
Asp	Val	Ala	Pro	Glu	Val	Leu	Glu	Gln	Val	Arg	Ala	Gly	Tyr	Thr	Thr			
		215				220				225								
ttg	gct	aag	cgc	gat	ggc	gtg	ttt	gtc	aat	act	tac	ttc	ggc	tct	ggc	835		
Leu	Ala	Lys	Arg	Asp	Gly	Val	Phe	Val	Asn	Thr	Tyr	Phe	Gly	Ser	Gly			
		230			235					240					245			
gat	cag	gcg	ctg	aac	act	ctt	gcg	ggc	atc	ggc	ctt	ggc	gcg	att	ggc	883		
Asp	Gln	Ala	Leu	Asn	Thr	Leu	Ala	Gly	Ile	Gly	Leu	Gly	Ala	Ile	Gly			
				250				255						260				

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt 931
 Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
 265 270 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc 979
 Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
 280 285 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc
 1027
 Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
 295 300 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac
 1075
 Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
 310 315 320 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc
 1123
 Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
 330 335 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta
 1171
 Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
 345 350 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att
 1219
 Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
 360 365 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc
 1267
 Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
 375 380 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag
 1315
 Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
 390 395 400 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc
 1363
 Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
 410 415 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa
 1411
 Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
 425 430 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat
 1459
 Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
 440 445 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac
 1507

Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
 455 460 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc
 1555

Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
 470 475 480 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc
 1603

Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
 490 495 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg
 1651

Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
 505 510 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag
 1699

Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
 520 525 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc
 1747

His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
 535 540 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca
 1795

Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
 550 555 560 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag
 1843

Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
 570 575 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg
 1891

Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
 585 590 595

aga cgt cga taagcctgcc tacctgcagt ggt
 1923

Arg Arg Arg
 600

<210> 228

<211> 600

<212> PRT

<213> Corynebacterium glutamicum

<400> 228

Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
 1 5 10 15

Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
 20 25 30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
 35 40 45
 Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
 50 55 60
 Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65 70 75 80
 Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
 85 90 95
 Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
 100 105 110
 Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
 115 120 125
 Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
 130 135 140
 Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
 145 150 155 160
 Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
 165 170 175
 Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
 180 185 190
 Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
 195 200 205
 Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
 210 215 220
 Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
 225 230 235 240
 Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
 245 250 255
 Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
 260 265 270
 Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
 275 280 285
 Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
 290 295 300
 Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
 305 310 315 320
 Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
 325 330 335
 Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
 340 345 350
 Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala

355					360					365						
Ala	Ser	Ala	Ala	Ile	Ala	Ser	Arg	Arg	Thr	Ser	Pro	Arg	Thr	Ala	Pro	
370					375					380						
Ile	Thr	Gln	Glu	Leu	Pro	Gly	Arg	Ser	Arg	Gly	Ser	Phe	Asp	Thr	Arg	
385					390					395					400	
Val	Thr	Leu	Gln	Glu	Lys	Ser	Leu	Glu	Leu	Pro	Ala	Leu	Pro	Thr	Thr	
405					410					415						
Thr	Ile	Gly	Ser	Phe	Pro	Gln	Thr	Pro	Ser	Ile	Arg	Ser	Ala	Arg	Ala	
420					425					430						
Arg	Leu	Arg	Lys	Glu	Ser	Ile	Thr	Leu	Glu	Gln	Tyr	Glu	Glu	Ala	Met	
435					440					445						
Arg	Glu	Glu	Ile	Asp	Leu	Val	Ile	Ala	Lys	Gln	Glu	Glu	Leu	Gly	Leu	
450					455					460						
Asp	Val	Leu	Val	His	Gly	Glu	Pro	Glu	Arg	Asn	Asp	Met	Val	Gln	Tyr	
465					470					475					480	
Phe	Ser	Glu	Leu	Leu	Asp	Gly	Phe	Leu	Ser	Thr	Ala	Asn	Gly	Trp	Val	
485					490					495						
Gln	Ser	Tyr	Gly	Ser	Arg	Cys	Val	Arg	Pro	Pro	Val	Leu	Phe	Gly	Asn	
500					505					510						
Val	Ser	Arg	Pro	Ala	Pro	Met	Thr	Val	Lys	Trp	Phe	Gln	Tyr	Ala	Gln	
515					520					525						
Ser	Leu	Thr	Gln	Lys	His	Val	Lys	Gly	Met	Leu	Thr	Gly	Pro	Val	Thr	
530					535					540						
Ile	Leu	Ala	Trp	Ser	Phe	Val	Arg	Asp	Asp	Gln	Pro	Leu	Ala	Thr	Thr	
545					550					555					560	
Ala	Asp	Gln	Val	Ala	Leu	Ala	Leu	Arg	Asp	Glu	Ile	Asn	Asp	Leu	Ile	
565					570					575						
Glu	Ala	Gly	Ala	Lys	Ile	Ile	Gln	Val	Asp	Glu	Pro	Ala	Ile	Arg	Glu	
580					585					590						
Leu	Leu	Pro	Ala	Thr	Arg	Arg	Arg									
595					600											

<210> 229

<211> 603

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(580)

<223> FRXA02086

<400> 229

gatgatcagc cgctggctac cactgctgac caggttgcac tggcactgcg cgatgaaatt 60

aacgatctca	tcgaggtctgg	cgcgaaagatc	atccaggtgg	atg	agc	ctg	cga	ttc								115	
				Met	Ser	Leu	Arg	Phe								5	
				1													
gtg	aac	tgt	tgc	ccg	cta	cga	gac	gtc	gat	aag	cct	gcc	tac	ctg	cag	163	
Val	Asn	Cys	Cys	Pro	Leu	Arg	Asp	Val	Asp	Lys	Pro	Ala	Tyr	Leu	Gln		
				10					15					20			
tgg	tcc	gtg	gac	tcc	ttc	cgc	ctg	gcg	act	gcc	ggc	gca	ccc	gac	gac	211	
Trp	Ser	Val	Asp	Ser	Phe	Arg	Leu	Ala	Thr	Ala	Gly	Ala	Pro	Asp	Asp		
			25					30					35				
gtc	caa	atc	cac	acc	cac	atg	tgc	tac	tcc	gag	ttc	aac	gaa	gtg	atc	259	
Val	Gln	Ile	His	Thr	His	Met	Cys	Tyr	Ser	Glu	Phe	Asn	Glu	Val	Ile		
		40					45					50					
tcc	tcg	gtc	atc	gcg	ttg	gat	gcc	gat	gtc	acc	acc	atc	gaa	gca	gca	307	
Ser	Ser	Val	Ile	Ala	Leu	Asp	Ala	Asp	Val	Thr	Thr	Ile	Glu	Ala	Ala		
	55					60					65						
cgt	tcc	gac	atg	cag	gtc	ctc	gct	gct	ctg	aaa	tct	tcc	ggc	ttc	gag	355	
Arg	Ser	Asp	Met	Gln	Val	Leu	Ala	Ala	Leu	Lys	Ser	Ser	Gly	Phe	Glu		
70					75					80					85		
ctc	ggc	gtc	gga	cct	ggg	gtg	tgg	gat	atc	cac	tcc	ccg	cgc	gtt	cct	403	
Leu	Gly	Val	Gly	Pro	Gly	Val	Trp	Asp	Ile	His	Ser	Pro	Arg	Val	Pro		
				90					95					100			
tcc	gcg	cag	aaa	gtg	gac	ggg	ctc	ctc	gag	gct	gca	ctg	cag	tcc	gtg	451	
Ser	Ala	Gln	Lys	Val	Asp	Gly	Leu	Leu	Glu	Ala	Ala	Leu	Gln	Ser	Val		
			105					110					115				
gat	cct	cgc	cag	ctg	tgg	gtc	aac	cca	gac	tgt	ggg	ctg	aag	acc	cgt	499	
Asp	Pro	Arg	Gln	Leu	Trp	Val	Asn	Pro	Asp	Cys	Gly	Leu	Lys	Thr	Arg		
		120					125					130					
gga	tgg	cca	gaa	gtg	gaa	gct	tcc	cta	aag	gtt	ctc	gtt	gag	tcc	gct	547	
Gly	Trp	Pro	Glu	Val	Glu	Ala	Ser	Leu	Lys	Val	Leu	Val	Glu	Ser	Ala		
	135					140					145						
aag	cag	gct	cgt	gag	aaa	atc	gga	gca	act	atc	taaattgggt				taccgctagg		600
Lys	Gln	Ala	Arg	Glu	Lys	Ile	Gly	Ala	Thr	Ile							
150					155					160							
aac																603	

<210> 230

<211> 160

<212> PRT

<213> Corynebacterium glutamicum

<400> 230

Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
1 5 10 15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
20 25 30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
35 40 45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
 50 55 60
 Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
 65 70 75 80
 Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
 85 90 95
 Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
 100 105 110
 Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
 115 120 125
 Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
 130 135 140
 Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
 145 150 155 160

<210> 231
 <211> 1326
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1303)
 <223> RXN02648

<400> 231
 atgaataaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcgggttag agtcgaatga 60
 gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5
 atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20
 gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35
 ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50
 gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg

70	75	80	85	
ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa				403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu				
	90	95	100	
gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat				451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp				
	105	110	115	
cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct				499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser				
	120	125	130	
ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga				547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly				
	135	140	145	
cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg				595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu				
	150	155	160	165
ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca				643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala				
	170	175	180	
gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac				691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp				
	185	190	195	
act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa				739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu				
	200	205	210	
tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg				787
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro				
	215	220	225	
gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag				835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys				
	230	235	240	245
gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca				883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala				
	250	255	260	
gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc				931
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly				
	265	270	275	
tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att				979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile				
	280	285	290	
ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca				
1027				
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala				
	295	300	305	
tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt				
1075				

Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
 310 315 320 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac
 1123

Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
 330 335 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc
 1171

Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
 345 350 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg
 1219

Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
 360 365 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta
 1267

Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
 375 380 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac
 1313

Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 390 395 400

aacgagggtt gct
 1326

<210> 232

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 232

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
 50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
 225 230 235 240
 Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
 245 250 255
 Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
 260 265 270
 His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
 275 280 285
 Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
 290 295 300
 Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
 305 310 315 320
 Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
 325 330 335
 Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
 340 345 350
 Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
 355 360 365
 Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
 370 375 380
 Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
 385 390 395 400
 Phe

<210> 233

<211> 548

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)...(525)

<223> FRXA02648

<400> 233

```

gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca      48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1              5              10              15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc      96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
              20              25              30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc     144
Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
              35              40              45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt     192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
              50              55              60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc     240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
              65              70              75              80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa     288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
              85              90              95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac     336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
              100              105              110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt     384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
              115              120              125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac     432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
              130              135              140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg     480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
              145              150              155              160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc         525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
              165              170              175

taagctagac aacgagggtt gct                                         548

```

<210> 234

<211> 175

<212> PRT

<213> Corynebacterium glutamicum

<400> 234

```

Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1              5              10              15

```

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
 20 25 30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
 35 40 45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
 50 55 60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65 70 75 80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
 85 90 95

Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
 100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
 115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
 130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
 145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
 165 170 175

<210> 235

<211> 784

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(784)

<223> FRXA02658

<400> 235

atgaataaaaa ttccgggtgc agtgaccgta ggtgaggtaa acgcggttag agtcgaatga 60

gagtttgata ctttcttttcg acttttagat tggattttca atg agc cag aac cgc 115
 Met Ser Gln Asn Arg
 1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
 Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
 10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
 Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
 25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
 Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
 40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
 Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
 55 60 65
 tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
 Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
 70 75 80 85
 ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
 Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
 90 95 100
 gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
 Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
 105 110 115
 cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
 Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
 120 125 130
 ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
 Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
 135 140 145
 cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
 Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
 150 155 160 165
 ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
 Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
 170 175 180
 gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
 Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
 185 190 195
 act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
 Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
 200 205 210
 tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
 Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
 215 220 225

<210> 236

<211> 228

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
 1 5 10 15
 Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
 20 25 30
 Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
 35 40 45
 Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu

50 55 60
 Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65 70 75 80
 Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
 85 90 95
 Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
 100 105 110
 Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
 115 120 125
 Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
 130 135 140
 Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
 145 150 155 160
 Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
 165 170 175
 Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
 180 185 190
 Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
 195 200 205
 Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
 210 215 220
 Gln Leu Asp Ala
 225

 <210> 237
 <211> 408
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(385)
 <223> RXC02238

 <400> 237
 ggcgcttagc caaaacatag agcggtaggg tatgcttatc cgattgagca acctttcccg 60

 ctcttaacac tactgtccat atacttttga aaagggtgtca gtg acc aac gtg agc 115
 Val Thr Asn Val Ser
 1 5

 aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
 Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
 10 15 20

 acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
 Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
 25 30 35

```

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Ph
      40              45              50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
      55              60              65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
      70              75              80              85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      90              95

cac 408

```

<210> 238
 <211> 95
 <212> PRT
 <213> Corynebacterium glutamicum

```

<400> 238
Val Thr Asn Val Ser Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp
  1              5              10              15

Pro Pro Val Gly Ile Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys
      20              25              30

Val Thr Ser Lys Tyr Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg
      35              40              45

Gln Ile Asn Ser Phe Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe
      50              55              60

Ile Gly Pro Leu Val Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile
      65              70              75              80

Ala Leu Arg Glu Ile Asn Ala Gly Leu Leu Asp His Glu Glu Gly
      85              90              95

```

<210> 239
 <211> 1827
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1804)
 <223> RXC00128

```

<400> 239
ccaattttccg tttggtcttg cctaaagaac cgcatggaaa ttatcgtgaa gcaccgatcc 60

cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
      1              5

```

acg	aaa	ctg	aag	gcc	ctc	acc	gcg	gtg	ctg	tct	gtg	acc	act	ctg	gtg	163
Thr	Lys	Leu	Lys	Ala	Leu	Thr	Ala	Val	Leu	Ser	Val	Thr	Thr	Leu	Val	
				10					15					20		
gct	ggg	tgt	tcc	acg	ctt	ccg	cag	aac	acg	gat	ccg	caa	gtg	ctg	cgc	211
Ala	Gly	Cys	Ser	Thr	Leu	Pro	Gln	Asn	Thr	Asp	Pro	Gln	Val	Leu	Arg	
			25					30					35			
tca	ttt	tcc	ggg	tcc	caa	agc	aca	caa	gag	ata	gca	ggg	ccg	acc	ccg	259
Ser	Phe	Ser	Gly	Ser	Gln	Ser	Thr	Gln	Glu	Ile	Ala	Gly	Pro	Thr	Pro	
		40					45					50				
aat	caa	gat	ccg	gat	ttg	ttg	atc	cgc	ggc	ttc	ttc	agc	gca	ggg	gcg	307
Asn	Gln	Asp	Pro	Asp	Leu	Leu	Ile	Arg	Gly	Phe	Phe	Ser	Ala	Gly	Ala	
	55					60					65					
tat	ccg	act	cag	cag	tat	gaa	gcg	gcg	aag	gcg	tat	ctg	acg	gaa	ggg	355
Tyr	Pro	Thr	Gln	Gln	Tyr	Glu	Ala	Ala	Lys	Ala	Tyr	Leu	Thr	Glu	Gly	
70					75					80					85	
acg	cgc	agc	acg	tgg	aat	ccg	gct	gcg	tcg	act	cgt	att	ttg	gat	cgc	403
Thr	Arg	Ser	Thr	Trp	Asn	Pro	Ala	Ala	Ser	Thr	Arg	Ile	Leu	Asp	Arg	
				90					95					100		
att	gat	ctg	aac	act	ctg	cca	ggt	tcg	acg	aat	gcg	gaa	cga	acg	att	451
Ile	Asp	Leu	Asn	Thr	Leu	Pro	Gly	Ser	Thr	Asn	Ala	Glu	Arg	Thr	Ile	
			105					110					115			
gcg	atc	cgt	gga	acg	cag	gtc	gga	acg	ttg	ctc	agc	ggt	ggc	gtg	tat	499
Ala	Ile	Arg	Gly	Thr	Gln	Val	Gly	Thr	Leu	Leu	Ser	Gly	Gly	Val	Tyr	
		120					125					130				
cag	ccg	gag	aat	gcg	gag	ttt	gaa	gct	gag	atc	acg	atg	cgt	cgg	gaa	547
Gln	Pro	Glu	Asn	Ala	Glu	Phe	Glu	Ala	Glu	Ile	Thr	Met	Arg	Arg	Glu	
	135					140					145					
gat	ggg	gag	tgg	cgt	atc	gat	gct	ttg	ccg	gac	ggg	att	tta	tta	gag	595
Asp	Gly	Glu	Trp	Arg	Ile	Asp	Ala	Leu	Pro	Asp	Gly	Ile	Leu	Leu	Glu	
150					155					160					165	
aga	aac	gat	ctg	cgg	aac	cat	tac	act	ccg	cac	gat	gtg	tat	ttc	ttt	643
Arg	Asn	Asp	Leu	Arg	Asn	His	Tyr	Thr	Pro	His	Asp	Val	Tyr	Phe	Phe	
				170					175					180		
gat	cct	tct	ggc	cag	gtg	ttg	gtg	ggg	gat	cgg	cgt	tgg	ttg	ttc	aat	691
Asp	Pro	Ser	Gly	Gln	Val	Leu	Val	Gly	Asp	Arg	Arg	Trp	Leu	Phe	Asn	
			185					190					195			
gag	tcg	cag	tcg	atg	tcc	acg	gtg	ctg	atg	gcc	ctt	ctg	ggt	aat	ggt	739
Glu	Ser	Gln	Ser	Met	Ser	Thr	Val	Leu	Met	Ala	Leu	Leu	Val	Asn	Gly	
		200					205					210				
cct	tcg	ccg	gca	att	tct	cct	ggt	gtg	gtc	aat	cag	ctg	tcc	acg	gat	787
Pro	Ser	Pro	Ala	Ile	Ser	Pro	Gly	Val	Val	Asn	Gln	Leu	Ser	Thr	Asp	
		215				220					225					
gcg	tcg	ttc	gtg	ggg	ttc	aat	gat	ggg	gag	tat	cag	ttc	act	ggt	ttg	835
Ala	Ser	Phe	Val	Gly	Phe	Asn	Asp	Gly	Glu	Tyr	Gln	Phe	Thr	Gly	Leu	
230					235					240					245	
gga	aat	ttg	gat	gat	gat	gcg	cgt	ttg	cgt	ttc	gcc	gcc	cag	gcc	gtg	883

Gly	Asn	Leu	Asp	Asp	Ala	Arg	Leu	Arg	Phe	Ala	Ala	Gln	Ala	Val				
															250	255	260	
tgg	acg	ttg	gcg	cat	gct	gat	gtc	gca	ggc	ccc	tac	act	ttg	gtc	gct	931		
Trp	Thr	Leu	Ala	His	Ala	Asp	Val	Ala	Gly	Pro	Tyr	Thr	Leu	Val	Ala			
															265	270	275	
gac	ggc	gcg	ccg	ttg	ctg	tcg	gag	ttc	cca	acg	ctc	acc	acc	gat	gac	979		
Asp	Gly	Ala	Pro	Leu	Leu	Ser	Glu	Phe	Pro	Thr	Leu	Thr	Thr	Asp	Asp			
															280	285	290	
ctc	gcc	gaa	tac	aac	cca	gag	gct	tac	acc	aac	acg	gtg	tcc	acg	ttg			
1027																		
Leu	Ala	Glu	Tyr	Asn	Pro	Glu	Ala	Tyr	Thr	Asn	Thr	Val	Ser	Thr	Leu			
															295	300	305	
ttt	gcg	ttg	cag	gat	gga	tcg	ttg	tcg	agg	gtc	agt	tcc	ggc	aat	gtg			
1075																		
Phe	Ala	Leu	Gln	Asp	Gly	Ser	Leu	Ser	Arg	Val	Ser	Ser	Gly	Asn	Val			
310																315	320	325
agt	cca	cta	cag	ggc	att	tgg	agc	ggg	gga	gat	atc	gat	tct	gca	gcg			
1123																		
Ser	Pro	Leu	Gln	Gly	Ile	Trp	Ser	Gly	Gly	Asp	Ile	Asp	Ser	Ala	Ala			
															330	335	340	
att	tcc	tcc	tcc	gcc	aat	gtg	gtg	gca	gcg	gta	cgc	cac	gaa	aac	aac			
1171																		
Ile	Ser	Ser	Ser	Ala	Asn	Val	Val	Ala	Ala	Val	Arg	His	Glu	Asn	Asn			
															345	350	355	
gag	gca	gtg	ctt	act	gtt	ggc	tcc	atg	gaa	ggc	gtg	act	tca	gat	gcg			
1219																		
Glu	Ala	Val	Leu	Thr	Val	Gly	Ser	Met	Glu	Gly	Val	Thr	Ser	Asp	Ala			
															360	365	370	
ttg	agg	agt	gaa	acg	atc	act	cgt	ccc	acc	ttt	gaa	tac	gcg	tcg	agt			
1267																		
Leu	Arg	Ser	Glu	Thr	Ile	Thr	Arg	Pro	Thr	Phe	Glu	Tyr	Ala	Ser	Ser			
															375	380	385	
ggg	ttg	tgg	gct	gtg	gtg	gat	ggg	gag	acg	cct	gtc	cga	gtc	gca	cga			
1315																		
Gly	Leu	Trp	Ala	Val	Val	Asp	Gly	Glu	Thr	Pro	Val	Arg	Val	Ala	Arg			
390																395	400	405
tcg	gca	aca	acc	ggg	gag	ctc	gtc	cag	acg	gag	gcg	gag	att	gtg	ctg			
1363																		
Ser	Ala	Thr	Thr	Gly	Glu	Leu	Val	Gln	Thr	Glu	Ala	Glu	Ile	Val	Leu			
															410	415	420	
cca	agg	gat	gtg	acg	ggg	ccg	atc	tct	gaa	ttc	caa	ctg	tca	cga	act			
1411																		
Pro	Arg	Asp	Val	Thr	Gly	Pro	Ile	Ser	Glu	Phe	Gln	Leu	Ser	Arg	Thr			
															425	430	435	
ggg	gtc	cgg	gcc	gcc	atg	atc	att	gaa	ggc	aag	gtg	tac	gtg	ggc	gtc			
1459																		
Gly	Val	Arg	Ala	Ala	Met	Ile	Ile	Glu	Gly	Lys	Val	Tyr	Val	Gly	Val			
															440	445	450	

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag
1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca
1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg
1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat
1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac
1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat
1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg
1795
Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc
1827
Val Ala Tyr

<210> 240

<211> 568

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 240

Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
1 5 10 15

Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
 85 90 95
 Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
 100 105 110
 Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
 115 120 125
 Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
 130 135 140
 Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
 145 150 155 160
 Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
 165 170 175
 Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
 180 185 190
 Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
 195 200 205
 Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
 210 215 220
 Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
 225 230 235 240
 Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
 245 250 255
 Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
 260 265 270
 Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
 275 280 285
 Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
 290 295 300
 Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
 305 310 315 320
 Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
 325 330 335
 Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
 340 345 350
 Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
 355 360 365
 Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
 370 375 380
 Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
 385 390 395 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
405 410 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
420 425 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
435 440 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
450 455 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465 470 475 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
485 490 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
500 505 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
515 520 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
530 535 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545 550 555 560

Arg Ala Ala Pro Val Val Ala Tyr
565

<210> 241
<211> 1344
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1321)
<223> RXA02240

<400> 241
cagctagacc actgacattg cagttttaga cagcttggtc tatattgggt ttttgtattt 60
aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115
Val Ala Gln Pro Thr
1 5
gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
10 15 20
aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
25 30 35
aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly

40	45	50	
atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile 55 60 65			307
cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser 70 75 80 85			355
gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly 90 95 100			403
gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala 105 110 115			451
cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp 120 125 130			499
cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met 135 140 145			547
cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln 150 155 160 165			595
gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr 170 175 180			643
cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp 185 190 195			691
acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp 200 205 210			739
ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp 215 220 225			787
gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn 230 235 240 245			835
cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu 250 255 260			883
acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His 265 270 275			931
ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser 280 285 290			979

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc
1027

Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
295 300 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca
1075

Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
310 315 320 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc
1123

Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
330 335 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg
1171

Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu
345 350 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac
1219

Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
360 365 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt
1267

Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu
375 380 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag
1315

Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys
390 395 400 405

ttg gcc taaaaatctg atgtagtatc ttc
1344

Leu Ala

<210> 242

<211> 407

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 242

Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr
1 5 10 15

Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu
20 25 30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr
35 40 45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser
50 55 60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile

65					70						75				80
Gly	Phe	Asn	Ser	Ser	Glu	Val	Gly	Phe	Asp	Gly	Arg	Thr	Cys	Gly	Val
				85					90					95	
Ser	Val	Ser	Ile	Gly	Glu	Gln	Ser	Gln	Glu	Ile	Ala	Asp	Gly	Val	Asp
			100					105					110		
Asn	Ser	Asp	Glu	Ala	Arg	Thr	Asn	Gly	Asp	Val	Glu	Glu	Asp	Asp	Arg
		115					120					125			
Ala	Gly	Ala	Gly	Asp	Gln	Gly	Leu	Met	Phe	Gly	Tyr	Ala	Thr	Asn	Glu
	130					135					140				
Thr	Glu	Glu	Tyr	Met	Pro	Leu	Pro	Ile	Ala	Leu	Ala	His	Arg	Leu	Ser
145					150					155					160
Arg	Arg	Leu	Thr	Gln	Val	Arg	Lys	Glu	Gly	Ile	Val	Pro	His	Leu	Arg
				165					170					175	
Pro	Asp	Gly	Lys	Thr	Gln	Val	Thr	Phe	Ala	Tyr	Asp	Ala	Gln	Asp	Arg
			180					185					190		
Pro	Ser	His	Leu	Asp	Thr	Val	Val	Ile	Ser	Thr	Gln	His	Asp	Pro	Glu
		195					200					205			
Val	Asp	Arg	Ala	Trp	Leu	Glu	Thr	Gln	Leu	Arg	Glu	His	Val	Ile	Asp
	210					215					220				
Trp	Val	Ile	Lys	Asp	Ala	Gly	Ile	Glu	Asp	Leu	Ala	Thr	Gly	Glu	Ile
225					230					235					240
Thr	Val	Leu	Ile	Asn	Pro	Ser	Gly	Ser	Phe	Ile	Leu	Gly	Gly	Pro	Met
				245					250					255	
Gly	Asp	Ala	Gly	Leu	Thr	Gly	Arg	Lys	Ile	Ile	Val	Asp	Thr	Tyr	Gly
			260					265					270		
Gly	Met	Ala	Arg	His	Gly	Gly	Gly	Ala	Phe	Ser	Gly	Lys	Asp	Pro	Ser
		275					280					285			
Lys	Val	Asp	Arg	Ser	Ala	Ala	Tyr	Ala	Met	Arg	Trp	Val	Ala	Lys	Asn
	290					295					300				
Ile	Val	Ala	Ala	Gly	Leu	Ala	Asp	Arg	Ala	Glu	Val	Gln	Val	Ala	Tyr
305					310					315					320
Ala	Ile	Gly	Arg	Ala	Lys	Pro	Val	Gly	Leu	Tyr	Val	Glu	Thr	Phe	Asp
				325					330					335	
Thr	Asn	Lys	Glu	Gly	Leu	Ser	Asp	Glu	Gln	Ile	Gln	Ala	Ala	Val	Leu
			340					345					350		
Glu	Val	Phe	Asp	Leu	Arg	Pro	Ala	Ala	Ile	Ile	Arg	Glu	Leu	Asp	Leu
		355					360					365			
Leu	Arg	Pro	Ile	Tyr	Ala	Asp	Thr	Ala	Ala	Tyr	Gly	His	Phe	Gly	Arg
	370					375					380				
Thr	Asp	Leu	Asp	Leu	Pro	Trp	Glu	Ala	Ile	Asp	Arg	Val	Asp	Glu	Leu
385					390					395					400

Arg Ala Ala Leu Lys Leu Ala
405

<210> 243
<211> 669
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(646)
<223> RXA00780

<400> 243
ccttttaagt ccttctttgc ccgtgaataa ttctctggat agtttccacg tgcagttaag 60
tcacgctgtt agacttgcct gcatgctctc gacaataaaaa atg atc cgt gaa gat 115
Met Ile Arg Glu Asp
1 5
ctc gca aac gct cgt gaa cac gat cca gca gcc cga ggc gat tta gaa 163
Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala Arg Gly Asp Leu Glu
10 15 20
aac gca gtg gtt tac tcc gga ctc cac gcc atc tgg gca cat cga gtt 211
Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile Trp Ala His Arg Val
25 30 35
gcc aac agc tgg tgg aaa tcc ggt ttc cgc ggc ccc gcc cgc gta tta 259
Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly Pro Ala Arg Val Leu
40 45 50
gcc caa ttc acc cga ttc ctc acc ggc att gaa att cac ccc ggt gcc 307
Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu Ile His Pro Gly Ala
55 60 65
acc att ggt cgt cgc ttt ttt att gac cac gga atg gga atc gtc atc 355
Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly Met Gly Ile Val Ile
70 75 80 85
ggc gaa acc gct gaa atc ggc gaa ggc gtc atg ctc tac cac ggc gtc 403
Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met Leu Tyr His Gly Val
90 95 100
acc ctc ggc gga cag gtt ctc acc caa acc aag cgc cac ccc acg ctc 451
Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys Arg His Pro Thr Leu
105 110 115
tgc gac aac gtg aca gtc ggc gcg ggc gca aaa atc tta ggt ccc atc 499
Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys Ile Leu Gly Pro Ile
120 125 130
acc atc ggc gaa ggc tcc gca att ggc gcc aat gca gtt gtc acc aaa 547
Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn Ala Val Val Thr Lys
135 140 145
gac gtg ccg gca gaa cac atc gca gtc gga att cct gcg gta gca cgc 595
Asp Val Pro Ala Glu His Ile Ala Val Gly Ile Pro Ala Val Ala Arg
150 155 160 165

cca cgt ggc aag aca gag aag atc aag ctc gtc gat ccg gac tat tac 643
 Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val Asp Pro Asp Tyr Tyr
 170 175 180

att taagaacagt tagcgcccta cct 669
 Ile

<210> 244

<211> 182

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 244

Met Ile Arg Glu Asp Leu Ala Asn Ala Arg Glu His Asp Pro Ala Ala
 1 5 10 15

Arg Gly Asp Leu Glu Asn Ala Val Val Tyr Ser Gly Leu His Ala Ile
 20 25 30

Trp Ala His Arg Val Ala Asn Ser Trp Trp Lys Ser Gly Phe Arg Gly
 35 40 45

Pro Ala Arg Val Leu Ala Gln Phe Thr Arg Phe Leu Thr Gly Ile Glu
 50 55 60

Ile His Pro Gly Ala Thr Ile Gly Arg Arg Phe Phe Ile Asp His Gly
 65 70 75 80

Met Gly Ile Val Ile Gly Glu Thr Ala Glu Ile Gly Glu Gly Val Met
 85 90 95

Leu Tyr His Gly Val Thr Leu Gly Gly Gln Val Leu Thr Gln Thr Lys
 100 105 110

Arg His Pro Thr Leu Cys Asp Asn Val Thr Val Gly Ala Gly Ala Lys
 115 120 125

Ile Leu Gly Pro Ile Thr Ile Gly Glu Gly Ser Ala Ile Gly Ala Asn
 130 135 140

Ala Val Val Thr Lys Asp Val Pro Ala Glu His Ile Ala Val Gly Ile
 145 150 155 160

Pro Ala Val Ala Arg Pro Arg Gly Lys Thr Glu Lys Ile Lys Leu Val
 165 170 175

Asp Pro Asp Tyr Tyr Ile
 180

<210> 245

<211> 1056

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1033)

ggc aag gct ggt cca cac aag atc cag ggc atc ggc gca aac ttc atc 787
 Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile Gly Ala Asn Phe Ile
 215 220 225

ccc gag gtc ctg gac cgc aag gtt ctc gac gac gtg ctg acc gtc tcc 835
 Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp Val Leu Thr Val Ser
 230 235 240 245

aac gaa gac gca atc gca ttc tcc cgc aag ctc gct acc gaa gag ggc 883
 Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu Ala Thr Glu Glu Gly
 250 255 260

atc ctc ggc ggt atc tcc acc ggc gca aac atc aag gca gct ctt gac 931
 Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile Lys Ala Ala Leu Asp
 265 270 275

ctt gca gca aag cca gag aac gct ggc aaa acc atc gtc acc gtt gtc 979
 Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr Ile Val Thr Val Val
 280 285 290

acc gac ttc ggc gag cgc tac gtc tcc acc gtt ctt tac gaa gac atc
 1027
 Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val Leu Tyr Glu Asp Ile
 295 300 305

cgc gac taattcttag cgactgttaa cca
 1056
 Arg Asp
 310

<210> 246

<211> 311

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 246

Met Gly Asn Val Tyr Asn Asn Ile Thr Glu Thr Ile Gly His Thr Pro
 1 5 10 15

Leu Val Lys Leu Asn Lys Leu Thr Glu Gly Leu Asp Ala Thr Val Leu
 20 25 30

Val Lys Leu Glu Ser Phe Asn Pro Ala Asn Ser Val Lys Asp Arg Ile
 35 40 45

Gly Leu Ala Ile Val Glu Asp Ala Glu Lys Ser Gly Ala Leu Lys Pro
 50 55 60

Gly Gly Thr Ile Val Glu Ala Thr Ser Gly Asn Thr Gly Ile Ala Leu
 65 70 75 80

Ala Met Val Gly Ala Ala Arg Gly Tyr Asn Val Val Leu Thr Met Pro
 85 90 95

Glu Thr Met Ser Asn Glu Arg Arg Val Leu Leu Arg Ala Tyr Gly Ala
 100 105 110

Glu Ile Val Leu Thr Pro Gly Ala Ala Gly Met Gln Gly Ala Lys Asp
 115 120 125

Lys Ala Asp Glu Ile Val Ala Glu Arg Glu Asn Ala Val Leu Ala Arg
 130 135 140
 Gln Phe Glu Asn Glu Ala Asn Pro Arg Val Asn Arg Asp Thr Thr Ala
 145 150 155 160
 Lys Glu Ile Leu Glu Asp Thr Asp Gly Thr Val Asp Ile Phe Val Ala
 165 170 175
 Ser Phe Gly Thr Gly Gly Thr Val Thr Gly Val Gly Gln Val Leu Lys
 180 185 190
 Glu Asn Asn Ala Asp Val Gln Val Tyr Thr Val Glu Pro Glu Ala Ser
 195 200 205
 Pro Leu Leu Thr Ala Gly Lys Ala Gly Pro His Lys Ile Gln Gly Ile
 210 215 220
 Gly Ala Asn Phe Ile Pro Glu Val Leu Asp Arg Lys Val Leu Asp Asp
 225 230 235 240
 Val Leu Thr Val Ser Asn Glu Asp Ala Ile Ala Phe Ser Arg Lys Leu
 245 250 255
 Ala Thr Glu Glu Gly Ile Leu Gly Gly Ile Ser Thr Gly Ala Asn Ile
 260 265 270
 Lys Ala Ala Leu Asp Leu Ala Ala Lys Pro Glu Asn Ala Gly Lys Thr
 275 280 285
 Ile Val Thr Val Val Thr Asp Phe Gly Glu Arg Tyr Val Ser Thr Val
 290 295 300
 Leu Tyr Glu Asp Ile Arg Asp
 305 310

<210> 247
 <211> 623
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(600)
 <223> RXN00402

<400> 247
 act gac gaa aag gat gga aag cca gta ttg ccc tac ttc gtc act cca 48
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 gat gct gct tac cac gga ttg aag tac gca gac ctt ggt gca cca gcc 96
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30
 ttc ggc ctc aag gtt cgc gtt ggc ctt cta cgc gac acc ggc tcc acc 144
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45
 ctc tcc gca ttc aac gca tgg gct gca gtc cag ggc atc gac acc ctt 192

Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 tcc ctg cgc ctg gag cgc cac aac gaa aac gcc atc aag gtt gca gaa 240
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80
 ttc ctc aac aac cac gag aag gtg gaa aag gtt aac ttc gca ggc ctg 288
 Phe Leu Asn Asn His Glu Lys Val Glu Lys Val Asn Phe Ala Gly Leu
 85 90 95
 aag gat tcc cct tgg tac gca acc aag gaa aag ctt ggc ctg aag tac 336
 Lys Asp Ser Pro Trp Tyr Ala Thr Lys Glu Lys Leu Gly Leu Lys Tyr
 100 105 110
 acc ggc tcc gtt ctc acc ttc gag atc aag ggc ggc aag gat gag gct 384
 Thr Gly Ser Val Leu Thr Phe Glu Ile Lys Gly Gly Lys Asp Glu Ala
 115 120 125
 tgg gca ttt atc gac gcc ctg aag cta cac tcc aac ctt gca aac atc 432
 Trp Ala Phe Ile Asp Ala Leu Lys Leu His Ser Asn Leu Ala Asn Ile
 130 135 140
 ggc gat gtt cgc tcc ctc gtt gtt cac cca gca acc acc acc cat tca 480
 Gly Asp Val Arg Ser Leu Val Val His Pro Ala Thr Thr Thr His Ser
 145 150 155 160
 cag tcc gac gaa gct ggc ctg gca cgc gcg ggc gtt acc cag tcc acc 528
 Gln Ser Asp Glu Ala Gly Leu Ala Arg Ala Gly Val Thr Gln Ser Thr
 165 170 175
 gtc cgc ctg tcc gtt ggc atc gag acc att gat gat atc atc gct gac 576
 Val Arg Leu Ser Val Gly Ile Glu Thr Ile Asp Asp Ile Ile Ala Asp
 180 185 190
 ctc gaa ggc ggc ttt gct gca atc tagctttaaa tagactcacc cca 623
 Leu Glu Gly Phe Ala Ala Ile
 195 200
 <210> 248
 <211> 200
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 248
 Thr Asp Glu Lys Asp Gly Lys Pro Val Leu Pro Tyr Phe Val Thr Pro
 1 5 10 15
 Asp Ala Ala Tyr His Gly Leu Lys Tyr Ala Asp Leu Gly Ala Pro Ala
 20 25 30
 Phe Gly Leu Lys Val Arg Val Gly Leu Leu Arg Asp Thr Gly Ser Thr
 35 40 45
 Leu Ser Ala Phe Asn Ala Trp Ala Ala Val Gln Gly Ile Asp Thr Leu
 50 55 60
 Ser Leu Arg Leu Glu Arg His Asn Glu Asn Ala Ile Lys Val Ala Glu
 65 70 75 80

Phe	Leu	Asn	Asn	His	Glu	Lys	Val	Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu
				85					90					95	
Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	Lys	Glu	Lys	Leu	Gly	Leu	Lys	Tyr
			100					105					110		
Thr	Gly	Ser	Val	Leu	Thr	Phe	Glu	Ile	Lys	Gly	Gly	Lys	Asp	Glu	Ala
			115				120					125			
Trp	Ala	Phe	Ile	Asp	Ala	Leu	Lys	Leu	His	Ser	Asn	Leu	Ala	Asn	Ile
	130					135					140				
Gly	Asp	Val	Arg	Ser	Leu	Val	Val	His	Pro	Ala	Thr	Thr	Thr	His	Ser
145					150					155					160
Gln	Ser	Asp	Glu	Ala	Gly	Leu	Ala	Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr
				165					170					175	
Val	Arg	Leu	Ser	Val	Gly	Ile	Glu	Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp
			180					185					190		
Leu	Glu	Gly	Gly	Phe	Ala	Ala	Ile								
		195					200								

```
<210> 249
<211> 599
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (1)..(576)
<223> FRXA00402
```

<400> 249																
gta	ttg	ccc	tac	ttc	gtc	act	cca	gat	gct	gct	tac	cac	gga	ttg	aag	48
Val	Leu	Pro	Tyr	Phe	Val	Thr	Pro	Asp	Ala	Ala	Tyr	His	Gly	Leu	Lys	
1				5				10						15		
tac	gca	gac	ctt	ggt	gca	cca	gcc	ttc	ggc	ctc	aag	gtt	cgc	gtt	ggc	96
Tyr	Ala	Asp	Leu	Gly	Ala	Pro	Ala	Phe	Gly	Leu	Lys	Val	Arg	Val	Gly	
			20				25						30			
ctt	cta	cgc	gac	acc	ggc	tcc	acc	ctc	tcc	gca	ttc	aac	gca	tgg	gct	144
Leu	Leu	Arg	Asp	Thr	Gly	Ser	Thr	Leu	Ser	Ala	Phe	Asn	Ala	Trp	Ala	
		35				40						45				
gca	gtc	cag	ggc	atc	gac	acc	ctt	tcc	ctg	cgc	ctg	gag	cgc	cac	aac	192
Ala	Val	Gln	Gly	Ile	Asp	Thr	Leu	Ser	Leu	Arg	Leu	Glu	Arg	His	Asn	
50						55						60				
gaa	aac	gcc	atc	aag	gtt	gca	gaa	ttc	ctc	aac	aac	cac	gag	aag	gtg	240
Glu	Asn	Ala	Ile	Lys	Val	Ala	Glu	Phe	Leu	Asn	Asn	His	Glu	Lys	Val	
65				70						75				80		
gaa	aag	gtt	aac	ttc	gca	ggc	ctg	aag	gat	tcc	cct	tgg	tac	gca	acc	288
Glu	Lys	Val	Asn	Phe	Ala	Gly	Leu	Lys	Asp	Ser	Pro	Trp	Tyr	Ala	Thr	
				85				90						95		
aag	gaa	aag	ctt	ggc	ctg	aag	tac	acc	ggc	tcc	gtt	ctc	acc	ttc	gag	336

Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 atc aag ggc ggc aag gat gag gct tgg gca ttt atc gac gcc ctg aag 384
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 cta cac tcc aac ctt gca aac atc ggc gat gtt cgc tcc ctc gtt gtt 432
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 cac cca gca acc acc acc cat tca cag tcc gac gaa gct ggc ctg gca 480
 His Pro Ala Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160
 cgc gcg ggc gtt acc cag tcc acc gtc cgc ctg tcc gtt ggc atc gag 528
 Arg Ala Gly Val Thr Gln Ser Thr Val Arg Leu Ser Val Gly Ile Glu
 165 170 175
 acc att gat gat atc atc gct gac ctc gaa ggc ggc ttt gct gca atc 576
 Thr Ile Asp Asp Ile Ile Ala Asp Leu Glu Gly Gly Phe Ala Ala Ile
 180 185 190
 tagctttaaa tagactcacc cca 599

<210> 250

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Val Leu Pro Tyr Phe Val Thr Pro Asp Ala Ala Tyr His Gly Leu Lys
 1 5 10 15
 Tyr Ala Asp Leu Gly Ala Pro Ala Phe Gly Leu Lys Val Arg Val Gly
 20 25 30
 Leu Leu Arg Asp Thr Gly Ser Thr Leu Ser Ala Phe Asn Ala Trp Ala
 35 40 45
 Ala Val Gln Gly Ile Asp Thr Leu Ser Leu Arg Leu Glu Arg His Asn
 50 55 60
 Glu Asn Ala Ile Lys Val Ala Glu Phe Leu Asn Asn His Glu Lys Val
 65 70 75 80
 Glu Lys Val Asn Phe Ala Gly Leu Lys Asp Ser Pro Trp Tyr Ala Thr
 85 90 95
 Lys Glu Lys Leu Gly Leu Lys Tyr Thr Gly Ser Val Leu Thr Phe Glu
 100 105 110
 Ile Lys Gly Gly Lys Asp Glu Ala Trp Ala Phe Ile Asp Ala Leu Lys
 115 120 125
 Leu His Ser Asn Leu Ala Asn Ile Gly Asp Val Arg Ser Leu Val Val
 130 135 140
 His Pro Ala Thr Thr Thr His Ser Gln Ser Asp Glu Ala Gly Leu Ala
 145 150 155 160

Arg	Ala	Gly	Val	Thr	Gln	Ser	Thr	Val	Arg	Leu	Ser	Val	Gly	Ile	Glu
				165					170					175	
Thr	Ile	Asp	Asp	Ile	Ile	Ala	Asp	Leu	Glu	Gly	Gly	Phe	Ala	Ala	Ile
			180					185					190		

```
<210> 251
<211> 613
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(613)  
<223> RXS00405
```

<400> 251																
agaataaaatt tataccacac agtctattgc aatagaccaa gctgttcagt aggggtgcatg																60
ggagaagaat ttcctaataa aaactcttaa ggacctccaa atg cca aag tac gac																115
Met Pro Lys Tyr Asp																5
1																
aat tcc aat gct gac cag tgg ggc ttt gaa acc cgc tcc att cac gca																163
Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr Arg Ser Ile His Ala																
10 15 20																
ggc cag tca gta gac gca cag acc agc gca cga aac ctt ccg atc tac																211
Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg Asn Leu Pro Ile Tyr																
25 30 35																
caa tcc acc gct ttc gtg ttc gac tcc gct gag cac gcc aag cag cgt																259
Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu His Ala Lys Gln Arg																
40 45 50																
ttc gca ctt gag gat cta ggc cct gtt tac tcc cgc ctc acc aac cca																307
Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser Arg Leu Thr Asn Pro																
55 60 65																
acc gtt gag gct ttg gaa aac cgc atc gct tcc ctc gaa ggt ggc gtc																355
Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser Leu Glu Gly Gly Val																
70 75 80 85																
cac gct gta gcg ttc tcc tcc gga cag gcc gca acc acc aac gcc att																403
His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala Thr Thr Asn Ala Ile																
90 95 100																
ttg aac ctg gca gga gcg ggc gac cac atc gtc acc tcc cca cgc ctc																451
Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val Thr Ser Pro Arg Leu																
105 110 115																
tac ggt ggc acc gag act cta ttc ctt atc act ctt aac cgc ctg ggt																499
Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr Leu Asn Arg Leu Gly																
120 125 130																
atc gat gtt tcc ttc gtg gaa aac ccc gac gac cct gag tcc tgg cag																547

Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp Pro Glu Ser Trp Gln
 135 140 145
 gca gcc gtt cag cca aac acc aaa gca ttc ttc ggc gag act ttc gcc 595
 Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe Gly Glu Thr Phe Ala
 150 155 160 165
 aac cca cag gca gac gtc 613
 Asn Pro Gln Ala Asp Val
 170

<210> 252
 <211> 171
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 252
 Met Pro Lys Tyr Asp Asn Ser Asn Ala Asp Gln Trp Gly Phe Glu Thr
 1 5 10 15
 Arg Ser Ile His Ala Gly Gln Ser Val Asp Ala Gln Thr Ser Ala Arg
 20 25 30
 Asn Leu Pro Ile Tyr Gln Ser Thr Ala Phe Val Phe Asp Ser Ala Glu
 35 40 45
 His Ala Lys Gln Arg Phe Ala Leu Glu Asp Leu Gly Pro Val Tyr Ser
 50 55 60
 Arg Leu Thr Asn Pro Thr Val Glu Ala Leu Glu Asn Arg Ile Ala Ser
 65 70 75 80
 Leu Glu Gly Gly Val His Ala Val Ala Phe Ser Ser Gly Gln Ala Ala
 85 90 95
 Thr Thr Asn Ala Ile Leu Asn Leu Ala Gly Ala Gly Asp His Ile Val
 100 105 110
 Thr Ser Pro Arg Leu Tyr Gly Gly Thr Glu Thr Leu Phe Leu Ile Thr
 115 120 125
 Leu Asn Arg Leu Gly Ile Asp Val Ser Phe Val Glu Asn Pro Asp Asp
 130 135 140
 Pro Glu Ser Trp Gln Ala Ala Val Gln Pro Asn Thr Lys Ala Phe Phe
 145 150 155 160
 Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val
 165 170

<210> 253
 <211> 1812
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1789)
 <223> RXC00164

<400> 253

ctgctttgcg ggaggttatg aaatgagtg ggagacgtcg aaaagcatgc gctttccgtt 60

ggccagcctg cgcgaagtgc ggcgcgaggt ggcccggcag gtg ggt cgt att ccg 115
 Val Gly Arg Ile Pro
 1 5

cgg gcg aag tgg tgg ttt tta ggc gcg ctg gtg ttg ctg agt gcg ggc 163
 Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val Leu Leu Ser Ala Gly
 10 15 20

gct tat gcg tcg gtg ctg gtg ccg cag gtg ctg ggg cgg att gtg gat 211
 Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu Gly Arg Ile Val Asp
 25 30 35

ctg gtg tcc gat ggc gcg cag atg cgt gat ttt gtt gag ctc agt gtg 259
 Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe Val Glu Leu Ser Val
 40 45 50

att ctc att gcg gtg gca att gcc ggc gcg gtg ctc agt gcg tgc ggg 307
 Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val Leu Ser Ala Cys Gly
 55 60 65

ttc tat gtg gtg tcg cgg att tct gag aag att atc gcc aat ttg agg 355
 Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile Ile Ala Asn Leu Arg
 70 75 80 85

gaa gat atg gtg ggc acc gcg ctt ggg ttg ccc acg cac cag gtg gaa 403
 Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro Thr His Gln Val Glu
 90 95 100

gat gcg ggc tct ggc gat ttg gtg agc cgc tcc acc gat gat gtc tcc 451
 Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser Thr Asp Asp Val Ser
 105 110 115

gag cta tcc gca gcg gtg aca gag acc gtc ccg att tta agt tcc tca 499
 Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro Ile Leu Ser Ser Ser
 120 125 130

ctg ttt acc att gcc gcg acg atc att gcg ctg ttt tct ttg gac tgg 547
 Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu Phe Ser Leu Asp Trp
 135 140 145

caa ttt gtg ctc att cct gtc gtg gtg gcg ccg gtg tac tac ttc gcg 595
 Gln Phe Val Leu Ile Pro Val Val Val Ala Pro Val Tyr Tyr Phe Ala
 150 155 160 165

tcc aag cac tat ttg agc aag gcg ccg gat cgg tat gcg gca gaa cgc 643
 Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg Tyr Ala Ala Glu Arg
 170 175 180

gcg gcg atg gcg gag cgt gcg cga aag gta ctt gag gct att cgc ggg 691
 Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu Glu Ala Ile Arg Gly
 185 190 195

cgt gca act gtg cgg gcg tat tcc atg gaa gat gcc atg cat aat cag 739
 Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp Ala Met His Asn Gln
 200 205 210

att gat cag gcg tcg tgg tct gtg gtg gtc aag ggt att cgt gcg cgc 787

Ile	Asp	Gln	Ala	Ser	Trp	Ser	Val	Val	Val	Lys	Gly	Ile	Arg	Ala	Arg		
215						220					225						
acc	acc	atg	ttg	att	ttg	aac	atg	tgg	atg	ctg	ttt	gcg	gaa	ttc	ctc	835	
Thr	Thr	Met	Leu	Ile	Leu	Asn	Met	Trp	Met	Leu	Phe	Ala	Glu	Phe	Leu		
230					235					240					245		
atg	ctc	gcg	gtc	gcg	ttg	gtg	atc	ggc	tac	aag	ctg	gtc	att	gat	aat	883	
Met	Leu	Ala	Val	Ala	Leu	Val	Ile	Gly	Tyr	Lys	Leu	Val	Ile	Asp	Asn		
				250					255						260		
gcg	ctg	acg	atc	ggc	gcg	gtt	acc	ggg	gcc	gtg	ctg	atg	att	att	cgt	931	
Ala	Leu	Thr	Ile	Gly	Ala	Val	Thr	Gly	Ala	Val	Leu	Met	Ile	Ile	Arg		
			265					270						275			
ctg	cgt	ggc	ccg	atg	aat	atg	ttc	atg	cgc	gtg	ctc	gac	acc	att	caa	979	
Leu	Arg	Gly	Pro	Met	Asn	Met	Phe	Met	Arg	Val	Leu	Asp	Thr	Ile	Gln		
		280					285					290					
tcc	ggc	tat	gcg	tcg	ctg	gcg	cgc	atc	gtg	gga	gtt	gtt	gcg	gat	ccg		
1027																	
Ser	Gly	Tyr	Ala	Ser	Leu	Ala	Arg	Ile	Val	Gly	Val	Val	Ala	Asp	Pro		
	295					300					305						
ccg	att	cct	gtg	ccc	gac	agc	ggg	gtg	aaa	gca	cct	cag	ggc	aaa	gtg		
1075																	
Pro	Ile	Pro	Val	Pro	Asp	Ser	Gly	Val	Lys	Ala	Pro	Gln	Gly	Lys	Val		
310					315					320					325		
gaa	ttg	cgc	aac	gtc	agc	ttt	agc	tat	ggc	gat	tcc	tgg	gcg	gtg	aaa		
1123																	
Glu	Leu	Arg	Asn	Val	Ser	Phe	Ser	Tyr	Gly	Asp	Ser	Trp	Ala	Val	Lys		
				330					335					340			
gac	atc	gac	atc	acg	atc	aat	tcc	ggc	gaa	act	gtc	gcg	ctc	gtg	ggc		
1171																	
Asp	Ile	Asp	Ile	Thr	Ile	Asn	Ser	Gly	Glu	Thr	Val	Ala	Leu	Val	Gly		
			345					350					355				
gca	tct	ggc	gca	ggg	aag	acg	acg	gtc	gcc	gcc	ttg	ctg	gcg	ggc	ttg		
1219																	
Ala	Ser	Gly	Ala	Gly	Lys	Thr	Thr	Val	Ala	Ala	Leu	Leu	Ala	Gly	Leu		
			360				365					370					
cgg	gtg	cca	gat	caa	ggg	caa	gtg	ctt	gtc	gac	gac	ttc	ccc	gtc	tct		
1267																	
Arg	Val	Pro	Asp	Gln	Gly	Gln	Val	Leu	Val	Asp	Asp	Phe	Pro	Val	Ser		
	375					380					385						
cac	ctc	tct	gac	cgc	gag	cgt	atc	gcc	cgc	ttg	gcc	atg	gtc	agc	cag		
1315																	
His	Leu	Ser	Asp	Arg	Glu	Arg	Ile	Ala	Arg	Leu	Ala	Met	Val	Ser	Gln		
390					395					400					405		
gag	gtt	cat	gtt	ttc	tcc	ggc	acg	ctg	cgc	cag	gat	ctc	acc	ttg	gct		
1363																	
Glu	Val	His	Val	Phe	Ser	Gly	Thr	Leu	Arg	Gln	Asp	Leu	Thr	Leu	Ala		
				410					415					420			
aaa	cca	gat	gcc	tcc	gat	gag	gaa	tta	gcg	cat	gct	ctt	ggg	caa	gtt		
1411																	

Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His Ala Leu Gly Gln Val
 425 430 435

aat gcc ctt gac tgg ttg gag agt ctt cca gaa gga ctg gac acg gtc
 1459

Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu Gly Leu Asp Thr Val
 440 445 450

gtt ggt gcg cga gga atc cag cta gaa cca gtg gtg gct cag cag ttg
 1507

Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val Val Ala Gln Gln Leu
 455 460 465

gcg ttg gcc cgg gtg ttg ttg ctc aat ccg gcg atc gtc atc atg gat
 1555

Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala Ile Val Ile Met Asp
 470 475 480 485

gaa gcc acg gca gaa gca gga tcg gcg ggt gcc agc gca ctg gaa gag
 1603

Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala Ser Ala Leu Glu Glu
 490 495 500

gct gca gat gca gtg agc aag aac cgt tcc gca ttg gtg gtg gcg cac
 1651

Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala Leu Val Val Ala His
 505 510 515

cgg ttg gat cag gca tcg cgg gct gat cag att ctg gtg atg gat aag
 1699

Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile Leu Val Met Asp Lys
 520 525 530

ggg gag gtt gtg gaa tcc ggt act cac cag gag tta ttg gat cac ggg
 1747

Gly Glu Val Val Glu Ser Gly Thr His Gln Glu Leu Leu Asp His Gly
 535 540 545

ggt att tat cag cgt ctg tgg act gcg tgg agt gtc gga aga
 1789

Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser Val Gly Arg
 550 555 560

tagttgactg ttcaatgcgt tga
 1812

<210> 254

<211> 563

<212> PRT

<213> Corynebacterium glutamicum

<400> 254

Val Gly Arg Ile Pro Arg Ala Lys Trp Trp Phe Leu Gly Ala Leu Val
 1 5 10 15

Leu Leu Ser Ala Gly Ala Tyr Ala Ser Val Leu Val Pro Gln Val Leu
 20 25 30

Gly Arg Ile Val Asp Leu Val Ser Asp Gly Ala Gln Met Arg Asp Phe
 35 40 45

Val Glu Leu Ser Val Ile Leu Ile Ala Val Ala Ile Ala Gly Ala Val
 50 55 60
 Leu Ser Ala Cys Gly Phe Tyr Val Val Ser Arg Ile Ser Glu Lys Ile
 65 70 75 80
 Ile Ala Asn Leu Arg Glu Asp Met Val Gly Thr Ala Leu Gly Leu Pro
 85 90 95
 Thr His Gln Val Glu Asp Ala Gly Ser Gly Asp Leu Val Ser Arg Ser
 100 105 110
 Thr Asp Asp Val Ser Glu Leu Ser Ala Ala Val Thr Glu Thr Val Pro
 115 120 125
 Ile Leu Ser Ser Ser Leu Phe Thr Ile Ala Ala Thr Ile Ile Ala Leu
 130 135 140
 Phe Ser Leu Asp Trp Gln Phe Val Leu Ile Pro Val Val Val Ala Pro
 145 150 155 160
 Val Tyr Tyr Phe Ala Ser Lys His Tyr Leu Ser Lys Ala Pro Asp Arg
 165 170 175
 Tyr Ala Ala Glu Arg Ala Ala Met Ala Glu Arg Ala Arg Lys Val Leu
 180 185 190
 Glu Ala Ile Arg Gly Arg Ala Thr Val Arg Ala Tyr Ser Met Glu Asp
 195 200 205
 Ala Met His Asn Gln Ile Asp Gln Ala Ser Trp Ser Val Val Val Lys
 210 215 220
 Gly Ile Arg Ala Arg Thr Thr Met Leu Ile Leu Asn Met Trp Met Leu
 225 230 235 240
 Phe Ala Glu Phe Leu Met Leu Ala Val Ala Leu Val Ile Gly Tyr Lys
 245 250 255
 Leu Val Ile Asp Asn Ala Leu Thr Ile Gly Ala Val Thr Gly Ala Val
 260 265 270
 Leu Met Ile Ile Arg Leu Arg Gly Pro Met Asn Met Phe Met Arg Val
 275 280 285
 Leu Asp Thr Ile Gln Ser Gly Tyr Ala Ser Leu Ala Arg Ile Val Gly
 290 295 300
 Val Val Ala Asp Pro Pro Ile Pro Val Pro Asp Ser Gly Val Lys Ala
 305 310 315 320
 Pro Gln Gly Lys Val Glu Leu Arg Asn Val Ser Phe Ser Tyr Gly Asp
 325 330 335
 Ser Trp Ala Val Lys Asp Ile Asp Ile Thr Ile Asn Ser Gly Glu Thr
 340 345 350
 Val Ala Leu Val Gly Ala Ser Gly Ala Gly Lys Thr Thr Val Ala Ala
 355 360 365

Leu Leu Ala Gly Leu Arg Val Pro Asp Gln Gly Gln Val Leu Val Asp
 370 375 380
 Asp Phe Pro Val Ser His Leu Ser Asp Arg Glu Arg Ile Ala Arg Leu
 385 390 395 400
 Ala Met Val Ser Gln Glu Val His Val Phe Ser Gly Thr Leu Arg Gln
 405 410 415
 Asp Leu Thr Leu Ala Lys Pro Asp Ala Ser Asp Glu Glu Leu Ala His
 420 425 430
 Ala Leu Gly Gln Val Asn Ala Leu Asp Trp Leu Glu Ser Leu Pro Glu
 435 440 445
 Gly Leu Asp Thr Val Val Gly Ala Arg Gly Ile Gln Leu Glu Pro Val
 450 455 460
 Val Ala Gln Gln Leu Ala Leu Ala Arg Val Leu Leu Leu Asn Pro Ala
 465 470 475 480
 Ile Val Ile Met Asp Glu Ala Thr Ala Glu Ala Gly Ser Ala Gly Ala
 485 490 495
 Ser Ala Leu Glu Glu Ala Ala Asp Ala Val Ser Lys Asn Arg Ser Ala
 500 505 510
 Leu Val Val Ala His Arg Leu Asp Gln Ala Ser Arg Ala Asp Gln Ile
 515 520 525
 Leu Val Met Asp Lys Gly Glu Val Val Glu Ser Gly Thr His Gln Glu
 530 535 540
 Leu Leu Asp His Gly Gly Ile Tyr Gln Arg Leu Trp Thr Ala Trp Ser
 545 550 555 560
 Val Gly Arg

<210> 255

<211> 1713

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1690)

<223> RXC01191

<400> 255

cgctgctttc acgcaactga aaccgcaccg gatcaagtta tttgggggttg ttcctttgtgg 60

cgtgttggtg gccgtcgcgg ggttggtagg gccctgggcg gtg ggt gga ctc gtc 115
 Val Gly Gly Leu Val
 1 5

gat aag ctc ctt gca acc ccg agc atg cgc gac gtt gta gtg ttc gcg 163
 Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp Val Val Val Phe Ala
 10 15 20

ctg ctt atc gtg gct ggc ggc gtt gtt tcg agc ctg ggc acg tgg tgg	211
Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser Leu Gly Thr Trp Trp	
25 30 35	
ggc agc gcg ctg atg gcg cgc gcg ttg gag ccg gcg atc gcg ggg ctg	259
Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro Ala Ile Ala Gly Leu	
40 45 50	
cgc gag gat gtg ttg cgc gcg gcg gtg agt ttg gat gcg aac acg att	307
Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu Asp Ala Asn Thr Ile	
55 60 65	
gaa acg gcg ggg cgc ggc gac gtg att tcg cgt atc gcg gat gat tcg	355
Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg Ile Ala Asp Asp Ser	
70 75 80 85	
cgg gag gtg tcc act gcg gcg agc acc gtg gtg ccg ctg atg gtg cag	403
Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val Pro Leu Met Val Gln	
90 95 100	
gcg ggc ttt acc gtg gtg att tcc gcg ttt ggc atg gcg gcg gtt gat	451
Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly Met Ala Ala Val Asp	
105 110 115	
tgg cgc ctc ggc ctt gtc ggt ttg gtc gcg atc ccg ctg tat tgg acc	499
Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile Pro Leu Tyr Trp Thr	
120 125 130	
acg ttg cgc gtc tat tta ccc cgc tca ggt ccg ctt tat acg cgt gag	547
Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro Leu Tyr Thr Arg Glu	
135 140 145	
cgc gag gcc ttt ggg gtg cgc acg cag ccg ctt gtc ggc gca gtc gaa	595
Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu Val Gly Ala Val Glu	
150 155 160 165	
ggc gcg gaa acc ttg cgc gct ttc cgc gca gaa gat aca gaa tta aag	643
Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu Asp Thr Glu Leu Lys	
170 175 180	
cgt atc gac gca gcc tcc ggc gaa gcc cgc gac att tcc att tct gtt	691
Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp Ile Ser Ile Ser Val	
185 190 195	
ttc agg ttc ctc aca tgg gca ttt tcc cgc aac aac cgc gcg gaa tgc	739
Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn Asn Arg Ala Glu Cys	
200 205 210	
atc acc ctc gtg ctc atc ttg ggc acc ggc ttt tac ctg gtc aac atc	787
Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe Tyr Leu Val Asn Ile	
215 220 225	
gat ctg gtc acc gtc ggc gca gtc tca acc gcc gca ctg atc ttc cac	835
Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala Ala Leu Ile Phe His	
230 235 240 245	
cga ctc ttc ggt cca atc ggc acg ctc gtg ggc atg ttc tcc gac atc	883
Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly Met Phe Ser Asp Ile	
250 255 260	
caa tcc gcc agc gca tcg ctg atc cgc atg gtg ggc gtt att aac gcg	931

Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val Gly Val Ile Asn Ala
 265 270 275
 gca tcg aac cag gtc agc ggc acc tcg ccg gcg tct gcc agc acc gct 979
 Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala Ser Ala Ser Thr Ala
 280 285 290
 tta acg ctt ttc gac gtc tcc cac cac tat cac act gca ccc gtc atc
 1027
 Leu Thr Leu Phe Asp Val Ser His His Tyr His Thr Ala Pro Val Ile
 295 300 305
 aag aat gca tcc gtg cag ctg gaa cca ggg gaa cac atc gcc att gtg
 1075
 Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu His Ile Ala Ile Val
 310 315 320 325
 ggt gcg acc ggc gct ggt aaa agc acg ctc gcc ctc att gcg gca ggc
 1123
 Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala Leu Ile Ala Ala Gly
 330 335 340
 ctg ctc agc cca act tcc ggg cag gtg gct ctc ggc gga tcg agt ttt
 1171
 Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu Gly Gly Ser Ser Phe
 345 350 355
 tct aac gtc gaa ccg gaa gca ttg cgc cag aag atc gcg atg gtc agc
 1219
 Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys Ile Ala Met Val Ser
 360 365 370
 caa gaa atc cac tgc ttc cga gga tct gtt tta gat aat ctt cgt atc
 1267
 Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu Asp Asn Leu Arg Ile
 375 380 385
 gca cgc ccc gaa gcc acc gat gcg gac atc cac gcc gtt ctc gcc gat
 1315
 Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His Ala Val Leu Ala Asp
 390 395 400 405
 att ggt gat tcc tgg ttg gag cgc tta ccg caa ggc ata gac acc atc
 1363
 Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln Gly Ile Asp Thr Ile
 410 415 420
 gtg ggt gat ggc gct ttc cgt tta acc tct gtg gaa aac cag atc atg
 1411
 Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val Glu Asn Gln Ile Met
 425 430 435
 gcg ctt gct cgc gta cat ttg gcc gac cta gca atc gtc atc ctt gat
 1459
 Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala Ile Val Ile Leu Asp
 440 445 450
 gaa gca acg gct gaa tca ggc tct gat cat gca aaa cag ctt gaa gat
 1507
 Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala Lys Gln Leu Glu Asp
 455 460 465

gca gcc ctt aaa gtc act gaa aac aga tca gcc atc atc gtg gct cac
1555

Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala Ile Ile Val Ala His
470 475 480 485

cgc ctc aac caa gcg aaa acc gcc gat cgc atc atc gtc atg gac tcc
1603

Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile Ile Val Met Asp Ser
490 495 500

gga gaa atc ata gaa tct gga acc cat gaa gag ctt cga gcg atc ggc
1651

Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu Leu Arg Ala Ile Gly
505 510 515

ggc cga tat gaa caa ctg tgg act gcg tgg tct gcg cgc taattagcca
1700

Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser Ala Arg
520 525 530

cccaagacca cgc
1713

<210> 256

<211> 530

<212> PRT

<213> Corynebacterium glutamicum

<400> 256

Val Gly Gly Leu Val Asp Lys Leu Leu Ala Thr Pro Ser Met Arg Asp
1 5 10 15

Val Val Val Phe Ala Leu Leu Ile Val Ala Gly Gly Val Val Ser Ser
20 25 30

Leu Gly Thr Trp Trp Gly Ser Ala Leu Met Ala Arg Ala Leu Glu Pro
35 40 45

Ala Ile Ala Gly Leu Arg Glu Asp Val Leu Arg Ala Ala Val Ser Leu
50 55 60

Asp Ala Asn Thr Ile Glu Thr Ala Gly Arg Gly Asp Val Ile Ser Arg
65 70 75 80

Ile Ala Asp Asp Ser Arg Glu Val Ser Thr Ala Ala Ser Thr Val Val
85 90 95

Pro Leu Met Val Gln Ala Gly Phe Thr Val Val Ile Ser Ala Phe Gly
100 105 110

Met Ala Ala Val Asp Trp Arg Leu Gly Leu Val Gly Leu Val Ala Ile
115 120 125

Pro Leu Tyr Trp Thr Thr Leu Arg Val Tyr Leu Pro Arg Ser Gly Pro
130 135 140

Leu Tyr Thr Arg Glu Arg Glu Ala Phe Gly Val Arg Thr Gln Arg Leu
145 150 155 160

Val Gly Ala Val Glu Gly Ala Glu Thr Leu Arg Ala Phe Arg Ala Glu
 165 170 175
 Asp Thr Glu Leu Lys Arg Ile Asp Ala Ala Ser Gly Glu Ala Arg Asp
 180 185 190
 Ile Ser Ile Ser Val Phe Arg Phe Leu Thr Trp Ala Phe Ser Arg Asn
 195 200 205
 Asn Arg Ala Glu Cys Ile Thr Leu Val Leu Ile Leu Gly Thr Gly Phe
 210 215 220
 Tyr Leu Val Asn Ile Asp Leu Val Thr Val Gly Ala Val Ser Thr Ala
 225 230 235 240
 Ala Leu Ile Phe His Arg Leu Phe Gly Pro Ile Gly Thr Leu Val Gly
 245 250 255
 Met Phe Ser Asp Ile Gln Ser Ala Ser Ala Ser Leu Ile Arg Met Val
 260 265 270
 Gly Val Ile Asn Ala Ala Ser Asn Gln Val Ser Gly Thr Ser Pro Ala
 275 280 285
 Ser Ala Ser Thr Ala Leu Thr Leu Phe Asp Val Ser His His Tyr His
 290 295 300
 Thr Ala Pro Val Ile Lys Asn Ala Ser Val Gln Leu Glu Pro Gly Glu
 305 310 315 320
 His Ile Ala Ile Val Gly Ala Thr Gly Ala Gly Lys Ser Thr Leu Ala
 325 330 335
 Leu Ile Ala Ala Gly Leu Leu Ser Pro Thr Ser Gly Gln Val Ala Leu
 340 345 350
 Gly Gly Ser Ser Phe Ser Asn Val Glu Pro Glu Ala Leu Arg Gln Lys
 355 360 365
 Ile Ala Met Val Ser Gln Glu Ile His Cys Phe Arg Gly Ser Val Leu
 370 375 380
 Asp Asn Leu Arg Ile Ala Arg Pro Glu Ala Thr Asp Ala Asp Ile His
 385 390 395 400
 Ala Val Leu Ala Asp Ile Gly Asp Ser Trp Leu Glu Arg Leu Pro Gln
 405 410 415
 Gly Ile Asp Thr Ile Val Gly Asp Gly Ala Phe Arg Leu Thr Ser Val
 420 425 430
 Glu Asn Gln Ile Met Ala Leu Ala Arg Val His Leu Ala Asp Leu Ala
 435 440 445
 Ile Val Ile Leu Asp Glu Ala Thr Ala Glu Ser Gly Ser Asp His Ala
 450 455 460
 Lys Gln Leu Glu Asp Ala Ala Leu Lys Val Thr Glu Asn Arg Ser Ala
 465 470 475 480
 Ile Ile Val Ala His Arg Leu Asn Gln Ala Lys Thr Ala Asp Arg Ile

485 490 495
 Ile Val Met Asp Ser Gly Glu Ile Ile Glu Ser Gly Thr His Glu Glu
 500 505 510
 Leu Arg Ala Ile Gly Gly Arg Tyr Glu Gln Leu Trp Thr Ala Trp Ser
 515 520 525
 Ala Arg
 530

 <210> 257
 <211> 1392
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1369)
 <223> RXA02646

 <400> 257
 ttggaaataa aacctatgcc aaagtaggtg caattctagg agaagattac actagtcaac 60

 catgagtgaacacatacgtgt ctgagaaaag tccaggagtg atg gct agc gga gcg 115
 Met Ala Ser Gly Ala
 1 5

 gag ctg att cgt gcc gcc gac att caa acg gcg cag gca cga att tcc 163
 Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala Gln Ala Arg Ile Ser
 10 15 20

 tcc gtc att gca cca act cca ttg cag tat tgc cct cgt ctt tct gag 211
 Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys Pro Arg Leu Ser Glu
 25 30 35

 gaa acc gga gcg gaa atc tac ctt aag cgt gag gat ctg cag gat gtt 259
 Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu Asp Leu Gln Asp Val
 40 45 50

 cgt tcc tac aag atc cgc ggt gcg ctg aac tct gga gcg cag ctc acc 307
 Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser Gly Ala Gln Leu Thr
 55 60 65

 caa gag cag cgc gat gca ggt atc gtt gcc gca tct gca ggt aac cat 355
 Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala Ser Ala Gly Asn His
 70 75 80 85

 gcc cag ggc gtg gcc tat gtg tgc aag tcc ttg ggc gtt cag gga gcg 403
 Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu Gly Val Gln Gly Arg
 90 95 100

 atc tat gtt cct gtg cag act cca aag caa aag cgt gac cgc atc atg 451
 Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys Arg Asp Arg Ile Met
 105 110 115

 gtt cac ggc gga gag ttt gtc tcc ttg gtg gtc act ggc aat aac ttc 499
 Val His Gly Gly Glu Phe Val Ser Leu Val Val Thr Gly Asn Asn Phe
 120 125 130

gac gaa gca tgc gct gca gcg cat gaa gat gca gag cgc acc ggc gca	547
Asp Glu Ala Ser Ala Ala His Glu Asp Ala Glu Arg Thr Gly Ala	
135 140 145	
acg ctg atc gag cct ttc gat gct cgc aac acc gtc atc ggt cag ggc	595
Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr Val Ile Gly Gln Gly	
150 155 160 165	
acc gtg gct gct gag atc ttg tgc cag ctg act tcc atg ggc aag agt	643
Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr Ser Met Gly Lys Ser	
170 175 180	
gca gat cac gtg atg gtt cca gtc ggc ggt ggc gga ctt ctt gca ggt	691
Ala Asp His Val Met Val Pro Val Gly Gly Gly Gly Leu Leu Ala Gly	
185 190 195	
gtg gtc agc tac atg gct gat atg gca cct cgc act gcg atc gtt ggt	739
Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg Thr Ala Ile Val Gly	
200 205 210	
atc gaa cca gcg gga gca gca tcc atg cag gct gca ttg cac aat ggt	787
Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala Ala Leu His Asn Gly	
215 220 225	
gga cca atc act ttg gag act gtt gat ccc ttt gtg gac ggc gca gca	835
Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe Val Asp Gly Ala Ala	
230 235 240 245	
gtc aaa cgt gtc gga gat ctc aac tac acc atc gtg gag aag aac cag	883
Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile Val Glu Lys Asn Gln	
250 255 260	
ggt cgc gtg cac atg atg agc gcg acc gag ggc gct gtg tgt act gag	931
Gly Arg Val His Met Met Ser Ala Thr Glu Gly Ala Val Cys Thr Glu	
265 270 275	
atg ctc gat ctt tac caa aac gaa ggc atc atc gcg gag cct gct ggc	979
Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile Ala Glu Pro Ala Gly	
280 285 290	
gcg ctg tct atc gct ggg ttg aag gaa atg tcc ttt gca gct cgc tct	
1027	
Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser Phe Ala Ala Arg Ser	
295 300 305	
gtc gtg gtg tgc atc atc tct ggt ggc aac aac gat gtg ctg cgt tat	
1075	
Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn Asp Val Leu Arg Tyr	
310 315 320 325	
gcg gaa atc gct gag cgc tcc ttg gtg cgc cgc ggt tta aag cac tac	
1123	
Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg Gly Leu Lys His Tyr	
330 335 340	
ttc ttg gtg aac ttc ccg caa aag cct ggt cag ttg cgt cac ttc ctg	
1171	
Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln Leu Arg His Phe Leu	
345 350 355	

gaa gat atc ctg gga ccg gat gat gac atc acg ctg ttt gag tac ctc
1219

Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr Leu Phe Glu Tyr Leu
360 365 370

aag cgc aac aac cgt gag acc ggt act gcg ttg gtg ggt att cac ttg
1267

Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu Val Gly Ile His Leu
375 380 385

agt gaa gca tca gga ttg gat tct ttg ctg gaa cgt atg gag gaa tcg
1315

Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu Arg Met Glu Glu Ser
390 395 400 405

gca att gat tcc cgt cgc ctc gag ccg ggc acc cct gag tac gaa tac
1363

Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr Pro Glu Tyr Glu Tyr
410 415 420

ttg acc taaacatagc tgaaggccac ctc
1392

Leu Thr

<210> 258

<211> 423

<212> PRT

<213> Corynebacterium glutamicum

<400> 258

Met Ala Ser Gly Ala Glu Leu Ile Arg Ala Ala Asp Ile Gln Thr Ala
1 5 10 15

Gln Ala Arg Ile Ser Ser Val Ile Ala Pro Thr Pro Leu Gln Tyr Cys
20 25 30

Pro Arg Leu Ser Glu Glu Thr Gly Ala Glu Ile Tyr Leu Lys Arg Glu
35 40 45

Asp Leu Gln Asp Val Arg Ser Tyr Lys Ile Arg Gly Ala Leu Asn Ser
50 55 60

Gly Ala Gln Leu Thr Gln Glu Gln Arg Asp Ala Gly Ile Val Ala Ala
65 70 75 80

Ser Ala Gly Asn His Ala Gln Gly Val Ala Tyr Val Cys Lys Ser Leu
85 90 95

Gly Val Gln Gly Arg Ile Tyr Val Pro Val Gln Thr Pro Lys Gln Lys
100 105 110

Arg Asp Arg Ile Met Val His Gly Gly Glu Phe Val Ser Leu Val Val
115 120 125

Thr Gly Asn Asn Phe Asp Glu Ala Ser Ala Ala Ala His Glu Asp Ala
130 135 140

Glu Arg Thr Gly Ala Thr Leu Ile Glu Pro Phe Asp Ala Arg Asn Thr
145 150 155 160

Val Ile Gly Gln Gly Thr Val Ala Ala Glu Ile Leu Ser Gln Leu Thr
 165 170 175
 Ser Met Gly Lys Ser Ala Asp His Val Met Val Pro Val Gly Gly Gly
 180 185 190
 Gly Leu Leu Ala Gly Val Val Ser Tyr Met Ala Asp Met Ala Pro Arg
 195 200 205
 Thr Ala Ile Val Gly Ile Glu Pro Ala Gly Ala Ala Ser Met Gln Ala
 210 215 220
 Ala Leu His Asn Gly Gly Pro Ile Thr Leu Glu Thr Val Asp Pro Phe
 225 230 235 240
 Val Asp Gly Ala Ala Val Lys Arg Val Gly Asp Leu Asn Tyr Thr Ile
 245 250 255
 Val Glu Lys Asn Gln Gly Arg Val His Met Met Ser Ala Thr Glu Gly
 260 265 270
 Ala Val Cys Thr Glu Met Leu Asp Leu Tyr Gln Asn Glu Gly Ile Ile
 275 280 285
 Ala Glu Pro Ala Gly Ala Leu Ser Ile Ala Gly Leu Lys Glu Met Ser
 290 295 300
 Phe Ala Ala Arg Ser Val Val Val Cys Ile Ile Ser Gly Gly Asn Asn
 305 310 315 320
 Asp Val Leu Arg Tyr Ala Glu Ile Ala Glu Arg Ser Leu Val Arg Arg
 325 330 335
 Gly Leu Lys His Tyr Phe Leu Val Asn Phe Pro Gln Lys Pro Gly Gln
 340 345 350
 Leu Arg His Phe Leu Glu Asp Ile Leu Gly Pro Asp Asp Asp Ile Thr
 355 360 365
 Leu Phe Glu Tyr Leu Lys Arg Asn Asn Arg Glu Thr Gly Thr Ala Leu
 370 375 380
 Val Gly Ile His Leu Ser Glu Ala Ser Gly Leu Asp Ser Leu Leu Glu
 385 390 395 400
 Arg Met Glu Glu Ser Ala Ile Asp Ser Arg Arg Leu Glu Pro Gly Thr
 405 410 415
 Pro Glu Tyr Glu Tyr Leu Thr
 420

<210> 259
 <211> 966
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(943)

<223> RXA00766

<400> 259

tatggcgctt gaaccacaaa taaagtctgc accgacgccg gtgatcttaa ttgtcgaacc 60

ctacggcggg tccatccggc aacaaaaccc caacctacca atg gtt ttt tgg gac 115
Met Val Phe Trp Asp
1 5

gat gca gcc tta acc cga ggc gat ggc atc ttt gaa aca ctc ctc atc 163
Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe Glu Thr Leu Leu Ile
10 15 20

cgc gac gga cat gcc tgc aac gtg cgc cga cac gga gaa cgc ttc aaa 211
Arg Asp Gly His Ala Cys Asn Val Arg Arg His Gly Glu Arg Phe Lys
25 30 35

gca tcg gca gca cta ttg gga ctg cca gag ccg atc ctg gaa gac tgg 259
Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro Ile Leu Glu Asp Trp
40 45 50

gaa aaa gcc acc caa atg ggc atc gaa tcc tgg tac tcc cac ccc aac 307
Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp Tyr Ser His Pro Asn
55 60 65

gca ggc gag gcc tca tgc acc tgg acg ctc agc cga ggt cgt tcc tcc 355
Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser Arg Gly Arg Ser Ser
70 75 80 85

acg ggg ctg gcc tca gga tgg tta acc atc acc cca gtc tcc tcc gac 403
Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr Pro Val Ser Ser Asp
90 95 100

aaa ctg gcg caa cgt gaa cac ggt gta tcg gtc atg acc agt tca aga 451
Lys Leu Ala Gln Arg Glu His Gly Val Ser Val Met Thr Ser Ser Arg
105 110 115

gga tat tcc atc gac acc ggc ctc ccc gga atc gga aaa gcc acc cga 499
Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile Gly Lys Ala Thr Arg
120 125 130

ggc gag cta tct aaa gtg gaa cga acc ccc gca cca tgg ctg aca gtc 547
Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala Pro Trp Leu Thr Val
135 140 145

ggc gcc aaa aca cta gcc tac gca gca aac atg gca gcc ctg cgc tac 595
Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met Ala Ala Leu Arg Tyr
150 155 160 165

gcc aaa tca aac gga ttc gac gat gtg atc ttc acc gat ggc gac cgc 643
Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe Thr Asp Gly Asp Arg
170 175 180

gtt cta gaa ggc gcc acc tcc acc gta gtg agt ttc aaa ggc gac aaa 691
Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser Phe Lys Gly Asp Lys
185 190 195

atc cgc acc cct tca ccc ggt ggc gac att ctc ccc gga acc acc caa 739
Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu Pro Gly Thr Thr Gln
200 205 210

gca gca ctc ttt gca cac gca acc gaa aaa gga tgg cga tgt aaa gaa 787
 Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly Trp Arg Cys Lys Glu
 215 220 225
 aaa gac tta agc att gac gat ctt ttc gga gcc gac agc gtg tgg cta 835
 Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala Asp Ser Val Trp Leu
 230 235 240 245
 gtg tcc tcc gtc cgc gga cca gtt cgg gtg acc agg ctc gat gga cac 883
 Val Ser Ser Val Arg Gly Pro Val Arg Val Thr Arg Leu Asp Gly His
 250 255 260
 aaa tta cgg aaa cca gac aat gaa aaa gaa atc aag gcg ctg att acc 931
 Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile Lys Ala Leu Ile Thr
 265 270 275
 aaa gct ctg ggg tagaggctgg cgctgggact tgc 966
 Lys Ala Leu Gly
 280

<210> 260
 <211> 281
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 260
 Met Val Phe Trp Asp Asp Ala Ala Leu Thr Arg Gly Asp Gly Ile Phe
 1 5 10 15
 Glu Thr Leu Leu Ile Arg Asp Gly His Ala Cys Asn Val Arg Arg His
 20 25 30
 Gly Glu Arg Phe Lys Ala Ser Ala Ala Leu Leu Gly Leu Pro Glu Pro
 35 40 45
 Ile Leu Glu Asp Trp Glu Lys Ala Thr Gln Met Gly Ile Glu Ser Trp
 50 55 60
 Tyr Ser His Pro Asn Ala Gly Glu Ala Ser Cys Thr Trp Thr Leu Ser
 65 70 75 80
 Arg Gly Arg Ser Ser Thr Gly Leu Ala Ser Gly Trp Leu Thr Ile Thr
 85 90 95
 Pro Val Ser Ser Asp Lys Leu Ala Gln Arg Glu His Gly Val Ser Val
 100 105 110
 Met Thr Ser Ser Arg Gly Tyr Ser Ile Asp Thr Gly Leu Pro Gly Ile
 115 120 125
 Gly Lys Ala Thr Arg Gly Glu Leu Ser Lys Val Glu Arg Thr Pro Ala
 130 135 140
 Pro Trp Leu Thr Val Gly Ala Lys Thr Leu Ala Tyr Ala Ala Asn Met
 145 150 155 160
 Ala Ala Leu Arg Tyr Ala Lys Ser Asn Gly Phe Asp Asp Val Ile Phe
 165 170 175
 Thr Asp Gly Asp Arg Val Leu Glu Gly Ala Thr Ser Thr Val Val Ser

180	185	190	
Phe Lys Gly Asp Lys Ile Arg Thr Pro Ser Pro Gly Gly Asp Ile Leu			
195	200	205	
Pro Gly Thr Thr Gln Ala Ala Leu Phe Ala His Ala Thr Glu Lys Gly			
210	215	220	
Trp Arg Cys Lys Glu Lys Asp Leu Ser Ile Asp Asp Leu Phe Gly Ala			
225	230	235	240
Asp Ser Val Trp Leu Val Ser Ser Val Arg Gly Pro Val Arg Val Thr			
245	250		255
Arg Leu Asp Gly His Lys Leu Arg Lys Pro Asp Asn Glu Lys Glu Ile			
260	265		270
Lys Ala Leu Ile Thr Lys Ala Leu Gly			
275	280		
<210> 261			
<211> 1224			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1201)			
<223> RXN01690			
<400> 261			
cctagccatt cctcaaaacc gtgagacgaa attggctatt catcccataa aatggggctg	60		
actagtgtat ctgtcaggta gcagggtgtac cttaaaatcc atg acg tca tta gag	115		
	Met Thr Ser Leu Glu		
	1 5		
ttc aca gta acc cgt acc gaa aat ccg acg tca ccc gat cgt ctg aag	163		
Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser Pro Asp Arg Leu Lys			
10 15 20			
gaa att ctt gcc gca ccg aag ttc ggt aag ttc ttc acc gac cac atg	211		
Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe Phe Thr Asp His Met			
25 30 35			
gtg acc att gac tgg aac gag tcg gaa ggc tgg cac aac gcc caa tta	259		
Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp His Asn Ala Gln Leu			
40 45 50			
gtg cca tac gcg ccg att cct atg gat cct gcc acc acc gta ttc cac	307		
Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala Thr Thr Val Phe His			
55 60 65			
tac gga cag gca att ttt gag gga att aag gcc tac cgc cat tcg gac	355		
Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala Tyr Arg His Ser Asp			
70 75 80 85			
gaa acc atc aag act ttc cgt cct gat gaa aac gcc gag cgt atg cag	403		
Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn Ala Glu Arg Met Gln			
90 95 100			

cgt tca gca gct cga atg gca atg cca cag ttg cca acc gag gac ttt	451
Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu Pro Thr Glu Asp Phe	
105 110 115	
att aaa gca ctt gaa ctg ctg gta gac gcg gat cag gat tgg gtt cct	499
Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp Gln Asp Trp Val Pro	
120 125 130	
gag tac ggc gga gaa gct tcc ctc tac ctg cgc cca ttc atg atc tcc	547
Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg Pro Phe Met Ile Ser	
135 140 145	
acc gaa att ggc ttg ggt gtc agc cca gct gat gcc tac aag ttc ctg	595
Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp Ala Tyr Lys Phe Leu	
150 155 160 165	
gtc atc gca tcc cca gtc ggc gct tac ttc acc ggt gga atc aag cct	643
Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr Gly Gly Ile Lys Pro	
170 175 180	
gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc gct gca ccc ggc gga	691
Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg Ala Ala Pro Gly Gly	
185 190 195	
act ggt gac gcc aaa ttt gct ggc aac tac gcg gct tct ttg ctt gcc	739
Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala Ala Ser Leu Leu Ala	
200 205 210	
cag tcc cag gct gcg gaa aag ggc tgt gac cag gtc gta tgg ttg gat	787
Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln Val Val Trp Leu Asp	
215 220 225	
gcc atc gag cac aag tac atc gaa gaa atg ggt ggc atg aac ctt ggg	835
Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly Gly Met Asn Leu Gly	
230 235 240 245	
ttc atc tac cgc aac ggc gac caa gtc aag cta gtc acc cct gaa ctt	883
Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu Val Thr Pro Glu Leu	
250 255 260	
tcc ggc tca cta ctt cca ggc atc acc cgc aag tca ctt cta caa gta	931
Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys Ser Leu Leu Gln Val	
265 270 275	
gca cgc gac ttg gga tac gaa gta gaa gag cga aag atc acc acc acc	979
Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg Lys Ile Thr Thr Thr	
280 285 290	
gag tgg gaa gaa gac gca aag tct ggc gcc atg acc gag gca ttt gct	
1027	
Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met Thr Glu Ala Phe Ala	
295 300 305	
tgc ggt act gca gct gtt atc acc cct gtt ggc acc gtg aaa tca gct	
1075	
Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly Thr Val Lys Ser Ala	
310 315 320 325	
cac ggc acc ttc gaa gtg aac aac aat gaa gtc gga gaa atc acg atg	
1123	

His Gly Thr Phe Glu Val Asn Asn Asn Glu Val Gly Glu Ile Thr Met
 330 335 340

aag ctt cgt gaa acc ctc acc gga att cag caa gga aac gtt gaa gac
 1171

Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln Gly Asn Val Glu Asp
 345 350 355

caa aac gga tgg ctt tac cca ctg gtt ggc taaatcaacc gggtttaaga
 1221

Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 360 365

ccc
 1224

<210> 262

<211> 367

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 262

Met Thr Ser Leu Glu Phe Thr Val Thr Arg Thr Glu Asn Pro Thr Ser
 1 5 10 15

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
 20 25 30

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
 35 40 45

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
 50 55 60

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
 65 70 75 80

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
 85 90 95

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
 100 105 110

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
 115 120 125

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
 130 135 140

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
 145 150 155 160

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
 165 170 175

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
 180 185 190

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
 195 200 205

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
 210 215 220

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly
 225 230 235 240

Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu
 245 250 255

Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys
 260 265 270

Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg
 275 280 285

Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met
 290 295 300

Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly
 305 310 315 320

Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val
 325 330 335

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
 340 345 350

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
 355 360 365

<210> 263

<211> 1076

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1053)

<223> FRXA01690

<400> 263

ccc gat cgt ctg aag gaa att ctt gcc gca ccg aag ttc ggt aag ttc 48

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe

1

5

10

15

ttc acc gac cac atg gtg acc att gac tgg aac gag tcg gaa ggc tgg 96

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp

20

25

30

cac aac gcc caa tta gtg cca tac gcg ccg att cct atg gat cct gcc 144

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala

35

40

45

acc acc gta ttc cac tac gga cag gca att ttt gag gga att aag gcc 192

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala

50

55

60

tac cgc cat tcg gac gaa acc atc aag act ttc cgt cct gat gaa aac 240

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn

65	70	75	80	
gcc gag cgt atg cag cgt tca gca gct cga atg gca atg cca cag ttg				288
Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu				
	85	90	95	
cca acc gag gac ttt att aaa gca ctt gaa ctg ctg gta gac gcg gat				336
Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp				
	100	105	110	
cag gat tgg gtt cct gag tac ggc gga gaa gct tcc ctc tac ctg cgc				384
Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg				
	115	120	125	
cca ttc atg atc tcc acc gaa att ggc ttg ggt gtc agc cca gct gat				432
Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp				
	130	135	140	
gcc tac aag ttc ctg gtc atc gca tcc cca gtc ggc gct tac ttc acc				480
Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr				
	145	150	155	160
ggg gga atc aag cct gtt tcc gtc tgg ctg agc gaa gat tac gtc cgc				528
Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg				
	165	170	175	
gct gca ccc ggc gga act ggt gac gcc aaa ttt gct ggc aac tac gcg				576
Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala				
	180	185	190	
gct tct ttg ctt gcc cag tcc cag gct gcg gaa aag ggc tgt gac cag				624
Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln				
	195	200	205	
gtc gta tgg ttg gat gcc atc gag cac aag tac atc gaa gaa atg ggt				672
Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly				
	210	215	220	
ggc atg aac ctt ggg ttc atc tac cgc aac ggc gac caa gtc aag cta				720
Gly Met Asn Leu Gly Phe Ile Tyr Arg Asn Gly Asp Gln Val Lys Leu				
	225	230	235	240
gtc acc cct gaa ctt tcc ggc tca cta ctt cca ggc atc acc cgc aag				768
Val Thr Pro Glu Leu Ser Gly Ser Leu Leu Pro Gly Ile Thr Arg Lys				
	245	250	255	
tca ctt cta caa gta gca cgc gac ttg gga tac gaa gta gaa gag cga				816
Ser Leu Leu Gln Val Ala Arg Asp Leu Gly Tyr Glu Val Glu Glu Arg				
	260	265	270	
aag atc acc acc acc gag tgg gaa gaa gac gca aag tct ggc gcc atg				864
Lys Ile Thr Thr Thr Glu Trp Glu Glu Asp Ala Lys Ser Gly Ala Met				
	275	280	285	
acc gag gca ttt gct tgc ggt act gca gct gtt atc acc cct gtt ggc				912
Thr Glu Ala Phe Ala Cys Gly Thr Ala Ala Val Ile Thr Pro Val Gly				
	290	295	300	
acc gtg aaa tca gct cac ggc acc ttc gaa gtg aac aac aat gaa gtc				960
Thr Val Lys Ser Ala His Gly Thr Phe Glu Val Asn Asn Asn Glu Val				
	305	310	315	320

gga gaa atc acg atg aag ctt cgt gaa acc ctc acc gga att cag caa
1008

Gly Glu Ile Thr Met Lys Leu Arg Glu Thr Leu Thr Gly Ile Gln Gln
325 330 335

gga aac gtt gaa gac caa aac gga tgg ctt tac cca ctg gtt ggc
1053

Gly Asn Val Glu Asp Gln Asn Gly Trp Leu Tyr Pro Leu Val Gly
340 345 350

taaatacaacc ggttttaaga ccc
1076

<210> 264

<211> 351

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 264

Pro Asp Arg Leu Lys Glu Ile Leu Ala Ala Pro Lys Phe Gly Lys Phe
1 5 10 15

Phe Thr Asp His Met Val Thr Ile Asp Trp Asn Glu Ser Glu Gly Trp
20 25 30

His Asn Ala Gln Leu Val Pro Tyr Ala Pro Ile Pro Met Asp Pro Ala
35 40 45

Thr Thr Val Phe His Tyr Gly Gln Ala Ile Phe Glu Gly Ile Lys Ala
50 55 60

Tyr Arg His Ser Asp Glu Thr Ile Lys Thr Phe Arg Pro Asp Glu Asn
65 70 75 80

Ala Glu Arg Met Gln Arg Ser Ala Ala Arg Met Ala Met Pro Gln Leu
85 90 95

Pro Thr Glu Asp Phe Ile Lys Ala Leu Glu Leu Leu Val Asp Ala Asp
100 105 110

Gln Asp Trp Val Pro Glu Tyr Gly Gly Glu Ala Ser Leu Tyr Leu Arg
115 120 125

Pro Phe Met Ile Ser Thr Glu Ile Gly Leu Gly Val Ser Pro Ala Asp
130 135 140

Ala Tyr Lys Phe Leu Val Ile Ala Ser Pro Val Gly Ala Tyr Phe Thr
145 150 155 160

Gly Gly Ile Lys Pro Val Ser Val Trp Leu Ser Glu Asp Tyr Val Arg
165 170 175

Ala Ala Pro Gly Gly Thr Gly Asp Ala Lys Phe Ala Gly Asn Tyr Ala
180 185 190

Ala Ser Leu Leu Ala Gln Ser Gln Ala Ala Glu Lys Gly Cys Asp Gln
195 200 205

Val Val Trp Leu Asp Ala Ile Glu His Lys Tyr Ile Glu Glu Met Gly

210	215	220
Gly Met Asn Leu Gly	Phe Ile Tyr Arg Asn	Gly Asp Gln Val Lys Leu
225	230	235 240
Val Thr Pro Glu Leu	Ser Gly Ser Leu Leu	Pro Gly Ile Thr Arg Lys
245	250	255
Ser Leu Leu Gln Val	Ala Arg Asp Leu Gly	Tyr Glu Val Glu Glu Arg
260	265	270
Lys Ile Thr Thr Thr	Glu Trp Glu Glu Asp	Ala Lys Ser Gly Ala Met
275	280	285
Thr Glu Ala Phe Ala	Cys Gly Thr Ala Ala	Val Ile Thr Pro Val Gly
290	295	300
Thr Val Lys Ser Ala	His Gly Thr Phe Glu	Val Asn Asn Asn Glu Val
305	310	315 320
Gly Glu Ile Thr Met	Lys Leu Arg Glu Thr	Leu Thr Gly Ile Gln Gln
325	330	335
Gly Asn Val Glu Asp	Gln Asn Gly Trp Leu	Tyr Pro Leu Val Gly
340	345	350

<210> 265

<211> 1782

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1759)

<223> RXN01026

<400> 265

gaggtgacat ttatgcctct taatagctat actgtcccat gaaacgatat tttaatctca 60

tatagtgaga	tttacagatt	tttaaaggac	ggtgagttcc	atg acc agc ccc gtg	115
				Met Thr Ser Pro Val	
				1 5	

gag aac agc acc tca act gag aag ctg acc ctg gca gag aag gtg tgg	163
Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu Ala Glu Lys Val Trp	
10 15 20	

cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac ctc ctc	211
Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp Leu Leu	
25 30 35	

tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag gca ttt	259
Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln Ala Phe	
40 45 50	

gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa ctg cac	307
Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu Leu His	
55 60 65	

ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag act ggc	355
---	-----

Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys	Thr	Gly		
70					75					80					85		
tca	ctg	ctg	gaa	atc	aac	gac	aag	att	tcc	cgc	ctg	cag	gta	tct	act	403	
Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val	Ser	Thr		
				90					95					100			
ctg	cgc	gac	aac	tgt	gaa	gaa	ttc	ggc	gtg	cgc	ctg	cac	cca	atg	ggc	451	
Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro	Met	Gly		
			105					110					115				
gat	gtc	cga	cag	ggc	atc	gtg	cac	acc	gtc	ggc	cca	cag	ctc	ggc	gca	499	
Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu	Gly	Ala		
		120					125					130					
acc	cag	cca	ggc	atg	acc	att	gtg	tgc	ggc	gac	tcc	cac	acc	tcc	acc	547	
Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr	Ser	Thr		
		135				140				145							
cac	ggc	gct	ttt	ggc	tcc	atg	gca	ttc	ggc	atc	ggc	acc	tca	gag	gtt	595	
His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser	Glu	Val		
150					155				160					165			
gag	cac	gtc	atg	gct	act	caa	acc	ctg	cca	ctg	aag	cct	ttc	aag	acc	643	
Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe	Lys	Thr		
				170				175					180				
atg	gcc	att	gaa	gtt	act	ggc	gaa	ctg	cag	cca	ggc	gtt	tcc	tcc	aag	691	
Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser	Ser	Lys		
			185				190						195				
gac	ctg	att	ctg	gcg	att	atc	gcc	aag	atc	ggc	acc	ggc	ggc	gga	cag	739	
Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly	Gly	Gln		
		200				205						210					
ggc	tac	gtt	ctg	gaa	tac	cgc	ggc	gaa	gca	atc	cgt	aag	atg	tcc	atg	787	
Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met	Ser	Met		
		215				220					225						
gat	gca	cgc	atg	acc	atg	tgc	aac	atg	tcc	atc	gaa	gct	ggc	gca	cgt	835	
Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly	Ala	Arg		
230					235				240					245			
gcc	ggc	atg	atc	gcc	cca	gac	caa	acc	acc	ttc	gac	tac	gtt	gaa	ggc	883	
Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val	Glu	Gly		
				250				255					260				
cgc	gaa	atg	gca	cca	aag	ggc	gcc	gac	tgg	gac	gaa	gca	gtt	gct	tac	931	
Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val	Ala	Tyr		
			265				270						275				
tgg	aag	acc	ctg	cca	acc	gac	gaa	ggc	gca	acc	ttt	gac	aag	gtc	gta	979	
Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys	Val	Val		
		280				285						290					
gaa	atc	gat	ggc	tcg	gca	ctg	acc	cca	ttc	atc	acc	tgg	ggc	acc	aac		
1027																	
Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly	Thr	Asn		
		295				300					305						

cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca gaa gac
1075
Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro Glu Asp
310 315 320 325

ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg cag tac
1123
Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu Gln Tyr
330 335 340

atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc gac acc
1171
Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile Asp Thr
345 350 355

gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg cag atc
1219
Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu Gln Ile
360 365 370

gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg cgc atg
1267
Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met Arg Met
375 380 385

atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa gcg ctc
1315
Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu Ala Leu
390 395 400 405

gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt acc gca
1363
Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg Thr Ala
410 415 420

ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag cca ggc
1411
Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys Pro Gly
425 430 435

gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc caa gga
1459
Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg Gln Gly
440 445 450

cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc gcc acc
1507
Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala Ala Thr
455 460 465

gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag gct aga
1555
Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys Ala Arg
470 475 480 485

aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc cac tgc
1603
Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe His Cys
490 495 500

agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct acc tca
 1651
 Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser Thr Ser
 505 510 515

agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca act ggc
 1699
 Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro Thr Gly
 520 525 530

gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca aga acg
 1747
 Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr Arg Thr
 535 540 545

gct ccg ttc tcg tagcaggccc tgactttggc acc
 1782
 Ala Pro Phe Ser
 550

<210> 266
 <211> 553
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 266
 Met Thr Ser Pro Val Glu Asn Ser Thr Ser Thr Glu Lys Leu Thr Leu
 1 5 10 15

Ala Glu Lys Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly
 20 25 30

Glu Pro Asp Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr
 35 40 45

Ser Pro Gln Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg
 50 55 60

His Pro Glu Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu
 65 70 75 80

Gly Ile Lys Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg
 85 90 95

Leu Gln Val Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg
 100 105 110

Leu His Pro Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly
 115 120 125

Pro Gln Leu Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp
 130 135 140

Ser His Thr Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile
 145 150 155 160

Gly Thr Ser Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu
 165 170 175

Lys Pro Phe Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro

180					185					190					
Gly	Val	Ser	Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly
	195						200					205			
Thr	Gly	Gly	Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile
	210					215					220				
Arg	Lys	Met	Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile
	225					230					235				240
Glu	Ala	Gly	Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe
				245					250					255	
Asp	Tyr	Val	Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp
			260					265					270		
Glu	Ala	Val	Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr
		275					280					285			
Phe	Asp	Lys	Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile
	290					295					300				
Thr	Trp	Gly	Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val
	305					310					315				320
Pro	Ser	Pro	Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu
				325					330					335	
Lys	Ala	Leu	Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp
			340					345					350		
Ile	Lys	Ile	Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile
		355					360					365			
Glu	Asp	Leu	Gln	Ile	Ala	Ala	Asp	Ile	Leu	Lys	Gly	His	Lys	Ile	Ala
	370					375					380				
Asp	Gly	Met	Arg	Met	Met	Val	Val	Pro	Ser	Ser	Thr	Trp	Ile	Lys	Gln
	385					390					395				400
Glu	Ala	Glu	Ala	Leu	Gly	Leu	Asp	Lys	Ile	Phe	Thr	Asp	Ala	Gly	Ala
				405					410					415	
Glu	Trp	Arg	Thr	Ala	Gly	Cys	Ser	Met	Cys	Leu	Gly	Met	Asn	Pro	Asp
			420					425					430		
Gln	Leu	Lys	Pro	Gly	Glu	Arg	Ser	Ala	Phe	Thr	Ser	Asn	Arg	Asn	Phe
		435					440					445			
Glu	Gly	Arg	Gln	Gly	Pro	Gly	Gly	Arg	Thr	His	Leu	Val	Ser	Pro	Ala
	450					455					460				
Val	Ala	Ala	Ala	Thr	Glu	Ser	Ala	Asp	Pro	Val	Leu	Thr	Cys	Arg	Tyr
	465					470					475				480
Leu	Arg	Lys	Ala	Arg	Lys	Gln	Trp	Lys	Asn	Leu	Pro	Pro	Thr	Pro	Ala
				485					490					495	
Leu	Ala	Phe	His	Cys	Ser	Asp	Pro	Thr	Trp	Thr	Pro	Thr	Arg	Ser	Ser
			500					505					510		

Gln Pro Ser Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp
 515 520 525

Cys Phe Pro Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro
 530 535 540

Thr Pro Thr Arg Thr Ala Pro Phe Ser
 545 550

<210> 267
 <211> 1625
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1) .. (1602)
 <223> FRXA01026

<400> 267

gtg tgg cgc gac cat gtc gtg tcc aag gga gaa aac ggc gag ccc gac	48
Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp	
1 5 10 15	
ctc ctc tac atc gac ctg cag ctg ctg cat gaa gtg acc tca cca cag	96
Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln	
20 25 30	
gca ttt gac ggc ctg cgc atg acc ggc cgt aaa ctg cgc cac cca gaa	144
Ala Phe Asp Gly Leu Arg Met Thr Gly Arg Lys Leu Arg His Pro Glu	
35 40 45	
ctg cac ctg gcc acc gaa gac cac aac gtg cca acc gaa ggc atc aag	192
Leu His Leu Ala Thr Glu Asp His Asn Val Pro Thr Glu Gly Ile Lys	
50 55 60	
act ggc tca ctg ctg gaa atc aac gac aag att tcc cgc ctg cag gta	240
Thr Gly Ser Leu Leu Glu Ile Asn Asp Lys Ile Ser Arg Leu Gln Val	
65 70 75 80	
tct act ctg cgc gac aac tgt gaa gaa ttc ggc gtg cgc ctg cac cca	288
Ser Thr Leu Arg Asp Asn Cys Glu Glu Phe Gly Val Arg Leu His Pro	
85 90 95	
atg ggt gat gtc cga cag ggc atc gtg cac acc gtc ggc cca cag ctc	336
Met Gly Asp Val Arg Gln Gly Ile Val His Thr Val Gly Pro Gln Leu	
100 105 110	
ggc gca acc cag cca ggc atg acc att gtg tgc ggt gac tcc cac acc	384
Gly Ala Thr Gln Pro Gly Met Thr Ile Val Cys Gly Asp Ser His Thr	
115 120 125	
tcc acc cac ggt gct ttt ggc tcc atg gca ttc ggc atc ggt acc tca	432
Ser Thr His Gly Ala Phe Gly Ser Met Ala Phe Gly Ile Gly Thr Ser	
130 135 140	
gag gtt gag cac gtc atg gct act caa acc ctg cca ctg aag cct ttc	480
Glu Val Glu His Val Met Ala Thr Gln Thr Leu Pro Leu Lys Pro Phe	
145 150 155 160	

aag acc atg gcc att gaa gtt act ggt gaa ctg cag cca ggt gtt tcc 528
Lys Thr Met Ala Ile Glu Val Thr Gly Glu Leu Gln Pro Gly Val Ser
165 170 175

tcc aag gac ctg att ctg gcg att atc gcc aag atc ggc acc ggc ggc 576
Ser Lys Asp Leu Ile Leu Ala Ile Ile Ala Lys Ile Gly Thr Gly Gly
180 185 190

gga cag ggc tac gtt ctg gaa tac cgc ggc gaa gca atc cgt aag atg 624
Gly Gln Gly Tyr Val Leu Glu Tyr Arg Gly Glu Ala Ile Arg Lys Met
195 200 205

tcc atg gat gca cgc atg acc atg tgc aac atg tcc atc gaa gct ggc 672
Ser Met Asp Ala Arg Met Thr Met Cys Asn Met Ser Ile Glu Ala Gly
210 215 220

gca cgt gcc ggc atg atc gcc cca gac caa acc acc ttc gac tac gtt 720
Ala Arg Ala Gly Met Ile Ala Pro Asp Gln Thr Thr Phe Asp Tyr Val
225 230 235 240

gaa ggc cgc gaa atg gca cca aag ggc gcc gac tgg gac gaa gca gtt 768
Glu Gly Arg Glu Met Ala Pro Lys Gly Ala Asp Trp Asp Glu Ala Val
245 250 255

gct tac tgg aag acc ctg cca acc gac gaa ggc gca acc ttt gac aag 816
Ala Tyr Trp Lys Thr Leu Pro Thr Asp Glu Gly Ala Thr Phe Asp Lys
260 265 270

gtc gta gaa atc gat ggc tcg gca ctg acc cca ttc atc acc tgg ggc 864
Val Val Glu Ile Asp Gly Ser Ala Leu Thr Pro Phe Ile Thr Trp Gly
275 280 285

acc aac cca ggc cag ggc ctg cca ctg ggc gaa tcc gta cca agc cca 912
Thr Asn Pro Gly Gln Gly Leu Pro Leu Gly Glu Ser Val Pro Ser Pro
290 295 300

gaa gac ttc acc aac gac aac gac aag gca gca gcc gaa aag gca ctg 960
Glu Asp Phe Thr Asn Asp Asn Asp Lys Ala Ala Ala Glu Lys Ala Leu
305 310 315 320

cag tac atg gac ctg gta cca gga acc cca ctg cgc gac atc aag atc
1008
Gln Tyr Met Asp Leu Val Pro Gly Thr Pro Leu Arg Asp Ile Lys Ile
325 330 335

gac acc gtc ttc ctg gga tcc tgc acc aac gcc cgc atc gaa gac ctg
1056
Asp Thr Val Phe Leu Gly Ser Cys Thr Asn Ala Arg Ile Glu Asp Leu
340 345 350

cag atc gcc gct gac atc ctc aag ggc cac aaa atc gcc gac ggc atg
1104
Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
355 360 365

cgc atg atg gtc gtg cct tcc tcc acc tgg atc aag caa gag gca gaa
1152
Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
370 375 380

gcg ctc gga ctg gac aaa atc ttc acc gac gct ggc gct gaa tgg cgt
 1200
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400

acc gca ggc tgc tcc atg tgc ctg ggc atg aac cca gac caa ctg aag
 1248
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415

cca ggc gag cgc tcc gca ttc acc tcc aac cga aac ttc gaa gga cgc
 1296
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430

caa gga cca gga ggc cgc acc cac ctg gta tcc cca gca gtc gca gcc
 1344
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445

gcc acc gaa tcc gcg gac cct gtc ctc acc tgc aga tat cta agg aag
 1392
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460

gct aga aaa caa tgg aaa aat tta cca cct aca ccg gcg ttg gcg ttc
 1440
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480

cac tgc agc gat cca acg tgg aca ccg acc aga tca tcc cag ccg tct
 1488
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495

acc tca agc gcg tca ccc gga ccg gct tcg aag acg gac tgt ttt cca
 1536
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510

act ggc gcc aaa acg acc cca act ttg tcc tca aca ccg aca cct aca
 1584
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525

aga acg gct ccg ttc tcg tagcaggccc tgactttggc acc
 1625
 Arg Thr Ala Pro Phe Ser
 530

<210> 268

<211> 534

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Val Trp Arg Asp His Val Val Ser Lys Gly Glu Asn Gly Glu Pro Asp
 1 5 10 15

Leu Leu Tyr Ile Asp Leu Gln Leu Leu His Glu Val Thr Ser Pro Gln

20				25				30							
Ala	Phe	Asp	Gly	Leu	Arg	Met	Thr	Gly	Arg	Lys	L u	Arg	His	Pro	Glu
		35					40					45			
Leu	His	Leu	Ala	Thr	Glu	Asp	His	Asn	Val	Pro	Thr	Glu	Gly	Ile	Lys
	50					55					60				
Thr	Gly	Ser	Leu	Leu	Glu	Ile	Asn	Asp	Lys	Ile	Ser	Arg	Leu	Gln	Val
65					70					75					80
Ser	Thr	Leu	Arg	Asp	Asn	Cys	Glu	Glu	Phe	Gly	Val	Arg	Leu	His	Pro
				85					90					95	
Met	Gly	Asp	Val	Arg	Gln	Gly	Ile	Val	His	Thr	Val	Gly	Pro	Gln	Leu
			100					105					110		
Gly	Ala	Thr	Gln	Pro	Gly	Met	Thr	Ile	Val	Cys	Gly	Asp	Ser	His	Thr
		115					120					125			
Ser	Thr	His	Gly	Ala	Phe	Gly	Ser	Met	Ala	Phe	Gly	Ile	Gly	Thr	Ser
	130					135					140				
Glu	Val	Glu	His	Val	Met	Ala	Thr	Gln	Thr	Leu	Pro	Leu	Lys	Pro	Phe
145					150					155					160
Lys	Thr	Met	Ala	Ile	Glu	Val	Thr	Gly	Glu	Leu	Gln	Pro	Gly	Val	Ser
				165					170					175	
Ser	Lys	Asp	Leu	Ile	Leu	Ala	Ile	Ile	Ala	Lys	Ile	Gly	Thr	Gly	Gly
			180					185					190		
Gly	Gln	Gly	Tyr	Val	Leu	Glu	Tyr	Arg	Gly	Glu	Ala	Ile	Arg	Lys	Met
		195					200					205			
Ser	Met	Asp	Ala	Arg	Met	Thr	Met	Cys	Asn	Met	Ser	Ile	Glu	Ala	Gly
	210					215					220				
Ala	Arg	Ala	Gly	Met	Ile	Ala	Pro	Asp	Gln	Thr	Thr	Phe	Asp	Tyr	Val
225					230					235					240
Glu	Gly	Arg	Glu	Met	Ala	Pro	Lys	Gly	Ala	Asp	Trp	Asp	Glu	Ala	Val
				245					250					255	
Ala	Tyr	Trp	Lys	Thr	Leu	Pro	Thr	Asp	Glu	Gly	Ala	Thr	Phe	Asp	Lys
			260					265					270		
Val	Val	Glu	Ile	Asp	Gly	Ser	Ala	Leu	Thr	Pro	Phe	Ile	Thr	Trp	Gly
		275					280					285			
Thr	Asn	Pro	Gly	Gln	Gly	Leu	Pro	Leu	Gly	Glu	Ser	Val	Pro	Ser	Pro
	290					295					300				
Glu	Asp	Phe	Thr	Asn	Asp	Asn	Asp	Lys	Ala	Ala	Ala	Glu	Lys	Ala	Leu
305					310					315					320
Gln	Tyr	Met	Asp	Leu	Val	Pro	Gly	Thr	Pro	Leu	Arg	Asp	Ile	Lys	Ile
				325					330					335	
Asp	Thr	Val	Phe	Leu	Gly	Ser	Cys	Thr	Asn	Ala	Arg	Ile	Glu	Asp	Leu
			340					345					350		

Gln Ile Ala Ala Asp Ile Leu Lys Gly His Lys Ile Ala Asp Gly Met
 355 360 365
 Arg Met Met Val Val Pro Ser Ser Thr Trp Ile Lys Gln Glu Ala Glu
 370 375 380
 Ala Leu Gly Leu Asp Lys Ile Phe Thr Asp Ala Gly Ala Glu Trp Arg
 385 390 395 400
 Thr Ala Gly Cys Ser Met Cys Leu Gly Met Asn Pro Asp Gln Leu Lys
 405 410 415
 Pro Gly Glu Arg Ser Ala Phe Thr Ser Asn Arg Asn Phe Glu Gly Arg
 420 425 430
 Gln Gly Pro Gly Gly Arg Thr His Leu Val Ser Pro Ala Val Ala Ala
 435 440 445
 Ala Thr Glu Ser Ala Asp Pro Val Leu Thr Cys Arg Tyr Leu Arg Lys
 450 455 460
 Ala Arg Lys Gln Trp Lys Asn Leu Pro Pro Thr Pro Ala Leu Ala Phe
 465 470 475 480
 His Cys Ser Asp Pro Thr Trp Thr Pro Thr Arg Ser Ser Gln Pro Ser
 485 490 495
 Thr Ser Ser Ala Ser Pro Gly Pro Ala Ser Lys Thr Asp Cys Phe Pro
 500 505 510
 Thr Gly Ala Lys Thr Thr Pro Thr Leu Ser Ser Thr Pro Thr Pro Thr
 515 520 525
 Arg Thr Ala Pro Phe Ser
 530

<210> 269
 <211> 1143
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1120)
 <223> RXN01127

<400> 269
 gccctgcatg atggggtagt gggggttggt gggcaggtac gagctgtgat caatcagcta 60
 cactagtga gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
 Met Lys Leu Ala Val
 1 5
 att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
 Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
 10 15 20
 gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
 Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu

25								30				35				
ggc	gca	cgc	cgt	tac	ctc	aaa	aat	ggc	gag	ctg	ctc	acc	gac	gag	gat	259
Gly	Ala	Arg	Arg	Tyr	Leu	Lys	Asn	Gly	Glu	Leu	Leu	Thr	Asp	Glu	Asp	
		40					45					50				
ctg	gca	tcc	ctg	cgc	gag	cat	gac	gcg	atc	ctt	ctt	ggc	gct	atc	ggc	307
Leu	Ala	Ser	Leu	Arg	Glu	His	Asp	Ala	Ile	Leu	Leu	Gly	Ala	Ile	Gly	
		55				60					65					
gca	cca	ggc	tcc	gtc	cct	cca	gga	att	ctc	gag	cgt	ggc	ttg	ctg	ctg	355
Ala	Pro	Gly	Ser	Val	Pro	Pro	Gly	Ile	Leu	Glu	Arg	Gly	Leu	Leu	Leu	
		70			75					80					85	
aag	atg	cga	ttc	gca	ctg	gat	cac	cac	gtg	aac	ctg	cgc	cca	tcc	aag	403
Lys	Met	Arg	Phe	Ala	Leu	Asp	His	His	Val	Asn	Leu	Arg	Pro	Ser	Lys	
				90					95					100		
ctg	tac	gac	ggc	gtg	gag	tcc	cca	ctg	cgt	aac	cca	ggc	aag	att	gat	451
Leu	Tyr	Asp	Gly	Val	Glu	Ser	Pro	Leu	Arg	Asn	Pro	Gly	Lys	Ile	Asp	
			105					110					115			
ttc	gtt	gtg	gtc	cgc	gaa	ggc	acc	gaa	ggc	gcc	tac	act	ggc	aac	ggc	499
Phe	Val	Val	Val	Arg	Glu	Gly	Thr	Glu	Gly	Ala	Tyr	Thr	Gly	Asn	Gly	
		120					125					130				
gga	gca	atc	cgc	gtg	gga	acc	cct	cac	gag	att	gcc	aac	gaa	acc	tcc	547
Gly	Ala	Ile	Arg	Val	Gly	Thr	Pro	His	Glu	Ile	Ala	Asn	Glu	Thr	Ser	
		135				140					145					
gtg	aac	act	cgc	tac	ggc	gct	gag	cgc	gtt	att	cgc	tac	gca	ttc	gag	595
Val	Asn	Thr	Arg	Tyr	Gly	Ala	Glu	Arg	Val	Ile	Arg	Tyr	Ala	Phe	Glu	
	150				155					160					165	
ctg	gca	cag	agc	cgc	cgc	aag	aag	ctc	acc	ctc	gtg	cac	aag	acc	aac	643
Leu	Ala	Gln	Ser	Arg	Arg	Lys	Lys	Leu	Thr	Leu	Val	His	Lys	Thr	Asn	
				170					175					180		
gtc	ctg	gtt	cac	ggc	ggc	ggc	ctg	tgg	cag	cgc	acc	gta	gat	gag	gtt	691
Val	Leu	Val	His	Gly	Gly	Gly	Leu	Trp	Gln	Arg	Thr	Val	Asp	Glu	Val	
			185					190					195			
gca	aag	gaa	tac	cca	gag	gta	gcc	gtc	gat	tac	aac	cac	atc	gat	gca	739
Ala	Lys	Glu	Tyr	Pro	Glu	Val	Ala	Val	Asp	Tyr	Asn	His	Ile	Asp	Ala	
		200					205					210				
gca	acc	atc	tat	ctg	gtc	act	gat	cct	tcc	cgc	ttc	gat	gtg	att	gtt	787
Ala	Thr	Ile	Tyr	Leu	Val	Thr	Asp	Pro	Ser	Arg	Phe	Asp	Val	Ile	Val	
		215				220					225					
acc	gat	aac	ctc	ttc	ggc	gac	atc	ctc	acc	gat	gag	gca	ggc	gca	gtc	835
Thr	Asp	Asn	Leu	Phe	Gly	Asp	Ile	Leu	Thr	Asp	Glu	Ala	Gly	Ala	Val	
	230				235					240					245	
tct	ggc	gga	att	ggc	ctc	gca	gca	tcc	ggc	aac	atc	gat	gcc	acg	ggc	883
Ser	Gly	Gly	Ile	Gly	Leu	Ala	Ala	Ser	Gly	Asn	Ile	Asp	Ala	Thr	Gly	
				250					255					260		
acc	aac	cct	tcc	atg	ttc	gag	cca	gtc	cac	ggc	tct	gca	cca	gat	atc	931
Thr	Asn	Pro	Ser	Met	Phe	Glu	Pro	Val	His	Gly	Ser	Ala	Pro	Asp	Ile	
			265					270					275			

gca ggc cag gga atc gca gac cca acg gca gca atc cta tcc gct gcg 979
 Ala Gly Gln Gly Ile Ala Asp Pro Thr Ala Ala Ile Leu Ser Ala Ala
 280 285 290

atg ctg ctg cgt cac tta ggt gat gaa gac aac gca gta cgt att gaa
 1027
 Met Leu Leu Arg His Leu Gly Asp Glu Asp Asn Ala Val Arg Ile Glu
 295 300 305

aca gcc atc gca gct gat gtg gct ggc cga gat aac tct cag ccg att
 1075
 Thr Ala Ile Ala Ala Asp Val Ala Gly Arg Asp Asn Ser Gln Pro Ile
 310 315 320 325

tct acc act gag gtg gga gac cgc atc gtc aag gcg ctg caa agc
 1120
 Ser Thr Thr Glu Val Gly Asp Arg Ile Val Lys Ala Leu Gln Ser
 330 335 340

taaatttcaa cgccgacccc ctt
 1143

<210> 270

<211> 340

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 270

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
 1 5 10 15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
 20 25 30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
 35 40 45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
 50 55 60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
 65 70 75 80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
 85 90 95

Leu Arg Pro Ser Lys Leu Tyr Asp Gly Val Glu Ser Pro Leu Arg Asn
 100 105 110

Pro Gly Lys Ile Asp Phe Val Val Val Arg Glu Gly Thr Glu Gly Ala
 115 120 125

Tyr Thr Gly Asn Gly Gly Ala Ile Arg Val Gly Thr Pro His Glu Ile
 130 135 140

Ala Asn Glu Thr Ser Val Asn Thr Arg Tyr Gly Ala Glu Arg Val Ile
 145 150 155 160

Arg Tyr Ala Phe Glu Leu Ala Gln Ser Arg Arg Lys Lys Leu Thr Leu

[illegible]

```
<210> 271
<211> 403
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(403)
<223> FRXA01132
```

```

<400> 271
gccctgcatg atggggtagt gggggttggt gggcaggtac gagctgtgat caatcagcta 60
cactagtgaa gtccatatag tgagaaggga atcccacaac atg aaa ctt gct gtt 115
Met Lys Leu Ala Val
1 5
att ggt gga gat ggt atc ggc cca gag gtt act gca gaa gcc ctc aag 163
Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr Ala Glu Ala Leu Lys
10 15 20
gtt cta aac gct gtc cgc gac gac atc gag acc acc gat tat gac ctt 211
Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr Thr Asp Tyr Asp Leu
25 30 35

```

```

ggc gca cgc cgt tac ctc aaa aat ggc gag ctg ctc acc gac gag gat 259
Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu Leu Thr Asp Glu Asp
      40                      45                      50

ctg gca tcc ctg cgc gag cat gac gcg atc ctt ctt ggc gct atc ggt 307
Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu Leu Gly Ala Ile Gly
      55                      60                      65

gca cca ggt tcc gtc cct cca gga att ctc gag cgt ggt ttg ctg ctg 355
Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu Arg Gly Leu Leu Leu
      70                      75                      80                      85

aag atg cga ttc gca ctg gat cac cac gtg aac ctg cgc cca tcc aag 403
Lys Met Arg Phe Ala Leu Asp His His Val Asn Leu Arg Pro Ser Lys
      90                      95                      100

```

<210> 272

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

```

Met Lys Leu Ala Val Ile Gly Gly Asp Gly Ile Gly Pro Glu Val Thr
  1                      5                      10                      15

Ala Glu Ala Leu Lys Val Leu Asn Ala Val Arg Asp Asp Ile Glu Thr
      20                      25                      30

Thr Asp Tyr Asp Leu Gly Ala Arg Arg Tyr Leu Lys Asn Gly Glu Leu
      35                      40                      45

Leu Thr Asp Glu Asp Leu Ala Ser Leu Arg Glu His Asp Ala Ile Leu
      50                      55                      60

Leu Gly Ala Ile Gly Ala Pro Gly Ser Val Pro Pro Gly Ile Leu Glu
      65                      70                      75                      80

Arg Gly Leu Leu Leu Lys Met Arg Phe Ala Leu Asp His His Val Asn
      85                      90                      95

Leu Arg Pro Ser Lys
      100

```

<210> 273

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1471)

<223> RXN00536

<400> 273

```

cggcggtgcc cagaggtctt aacacgaccg gcatcccgtc gcggagtgttg gtgttgccgg 60

tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115
Met Ser Pro Asn Asp
      1                      5

```

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc	163
Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg	
10 15 20	
aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
gtt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
gtt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	

ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc 883
 Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser
 250 255 260

att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg 931
 Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275

tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290

ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305

aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325

atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340

cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355

cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370

cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385

cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405

acc cga atg gga ggt tcc tta cct gcc tat cga tcc aaa gga tgt cgg
 1363
 Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg Ser Lys Gly Cys Arg
 410 415 420

tcg cga cta cga ggc tgt tat ccg cgt gaa ctc cca gtc cgg caa ggg
 1411
 Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu Pro Val Arg Gln Gly
 425 430 435

cgg cgt tgc tta cat cat gaa gac cga tca cgg tct gca gat ccc tcg
 1459
 Arg Arg Cys Leu His His Glu Asp Arg Ser Arg Ser Ala Asp Pro Ser
 440 445 450

ctc cat gca ggt tgagttctcc accgttgtcc aga

1494

Leu His Ala Gly

455

<210> 274

<211> 457

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 274

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val
35 40 45

Glu Asp Ile Ser Leu Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr
50 55 60

Val Ala Pro Gln Trp Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala
65 70 75 80

Leu Ile Asp Pro Met Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu
85 90 95

Leu Val Gln Met Gly Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala
100 105 110

Ser Gln Thr Asp Phe Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met
115 120 125

Ile Pro Asp Asp Val Thr Ile Gln Val Leu Val Gln Ala Arg Glu His
130 135 140

Leu Ile Arg Arg Thr Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile
145 150 155 160

Val His Phe Tyr Asn Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe
165 170 175

Arg Met Asp Lys Val Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu
180 185 190

Leu Ile Lys Thr Ile Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp
195 200 205

Gln Tyr Ser Pro Glu Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys
210 215 220

Glu Val Val Asp Ala Val Val Glu Val Met Asp Pro Thr Pro Glu Asn
225 230 235 240

Pro Met Ile Ile Asn Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn
245 250 255

Val Tyr Ala Asp Ser Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg
 260 265 270

Asp Ser Ile Ile Leu Ser Leu His Pro His Asn Asp Arg Gly Thr Gly
 275 280 285

Val Gly Ala Ala Glu Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu
 290 295 300

Gly Cys Leu Phe Gly Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val
 305 310 315 320

Thr Leu Ala Leu Asn Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp
 325 330 335

Phe Thr Asp Ile Arg Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln
 340 345 350

Leu Arg Val Pro Glu Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr
 355 360 365

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
 370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
 385 390 395 400

Glu Gln Leu Arg Asp Thr Arg Met Gly Gly Ser Leu Pro Ala Tyr Arg
 405 410 415

Ser Lys Gly Cys Arg Ser Arg Leu Arg Gly Cys Tyr Pro Arg Glu Leu
 420 425 430

Pro Val Arg Gln Gly Arg Arg Cys Leu His His Glu Asp Arg Ser Arg
 435 440 445

Ser Ala Asp Pro Ser Leu His Ala Gly
 450 455

<210> 275

<211> 1333

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1333)

<223> FRXA00536

<400> 275

cggcgggtcc cagaggtctt aacacgaccg gcatcccgtc gcggagtttg gtgttgccgg 60

tcgtggaccc acccaaaact ttttaagaag gttgaacaca atg tct cct aac gat 115
 Met Ser Pro Asn Asp
 1 5

gca ttc atc tcc gca cct gcc aag atc gaa acc cca gtt ggg cct cgc 163
 Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr Pro Val Gly Pro Arg
 10 15 20

aac gaa ggc cag cca gca tgg aat aag cag cgt ggc tcc tca atg cca	211
Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg Gly Ser Ser Met Pro	
25 30 35	
ggt aac cgc tac atg cct ttc gag gtt gag gta gaa gat att tct ctg	259
Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val Glu Asp Ile Ser Leu	
40 45 50	
ccg gac cgc act tgg cca gat aaa aaa atc acc gtt gca cct cag tgg	307
Pro Asp Arg Thr Trp Pro Asp Lys Lys Ile Thr Val Ala Pro Gln Trp	
55 60 65	
tgt gct gtt gac ctg cgt gac ggc aac cag gct ctg att gat ccg atg	355
Cys Ala Val Asp Leu Arg Asp Gly Asn Gln Ala Leu Ile Asp Pro Met	
70 75 80 85	
tct cct gag cgt aag cgc cgc atg ttt gag ctg ctg gtt cag atg ggc	403
Ser Pro Glu Arg Lys Arg Arg Met Phe Glu Leu Leu Val Gln Met Gly	
90 95 100	
ttc aaa gaa atc gag gtc ggt ttc cct tca gct tcc cag act gat ttt	451
Phe Lys Glu Ile Glu Val Gly Phe Pro Ser Ala Ser Gln Thr Asp Phe	
105 110 115	
gat ttc gtt cgt gag atc atc gaa aag ggc atg atc cct gac gat gtc	499
Asp Phe Val Arg Glu Ile Ile Glu Lys Gly Met Ile Pro Asp Asp Val	
120 125 130	
acc att cag gtt ctg gtt cag gct cgt gag cac ctg att cgc cgt act	547
Thr Ile Gln Val Leu Val Gln Ala Arg Glu His Leu Ile Arg Arg Thr	
135 140 145	
ttt gaa gct tgc gaa ggc gca aaa aac gtt atc gtg cac ttc tac aac	595
Phe Glu Ala Cys Glu Gly Ala Lys Asn Val Ile Val His Phe Tyr Asn	
150 155 160 165	
tcc acc tcc atc ctg cag cgc aac gtg gtg ttc cgc atg gac aag gtg	643
Ser Thr Ser Ile Leu Gln Arg Asn Val Val Phe Arg Met Asp Lys Val	
170 175 180	
cag gtg aag aag ctg gct acc gat gcc gct gaa cta atc aag acc atc	691
Gln Val Lys Lys Leu Ala Thr Asp Ala Ala Glu Leu Ile Lys Thr Ile	
185 190 195	
gct cag gat tac cca gac acc aac tgg cgc tgg cag tac tcc cct gag	739
Ala Gln Asp Tyr Pro Asp Thr Asn Trp Arg Trp Gln Tyr Ser Pro Glu	
200 205 210	
tcc ttc acc ggc act gag gtt gag tac gcc aag gaa gtt gtg gac gca	787
Ser Phe Thr Gly Thr Glu Val Glu Tyr Ala Lys Glu Val Val Asp Ala	
215 220 225	
ggt gtt gag gtc atg gat cca act cct gag aac cca atg atc atc aac	835
Val Val Glu Val Met Asp Pro Thr Pro Glu Asn Pro Met Ile Ile Asn	
230 235 240 245	
ctg cct tcc acc gtt gag atg atc acc cct aac gtt tac gca gac tcc	883
Leu Pro Ser Thr Val Glu Met Ile Thr Pro Asn Val Tyr Ala Asp Ser	
250 255 260	
att gaa tgg atg cac cgc aat cta aac cgt cgt gat tcc att atc ctg	931

Ile Glu Trp Met His Arg Asn Leu Asn Arg Arg Asp Ser Ile Ile Leu
 265 270 275
 tcc ctg cac ccg cac aat gac cgt ggc acc ggc gtt ggc gca gct gag 979
 Ser Leu His Pro His Asn Asp Arg Gly Thr Gly Val Gly Ala Ala Glu
 280 285 290
 ctg ggc tac atg gct ggc gct gac cgc atc gaa ggc tgc ctg ttc ggc
 1027
 Leu Gly Tyr Met Ala Gly Ala Asp Arg Ile Glu Gly Cys Leu Phe Gly
 295 300 305
 aac ggc gag cgc acc ggc aac gtc tgc ctg gtc acc ctg gca ctg aac
 1075
 Asn Gly Glu Arg Thr Gly Asn Val Cys Leu Val Thr Leu Ala Leu Asn
 310 315 320 325
 atg ctg acc cag ggc gtt gac cct cag ctg gac ttc acc gat ata cgc
 1123
 Met Leu Thr Gln Gly Val Asp Pro Gln Leu Asp Phe Thr Asp Ile Arg
 330 335 340
 cag atc cgc agc acc gtt gaa tac tgc aac cag ctg cgc gtt cct gag
 1171
 Gln Ile Arg Ser Thr Val Glu Tyr Cys Asn Gln Leu Arg Val Pro Glu
 345 350 355
 cgc cac cca tac ggc ggt gac ctg gtc ttc acc gct ttc tcc ggt tcc
 1219
 Arg His Pro Tyr Gly Gly Asp Leu Val Phe Thr Ala Phe Ser Gly Ser
 360 365 370
 cac cag gac gct gtg aac aag ggt ctg gac gcc atg gct gcc aag gtt
 1267
 His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala Met Ala Ala Lys Val
 375 380 385
 cag cca ggt gct agc tcc act gaa gtt tct tgg gag cag ctg cgc gac
 1315
 Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp Glu Gln Leu Arg Asp
 390 395 400 405
 acc gaa tgg gag gtt cct
 1333
 Thr Glu Trp Glu Val Pro
 410

<210> 276

<211> 411

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Met Ser Pro Asn Asp Ala Phe Ile Ser Ala Pro Ala Lys Ile Glu Thr
 1 5 10 15

Pro Val Gly Pro Arg Asn Glu Gly Gln Pro Ala Trp Asn Lys Gln Arg
 20 25 30

Gly Ser Ser Met Pro Val Asn Arg Tyr Met Pro Phe Glu Val Glu Val

35					40					45					
Glu	Asp	Ile	Ser	Leu	Pro	Asp	Arg	Thr	Trp	Pro	Asp	Lys	Lys	Ile	Thr
50					55					60					
Val	Ala	Pro	Gln	Trp	Cys	Ala	Val	Asp	Leu	Arg	Asp	Gly	Asn	Gln	Ala
65					70					75					80
Leu	Ile	Asp	Pro	Met	Ser	Pro	Glu	Arg	Lys	Arg	Arg	Met	Phe	Glu	Leu
				85					90					95	
Leu	Val	Gln	Met	Gly	Phe	Lys	Glu	Ile	Glu	Val	Gly	Phe	Pro	Ser	Ala
			100					105					110		
Ser	Gln	Thr	Asp	Phe	Asp	Phe	Val	Arg	Glu	Ile	Ile	Glu	Lys	Gly	Met
		115					120					125			
Ile	Pro	Asp	Asp	Val	Thr	Ile	Gln	Val	Leu	Val	Gln	Ala	Arg	Glu	His
	130					135					140				
Leu	Ile	Arg	Arg	Thr	Phe	Glu	Ala	Cys	Glu	Gly	Ala	Lys	Asn	Val	Ile
145					150					155					160
Val	His	Phe	Tyr	Asn	Ser	Thr	Ser	Ile	Leu	Gln	Arg	Asn	Val	Val	Phe
				165					170					175	
Arg	Met	Asp	Lys	Val	Gln	Val	Lys	Lys	Leu	Ala	Thr	Asp	Ala	Ala	Glu
			180					185					190		
Leu	Ile	Lys	Thr	Ile	Ala	Gln	Asp	Tyr	Pro	Asp	Thr	Asn	Trp	Arg	Trp
		195					200					205			
Gln	Tyr	Ser	Pro	Glu	Ser	Phe	Thr	Gly	Thr	Glu	Val	Glu	Tyr	Ala	Lys
	210					215					220				
Glu	Val	Val	Asp	Ala	Val	Val	Glu	Val	Met	Asp	Pro	Thr	Pro	Glu	Asn
225					230					235					240
Pro	Met	Ile	Ile	Asn	Leu	Pro	Ser	Thr	Val	Glu	Met	Ile	Thr	Pro	Asn
				245					250					255	
Val	Tyr	Ala	Asp	Ser	Ile	Glu	Trp	Met	His	Arg	Asn	Leu	Asn	Arg	Arg
			260					265					270		
Asp	Ser	Ile	Ile	Leu	Ser	Leu	His	Pro	His	Asn	Asp	Arg	Gly	Thr	Gly
		275					280					285			
Val	Gly	Ala	Ala	Glu	Leu	Gly	Tyr	Met	Ala	Gly	Ala	Asp	Arg	Ile	Glu
	290					295					300				
Gly	Cys	Leu	Phe	Gly	Asn	Gly	Glu	Arg	Thr	Gly	Asn	Val	Cys	Leu	Val
305					310					315					320
Thr	Leu	Ala	Leu	Asn	Met	Leu	Thr	Gln	Gly	Val	Asp	Pro	Gln	Leu	Asp
				325					330					335	
Phe	Thr	Asp	Ile	Arg	Gln	Ile	Arg	Ser	Thr	Val	Glu	Tyr	Cys	Asn	Gln
			340					345					350		
Leu	Arg	Val	Pro	Glu	Arg	His	Pro	Tyr	Gly	Gly	Asp	Leu	Val	Phe	Thr
		355					360					365			

Ala Phe Ser Gly Ser His Gln Asp Ala Val Asn Lys Gly Leu Asp Ala
370 375 380

Met Ala Ala Lys Val Gln Pro Gly Ala Ser Ser Thr Glu Val Ser Trp
385 390 395 400

Glu Gln Leu Arg Asp Thr Glu Trp Glu Val Pro
405 410

<210> 277

<211> 714

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(691)

<223> RXN02965

<400> 277

caggaggccg caccacacctg gtatccccag cagtcgcagc cgccaccgaa tccgcggacc 60

ctgtcctcac ctgcagatat ctaaggaagg ctagaaaaca atg gaa aaa ttt acc 115
Met Glu Lys Phe Thr
1 5

acc tac acc ggc gtt ggc gtt cca ctg cag cga tcc aac gtg gac acc 163
Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg Ser Asn Val Asp Thr
10 15 20

gac cag atc atc cca gcc gtc tac ctc aag cgc gtc acc cgg acc ggc 211
Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg Val Thr Arg Thr Gly
25 30 35

ttc gaa gac gga ctg ttt tcc aac tgg cgc caa aac gac ccc aac ttt 259
Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln Asn Asp Pro Asn Phe
40 45 50

gtc ctc aac acc gac acc tac aag aac ggc tcc gtt ctc gta gca ggc 307
Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser Val Leu Val Ala Gly
55 60 65

cct gac ttt ggc acc ggc tcc tcc cgc gag cac gcc gtc tgg gca ctc 355
Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His Ala Val Trp Ala Leu
70 75 80 85

atg gac tac ggc ttc cgc gct gtc ttc tcc tca cga ttc gcc gac atc 403
Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser Arg Phe Ala Asp Ile
90 95 100

ttc cgc ggc aac tcc gga aaa gcg ggc atg ctc acc ggc atc atg gaa 451
Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu Thr Gly Ile Met Glu
105 110 115

cag tcc gac atc gaa ctt ctg tgg aag ctc atg gaa caa acc cca ggc 499
Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met Glu Gln Thr Pro Gly
120 125 130

ctc gaa ctg acc gtg aac ctg gaa aag cag atc gtc acc gca ggc gac 547

Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile Val Thr Ala Gly Asp
 135 140 145
 gta gtg atc agc ttc gaa gtt gac ccc tac atc cgc tgg cgt ttg atg 595
 Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile Arg Trp Arg Leu Met
 150 155 160 165
 gaa ggc ctc gac gac gct ggc ctg acc ctg cgc aag ctc gat gaa att 643
 Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg Lys Leu Asp Glu Ile
 170 175 180
 gaa gac tac gag gct aag cgc cct gcg ttt aag cca cgc act aac gct 691
 Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys Pro Arg Thr Asn Ala
 185 190 195
 taagtttcag tctgatagcg aaa 714

<210> 278

<211> 197

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 278

Met Glu Lys Phe Thr Thr Tyr Thr Gly Val Gly Val Pro Leu Gln Arg
 1 5 10 15
 Ser Asn Val Asp Thr Asp Gln Ile Ile Pro Ala Val Tyr Leu Lys Arg
 20 25 30
 Val Thr Arg Thr Gly Phe Glu Asp Gly Leu Phe Ser Asn Trp Arg Gln
 35 40 45
 Asn Asp Pro Asn Phe Val Leu Asn Thr Asp Thr Tyr Lys Asn Gly Ser
 50 55 60
 Val Leu Val Ala Gly Pro Asp Phe Gly Thr Gly Ser Ser Arg Glu His
 65 70 75 80
 Ala Val Trp Ala Leu Met Asp Tyr Gly Phe Arg Ala Val Phe Ser Ser
 85 90 95
 Arg Phe Ala Asp Ile Phe Arg Gly Asn Ser Gly Lys Ala Gly Met Leu
 100 105 110
 Thr Gly Ile Met Glu Gln Ser Asp Ile Glu Leu Leu Trp Lys Leu Met
 115 120 125
 Glu Gln Thr Pro Gly Leu Glu Leu Thr Val Asn Leu Glu Lys Gln Ile
 130 135 140
 Val Thr Ala Gly Asp Val Val Ile Ser Phe Glu Val Asp Pro Tyr Ile
 145 150 155 160
 Arg Trp Arg Leu Met Glu Gly Leu Asp Asp Ala Gly Leu Thr Leu Arg
 165 170 175
 Lys Leu Asp Glu Ile Glu Asp Tyr Glu Ala Lys Arg Pro Ala Phe Lys
 180 185 190
 Pro Arg Thr Asn Ala

195

```
<210> 279
<211> 936
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(913)
<223> RXN01929
```

<400> 279																
aaaatttgac tccataacga gaacttaatc gagcaacacc cctgaacagt gaatcaaatc 60																
ggaattttatt tattctgagc tgggtcatcac atctatactc atg ccc atg tca ggc 115																
Met Pro Met Ser Gly 1 5																
att gat gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta 163																
Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val 10 15 20																
aac ggc cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg 211																
Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala 25 30 35																
cgc att ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc 259																
Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser 40 45 50																
gct gcc aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg 307																
Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu 55 60 65																
gat gag atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt 355																
Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala Thr Lys Arg 70 75 80 85																
gcg ctt gtg gtg gtt gat ctg ccg ttt ggt acc tat gag gtg agc cca 403																
Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu Val Ser Pro 90 95 100																
aat cag gcg gtg gag tcc gcg atc cgg gtc atg cgt gaa acg ggt gcg 451																
Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu Thr Gly Ala 105 110 115																
gct gcg gtg aag atc gag ggt ggc gtg gag atc gcg cag acg att cga 499																
Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln Thr Ile Arg 120 125 130																
cgc att gtt gat gct gga att ccg gtt gtc ggc cac atc ggg tac acc 547																
Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile Gly Tyr Thr 135 140 145																
ccg cag tcc gag cat tcc ttg ggc ggc cac gtg gtt cag ggt cgt ggc 595																
Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln Gly Arg Gly 150 155 160 165																
gcg agt tct gga aag ctc atc gcc gat gcc cgc gcg ttg gag cag gcg 643																

Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu Glu Gln Ala
 170 175 180

ggt gcg ttt gcg gtt gtg ttg gag atg gtt cca gca gag gca gcg cgc 691
 Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu Ala Ala Arg
 185 190 195

gag gtt acc gag gat ctt tcc atc acc act atc gga atc ggt gcc ggc 739
 Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile Gly Ala Gly
 200 205 210

aat ggc aca gat ggg cag gtt ttg gtg tgg cag gat gcc ttc ggc ctc 787
 Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala Phe Gly Leu
 215 220 225

aac cgc ggc aag aag cca cgc ttc gtc cgc gag tac gcc acc ttg ggc 835
 Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala Thr Leu Gly
 230 235 240 245

gat tcc ttg cac gac gcc gcg cag gcc tac atc gcc gat atc cac gcg 883
 Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp Ile His Ala
 250 255 260

ggt acc ttc cca ggc gaa gcg gag tcc ttt taatgcaggt agcaaccaca 933
 Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 265 270

aag 936

<210> 280

<211> 271

<212> PRT

<213> Corynebacterium glutamicum

<400> 280

Met Pro Met Ser Gly Ile Asp Ala Lys Lys Ile Arg Thr Arg His Phe
 1 5 10 15

Arg Glu Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr
 20 25 30

Asp Ala Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu
 35 40 45

Leu Val Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr
 50 55 60

Leu Ser Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr
 65 70 75 80

Ile Ala Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr
 85 90 95

Tyr Glu Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met
 100 105 110

Arg Glu Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile
 115 120 125

Ala Gln Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly

130	135	140
His Ile Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val 145 150 155 160		
Val Gln Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg 165 170 175		
Ala Leu Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro 180 185 190		
Ala Glu Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile 195 200 205		
Gly Ile Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln 210 215 220		
Asp Ala Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu 225 230 235 240		
Tyr Ala Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile 245 250 255		
Ala Asp Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe 260 265 270		

<210> 281
 <211> 930
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(907)
 <223> FRXA01929

<400> 281
 tgactccata acgagaactt aatcgagcaa caccctgaa cagtgaatca aatcggaatt 60
 tatttattct gagctgggtca tcacatctat actcatgccc atg tca ggc att gat 115
 Met Ser Gly Ile Asp
 1 5
 gca aag aaa atc cgc acc cgt cat ttc cgc gaa gct aaa gta aac ggc 163
 Ala Lys Lys Ile Arg Thr Arg His Phe Arg Glu Ala Lys Val Asn Gly
 10 15 20
 cag aaa gtt tcg gtt ctc acc agc tat gat gcg ctt tcg gcg cgc att 211
 Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala Leu Ser Ala Arg Ile
 25 30 35
 ttt gat gag gct ggc gtc gat atg ctc ctt gtt ggt gat tcc gct gcc 259
 Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val Gly Asp Ser Ala Ala
 40 45 50
 aac gtt gtg ctg ggt cgc gat acc acc ttg tcg atc acc ttg gat gag 307
 Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser Ile Thr Leu Asp Glu
 55 60 65
 atg att gtg ctg gcc aag gcg gtg acg atc gct acg aag cgt gcg ctt 355

Met	Ile	Val	Leu	Ala	Lys	Ala	Val	Thr	Ile	Ala	Thr	Lys	Arg	Ala	Leu		
70					75					80					85		
gtg	gtg	gtt	gat	ctg	ccg	ttt	ggg	acc	tat	gag	gtg	agc	cca	aat	cag	403	
Val	Val	Val	Asp	Leu	Pro	Phe	Gly	Thr	Tyr	Glu	Val	Ser	Pro	Asn	Gln		
				90				95						100			
gcg	gtg	gag	tcc	gcg	atc	cgg	gtc	atg	cgt	gaa	acg	ggg	gcg	gct	gcg	451	
Ala	Val	Glu	Ser	Ala	Ile	Arg	Val	Met	Arg	Glu	Thr	Gly	Ala	Ala	Ala		
			105					110					115				
gtg	aag	atc	gag	ggg	ggc	gtg	gag	atc	gcg	cag	acg	att	cga	cgc	att	499	
Val	Lys	Ile	Glu	Gly	Gly	Val	Glu	Ile	Ala	Gln	Thr	Ile	Arg	Arg	Ile		
		120					125					130					
gtt	gat	gct	gga	att	ccg	gtt	gtc	ggc	cac	atc	ggg	tac	acc	ccg	cag	547	
Val	Asp	Ala	Gly	Ile	Pro	Val	Val	Gly	His	Ile	Gly	Tyr	Thr	Pro	Gln		
	135					140					145						
tcc	gag	cat	tcc	ttg	ggc	ggc	cac	gtg	gtt	cag	ggg	cgt	ggc	gcg	agt	595	
Ser	Glu	His	Ser	Leu	Gly	Gly	His	Val	Val	Gln	Gly	Arg	Gly	Ala	Ser		
150					155					160					165		
tct	gga	aag	ctc	atc	gcc	gat	gcc	cgc	gcg	ttg	gag	cag	gcg	ggg	gcg	643	
Ser	Gly	Lys	Leu	Ile	Ala	Asp	Ala	Arg	Ala	Leu	Glu	Gln	Ala	Gly	Ala		
			170					175						180			
ttt	gcg	gtt	gtg	ttg	gag	atg	gtt	cca	gca	gag	gca	gcg	cgc	gag	gtt	691	
Phe	Ala	Val	Val	Leu	Glu	Met	Val	Pro	Ala	Glu	Ala	Ala	Arg	Glu	Val		
			185					190					195				
acc	gag	gat	ctt	tcc	atc	acc	act	atc	gga	atc	ggg	gcc	ggc	aat	ggc	739	
Thr	Glu	Asp	Leu	Ser	Ile	Thr	Thr	Ile	Gly	Ile	Gly	Ala	Gly	Asn	Gly		
		200					205					210					
aca	gat	ggg	cag	gtt	ttg	gtg	tgg	cag	gat	gcc	ttc	ggc	ctc	aac	cgc	787	
Thr	Asp	Gly	Gln	Val	Leu	Val	Trp	Gln	Asp	Ala	Phe	Gly	Leu	Asn	Arg		
	215					220					225						
ggc	aag	aag	cca	cgc	ttc	gtc	cgc	gag	tac	gcc	acc	ttg	ggc	gat	tcc	835	
Gly	Lys	Lys	Pro	Arg	Phe	Val	Arg	Glu	Tyr	Ala	Thr	Leu	Gly	Asp	Ser		
230					235					240					245		
ttg	cac	gac	gcc	gcg	cag	gcc	tac	atc	gcc	gat	atc	cac	gcg	ggg	acc	883	
Leu	His	Asp	Ala	Ala	Gln	Ala	Tyr	Ile	Ala	Asp	Ile	His	Ala	Gly	Thr		
			250					255						260			
ttc	cca	ggc	gaa	gcg	gag	tcc	ttt	taatgcaggt	agcaaccaca	aag						930	
Phe	Pro	Gly	Glu	Ala	Glu	Ser	Phe										
			265														

<210> 282

<211> 269

<212> PRT

<213> Corynebacterium glutamicum

<400> 282

Met	Ser	Gly	Ile	Asp	Ala	Lys	Lys	Ile	Arg	Thr	Arg	His	Phe	Arg	Glu
1					5				10					15	

Ala Lys Val Asn Gly Gln Lys Val Ser Val Leu Thr Ser Tyr Asp Ala
 20 25 30
 Leu Ser Ala Arg Ile Phe Asp Glu Ala Gly Val Asp Met Leu Leu Val
 35 40 45
 Gly Asp Ser Ala Ala Asn Val Val Leu Gly Arg Asp Thr Thr Leu Ser
 50 55 60
 Ile Thr Leu Asp Glu Met Ile Val Leu Ala Lys Ala Val Thr Ile Ala
 65 70 75 80
 Thr Lys Arg Ala Leu Val Val Val Asp Leu Pro Phe Gly Thr Tyr Glu
 85 90 95
 Val Ser Pro Asn Gln Ala Val Glu Ser Ala Ile Arg Val Met Arg Glu
 100 105 110
 Thr Gly Ala Ala Ala Val Lys Ile Glu Gly Gly Val Glu Ile Ala Gln
 115 120 125
 Thr Ile Arg Arg Ile Val Asp Ala Gly Ile Pro Val Val Gly His Ile
 130 135 140
 Gly Tyr Thr Pro Gln Ser Glu His Ser Leu Gly Gly His Val Val Gln
 145 150 155 160
 Gly Arg Gly Ala Ser Ser Gly Lys Leu Ile Ala Asp Ala Arg Ala Leu
 165 170 175
 Glu Gln Ala Gly Ala Phe Ala Val Val Leu Glu Met Val Pro Ala Glu
 180 185 190
 Ala Ala Arg Glu Val Thr Glu Asp Leu Ser Ile Thr Thr Ile Gly Ile
 195 200 205
 Gly Ala Gly Asn Gly Thr Asp Gly Gln Val Leu Val Trp Gln Asp Ala
 210 215 220
 Phe Gly Leu Asn Arg Gly Lys Lys Pro Arg Phe Val Arg Glu Tyr Ala
 225 230 235 240
 Thr Leu Gly Asp Ser Leu His Asp Ala Ala Gln Ala Tyr Ile Ala Asp
 245 250 255
 Ile His Ala Gly Thr Phe Pro Gly Glu Ala Glu Ser Phe
 260 265

<210> 283

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXN01420

<400> 283

cgaagttcac gactacaggc attacctggg tgctgatttt gcgcgagtaa agctgtggct 60

gcggaatgcg	ctgctcatcc	acacgtggaa	tcctgattgg	gtg	acg	ctg	ggg	gga	115
				Val	Thr	Leu	Gly	Gly	
				1				5	
ttg	aat	gta	cca	tcg	tgg	tcg	ctg	ggc	163
Leu	Asn	Val	Pro	Ser	Trp	Ser	Leu	Gly	
				10				15	
acg	ttc	ccg	ctg	ttt	att	ccg	tta	gtg	211
Thr	Phe	Pro	Leu	Phe	Ile	Pro	Leu	Val	
				25				30	
aac	tgg	tgg	gca	ttt	ggc	atc	acc	ttt	259
Asn	Trp	Trp	Ala	Phe	Gly	Ile	Thr	Phe	
				40				45	
aca	gtg	att	cac	ttt	tat	gcg	gac	gga	307
Thr	Val	Ile	His	Phe	Tyr	Ala	Asp	Gly	
				55				60	
ttt	gtt	cct	cg	ctg	tgg	gac	acc	aat	355
Phe	Val	Pro	Arg	Leu	Trp	Asp	Thr	Asn	
				70				75	
cac	gcc	gat	cca	gtg	tgg	ttt	atg	cag	403
His	Ala	Asp	Pro	Val	Trp	Phe	Met	Gln	
				90				95	
tct	tac	tgg	ctg	tct	tac	tac	ttc	ccg	451
Ser	Tyr	Trp	Leu	Ser	Tyr	Tyr	Phe	Pro	
				105				110	
tac	ctc	ggg	gtg	ttt	ggc	gcg	aag	ctg	499
Tyr	Leu	Gly	Val	Phe	Gly	Ala	Lys	Leu	
				120				125	
aac	acc	aac	atc	acc	atc	ccg	ctg	atc	547
Asn	Thr	Asn	Ile	Thr	Ile	Pro	Leu	Ile	
				135				140	
gct	act	tgg	ttt	gtg	cca	ctg	gca	ttc	595
Ala	Thr	Trp	Phe	Val	Pro	Leu	Ala	Phe	
				150				155	
ctg	cca	atg	gct	ttt	gtt	gtg	gca	acg	643
Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	
				170				175	
ggc	aag	agt	ggg	gaa	atc	gcc	tcg	cct	691
Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	
				185				190	
att	tcc	ttt	gcc	ttc	tac	atg	gtg	caa	739
Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	
				200				205	
cag	cg	tat	ttc	att	gct	ggc	aaa	gaa	787
Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	
				215				220	

ttc tat gca gtg gtg tgt ttc atc gtg tcg gtc att ctc gcg tgg gtg 835
 Phe Tyr Ala Val Val Cys Phe Ile Val Ser Val Ile Leu Ala Trp Val
 230 235 240 245

 ctg ttt acc ttc gtt gat gat cct ttg atg aag gcc acg gcg cgc aag 883
 Leu Phe Thr Phe Val Asp Asp Pro Leu Met Lys Ala Thr Ala Arg Lys
 250 255 260

 aag ggg agt agg cgc ttg aag cag tcc aat att ttg gtc cgt gac ctg 931
 Lys Gly Ser Arg Arg Leu Lys Gln Ser Asn Ile Leu Val Arg Asp Leu
 265 270 275

 aaa gtt ctc ttc ggc aaa agc ccc gaa aag ccg tta aaa gtt gag act 979
 Lys Val Leu Phe Gly Lys Ser Pro Glu Lys Pro Leu Lys Val Glu Thr
 280 285 290

 cgc gct gag aat ctc aca gaa aac tcc gaa gct ccc gct aag gta gct
 1027
 Arg Ala Glu Asn Leu Thr Glu Asn Ser Glu Ala Pro Ala Lys Val Ala
 295 300 305

 acc gga atc aaa tct tagggaagga aaacatatgg cta
 1065
 Thr Gly Ile Lys Ser
 310

<210> 284

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 284

Val Thr Leu Gly Gly Leu Asn Val Pro Ser Trp Ser Leu Gly Ala Glu
 1 5 10 15

 Met Leu Phe Tyr Leu Thr Phe Pro Leu Phe Ile Pro Leu Val Arg Lys
 20 25 30

 Val Lys Gly Val Gly Asn Trp Trp Ala Phe Gly Ile Thr Phe Ala Val
 35 40 45

 Ser Leu Ala Leu Ile Thr Val Ile His Phe Tyr Ala Asp Gly Pro Lys
 50 55 60

 Gly Ile Glu Asn Phe Phe Val Pro Arg Leu Trp Asp Thr Asn Val Ser
 65 70 75 80

 Pro Val Ala Glu Val His Ala Asp Pro Val Trp Phe Met Gln Glu Glu
 85 90 95

 Ile Pro Val Leu Glu Ser Tyr Trp Leu Ser Tyr Tyr Phe Pro Leu Thr
 100 105 110

 Arg Leu Ile Glu Phe Tyr Leu Gly Val Phe Gly Ala Lys Leu Val Ala
 115 120 125

 Glu Gly Met Phe Lys Asn Thr Asn Ile Thr Ile Pro Leu Ile Ala Leu
 130 135 140

 Ala Val Ser Phe Val Ala Thr Trp Phe Val Pro Leu Ala Phe Lys Met

145				150				155				160			
Ser	Val	Ile	Met	Ser	Leu	Pro	Met	Ala	Phe	Val	Val	Ala	Thr	Leu	Ala
165								170				175			
Val	Arg	Asp	Ile	Glu	Gly	Lys	Ser	Gly	Glu	Ile	Ala	Ser	Pro	Arg	Ala
180								185				190			
Val	Leu	Leu	Gly	Asn	Ile	Ser	Phe	Ala	Phe	Tyr	Met	Val	Gln	Phe	Pro
195								200				205			
Val	Met	Val	Phe	Val	Gln	Arg	Tyr	Phe	Ile	Ala	Gly	Lys	Glu	Tyr	Gly
210												220			
Phe	Leu	Gly	Trp	Ala	Phe	Tyr	Ala	Val	Val	Cys	Phe	Ile	Val	Ser	Val
225												235			
Ile	Leu	Ala	Trp	Val	Leu	Phe	Thr	Phe	Val	Asp	Asp	Pro	Leu	Met	Lys
												245			
Ala	Thr	Ala	Arg	Lys	Lys	Gly	Ser	Arg	Arg	Leu	Lys	Gln	Ser	Asn	Ile
												260			
Leu	Val	Arg	Asp	Leu	Lys	Val	Leu	Phe	Gly	Lys	Ser	Pro	Glu	Lys	Pro
												275			
Leu	Lys	Val	Glu	Thr	Arg	Ala	Glu	Asn	Leu	Thr	Glu	Asn	Ser	Glu	Ala
												290			
Pro	Ala	Lys	Val	Ala	Thr	Gly	Ile	Lys	Ser						
												305			
												310			

```
<210> 285
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1114)
<223> RXS01145
```

```

<400> 285
taatgtagtt gtctgcccac gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60

cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
Met Ala Ile Glu Leu
1 5

ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
10 15 20

gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
25 30 35

cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
40 45 50

```

tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct	307
Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala	
55 60 65	
gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc	355
Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr	
70 75 80 85	
tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca	403
Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala	
90 95 100	
ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg	451
Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu	
105 110 115	
atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc	499
Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly	
120 125 130	
cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct	547
Pro Gly His Leu Val Arg Arg Gln Phe Val Asp Gly Lys Gly Val Pro	
135 140 145	
tgc ctc atc gca gtc gac cag gac cca acc gga acc gca cag gct ctg	595
Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly Thr Ala Gln Ala Leu	
150 155 160 165	
acc ctg tcc tac gca gca gca atc ggt ggc gca cgc gca ggc gtt atc	643
Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala Arg Ala Gly Val Ile	
170 175 180	
cca acc acc ttc gaa gct gag acc gtc acc gac ctc ttc ggc gag cag	691
Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp Leu Phe Gly Glu Gln	
185 190 195	
gct gtt ctc tgc ggt ggc acc gag gaa ctg gtc aag gtt ggc ttc gag	739
Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val Lys Val Gly Phe Glu	
200 205 210	
gtt ctc acc gaa gct ggc tac gag cca gag atg gca tac ttc gag gtt	787
Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met Ala Tyr Phe Glu Val	
215 220 225	
ctt cac gag ctc aag ctc atc gtt gac ctc atg ttc gaa ggt ggc atc	835
Leu His Glu Leu Lys Leu Ile Val Asp Leu Met Phe Glu Gly Gly Ile	
230 235 240 245	
agc aac atg aac tac tct gtt tct gac acc gct gag ttc ggt ggc tac	883
Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala Glu Phe Gly Gly Tyr	
250 255 260	
ctc tcc ggc cca cgc gtc atc gat gca gac acc aag tcc cgc atg aag	931
Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr Lys Ser Arg Met Lys	
265 270 275	
gac atc ctg acc gat atc cag gac ggc acc ttc acc aag cgc ctc atc	979
Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe Thr Lys Arg Leu Ile	
280 285 290	

gca aac gtt gag aac ggc aac acc gag ctt gag ggc ctt cgt gct tcc
1027

Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu Gly Leu Arg Ala Ser
295 300 305

tac aac aac cac cca atc gag gag acc ggc gct aag ctc cgc gac ctc
1075

Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala Lys Leu Arg Asp Leu
310 315 320 325

atg agc tgg gtc aag gtt gac gct cgc gca gaa acc gct taagtttcac
1124

Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu Thr Ala
330 335

ccctttgacg gct
1137

<210> 286

<211> 338

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
130 135 140

Gly Lys Gly Val Pro Cys Leu Ile Ala Val Asp Gln Asp Pro Thr Gly
145 150 155 160

Thr Ala Gln Ala Leu Thr Leu Ser Tyr Ala Ala Ala Ile Gly Gly Ala
165 170 175

Arg Ala Gly Val Ile Pro Thr Thr Phe Glu Ala Glu Thr Val Thr Asp
180 185 190

Leu Phe Gly Glu Gln Ala Val Leu Cys Gly Gly Thr Glu Glu Leu Val
 195 200 205
 Lys Val Gly Phe Glu Val Leu Thr Glu Ala Gly Tyr Glu Pro Glu Met
 210 215 220
 Ala Tyr Phe Glu Val Leu His Glu Leu Lys Leu Ile Val Asp Leu Met
 225 230 235 240
 Phe Glu Gly Gly Ile Ser Asn Met Asn Tyr Ser Val Ser Asp Thr Ala
 245 250 255
 Glu Phe Gly Gly Tyr Leu Ser Gly Pro Arg Val Ile Asp Ala Asp Thr
 260 265 270
 Lys Ser Arg Met Lys Asp Ile Leu Thr Asp Ile Gln Asp Gly Thr Phe
 275 280 285
 Thr Lys Arg Leu Ile Ala Asn Val Glu Asn Gly Asn Thr Glu Leu Glu
 290 295 300
 Gly Leu Arg Ala Ser Tyr Asn Asn His Pro Ile Glu Glu Thr Gly Ala
 305 310 315 320
 Lys Leu Arg Asp Leu Met Ser Trp Val Lys Val Asp Ala Arg Ala Glu
 325 330 335
 Thr Ala

<210> 287
 <211> 556
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(556)
 <223> FRXA01145

<400> 287
 taatgtagtt gtctgcccac gcgagttaaa ctcccacgat ttacagtggg gggcagacat 60
 cttttcacca aaatttttac gaaaggcgag attttctccc atg gct att gaa ctg 115
 Met Ala Ile Glu Leu
 1 5
 ctt tat gat gct gac gct gac ctc tcc ttg atc cag ggc cgt aag gtt 163
 Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile Gln Gly Arg Lys Val
 10 15 20
 gcc atc gtt ggc tac ggc tcc cag ggc cac gca cac tcc cag aac ctc 211
 Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala His Ser Gln Asn Leu
 25 30 35
 cgc gat tct ggc gtt gag gtt gtc att ggt ctg cgc gag ggc tcc aag 259
 Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu Arg Glu Gly Ser Lys
 40 45 50
 tcc gca gag aag gca aag gaa gca ggc ttc gag gtc aag acc acc gct 307

Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu Val Lys Thr Thr Ala
 55 60 65

gag gct gca gct tgg gct gac gtc atc atg ctc ctg gct cca gac acc 355
 Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu Leu Ala Pro Asp Thr
 70 75 80 85

tcc cag gca gaa atc ttc acc aac gac atc gag cca aac ctg aac gca 403
 Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu Pro Asn Leu Asn Ala
 90 95 100

ggc gac gca ctg ctg ttc ggc cac ggc ctg aac att cac ttc gac ctg 451
 Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn Ile His Phe Asp Leu
 105 110 115

atc aag cca gct gac gac atc atc gtt ggc atg gtt gcg cca aag ggc 499
 Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met Val Ala Pro Lys Gly
 120 125 130

cca ggc cac ttg gtt cgc cgt cag ttc gtt gat ggc aag ggt gtt cct 547
 Pro Gly His Leu Val Arg Gln Phe Val Asp Gly Lys Gly Val Pro
 135 140 145

tgc ctc atc 556
 Cys Leu Ile
 150

<210> 288

<211> 152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 288

Met Ala Ile Glu Leu Leu Tyr Asp Ala Asp Ala Asp Leu Ser Leu Ile
 1 5 10 15

Gln Gly Arg Lys Val Ala Ile Val Gly Tyr Gly Ser Gln Gly His Ala
 20 25 30

His Ser Gln Asn Leu Arg Asp Ser Gly Val Glu Val Val Ile Gly Leu
 35 40 45

Arg Glu Gly Ser Lys Ser Ala Glu Lys Ala Lys Glu Ala Gly Phe Glu
 50 55 60

Val Lys Thr Thr Ala Glu Ala Ala Ala Trp Ala Asp Val Ile Met Leu
 65 70 75 80

Leu Ala Pro Asp Thr Ser Gln Ala Glu Ile Phe Thr Asn Asp Ile Glu
 85 90 95

Pro Asn Leu Asn Ala Gly Asp Ala Leu Leu Phe Gly His Gly Leu Asn
 100 105 110

Ile His Phe Asp Leu Ile Lys Pro Ala Asp Asp Ile Ile Val Gly Met
 115 120 125

Val Ala Pro Lys Gly Pro Gly His Leu Val Arg Arg Gln Phe Val Asp
 130 135 140

Gly Lys Gly Val Pro Cys Leu Ile
145 150

<210> 289

<211> 1350

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02375

<400> 289

cttttcaggt ctacgtgtat acgatggtaa cgctatgaat gatacgcaga acacacctga 60

aagcgttcga ttacgggata atctcccaac gccaacccaa atg gcg ccg gtg aca 115
Met Ala Pro Val Thr
1 5

ggg ctt cct gtc acc ccc tac agc cag gaa gca agc atc ggt gcg agc 163
Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala Ser Ile Gly Ala Ser
10 15 20

ttc ccg gca gtg gat ccg gac acc aaa gac agc gcc gca tac gga cat 211
Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser Ala Ala Tyr Gly His
25 30 35

gaa tcc gga atg cgt gag cgc atc tcc aac gct aag cga gtg gtg gtg 259
Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala Lys Arg Val Val Val
40 45 50

aaa att ggt tcg tcc tca ttg act aac gat gag gac gga cac acc gtc 307
Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu Asp Gly His Thr Val
55 60 65

gat ccc aac cgc atc aac act att gtc aat gcc ttg caa gca cgc atg 355
Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala Leu Gln Ala Arg Met
70 75 80 85

gaa gct ggc tcg gac ctc atc gtt gtg tcc tct ggc gca gtg gcc gcg 403
Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser Gly Ala Val Ala Ala
90 95 100

gga atg gcc ccg ctt gga ttg agc acc cgg ccc acg gaa ttg gca gtc 451
Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro Thr Glu Leu Ala Val
105 110 115

aag cag gct gca gca gca gtg ggg caa gtt cac ctc atg cac cag tgg 499
Lys Gln Ala Ala Ala Val Gly Gln Val His Leu Met His Gln Trp
120 125 130

gga cgt tct ttt gcc cgg tat ggt cgc ccc atc ggc cag gtg ctt ctt 547
Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile Gly Gln Val Leu Leu
135 140 145

acc gca gct gat gca gga aag cgt gat cgt gcg agg aat gcg cag cgt 595
Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala Arg Asn Ala Gln Arg
150 155 160 165

acc atc gac aag ctg cgc att ttg ggc gcg gtt cct atc gtc aat gaa	643
Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val Pro Ile Val Asn Glu	
170 175 180	
aat gac acc gtg gca acc acc ggt gtg aat ttt ggt gac aac gac cga	691
Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe Gly Asp Asn Asp Arg	
185 190 195	
ctt gct gca att gtg gcg cac ctg gtg tct gct gat gct ttg gtg ctg	739
Leu Ala Ala Ile Val Ala His Leu Val Ser Ala Asp Ala Leu Val Leu	
200 205 210	
ctc agt gac gtg gat gga ctt ttt gat aaa aac cct act gat ccc acc	787
Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn Pro Thr Asp Pro Thr	
215 220 225	
gcg aag ttt att tcc gag gtt cgt gac ggc aat gat ttg aaa ggt gtc	835
Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn Asp Leu Lys Gly Val	
230 235 240 245	
att gcc ggc gac ggc gga aaa gtg ggc acc ggt ggc atg gca tca aag	883
Ile Ala Gly Asp Gly Gly Lys Val Gly Thr Gly Gly Met Ala Ser Lys	
250 255 260	
gtg tct gct gca cgt ttg gct tcc cga agt ggc gtg cct gtg ctg ttg	931
Val Ser Ala Ala Arg Leu Ala Ser Arg Ser Gly Val Pro Val Leu Leu	
265 270 275	
acc tct gcg gca aac att ggc cca gca ctg gaa gac gcc cag gtg ggc	979
Thr Ser Ala Ala Asn Ile Gly Pro Ala Leu Glu Asp Ala Gln Val Gly	
280 285 290	
act gta ttc cac ccc aag gac aac cgc ctc tcc gcg tgg aag ttc tgg	
1027	
Thr Val Phe His Pro Lys Asp Asn Arg Leu Ser Ala Trp Lys Phe Trp	
295 300 305	
gct ttg tat gcc gca gat act gca gga aag atc cga ctc gat gac ggc	
1075	
Ala Leu Tyr Ala Ala Asp Thr Ala Gly Lys Ile Arg Leu Asp Asp Gly	
310 315 320 325	
gcg gtg gaa gca gtg acc tcc ggt ggt aaa tct ttg ctg gct gtg ggc	
1123	
Ala Val Glu Ala Val Thr Ser Gly Gly Lys Ser Leu Leu Ala Val Gly	
330 335 340	
att act gaa atc att ggt gat ttc cag cag ggt gag atc gtg gag atc	
1171	
Ile Thr Glu Ile Ile Gly Asp Phe Gln Gln Gly Glu Ile Val Glu Ile	
345 350 355	
ttg gga cct gcc ggc caa atc atc ggg cga ggc gag gtg tcc tac gat	
1219	
Leu Gly Pro Ala Gly Gln Ile Ile Gly Arg Gly Glu Val Ser Tyr Asp	
360 365 370	
tct gat acc ttg caa tca atg gtt ggt atg caa acg cag gac ctt cca	
1267	
Ser Asp Thr Leu Gln Ser Met Val Gly Met Gln Thr Gln Asp Leu Pro	
375 380 385	

gat ggc atg cag cgc ccg gta gtg cat gca gat tat ctg tcc aac tac
1315

Asp Gly Met Gln Arg Pro Val Val His Ala Asp Tyr Leu Ser Asn Tyr
390 395 400 405

gcc agc cgc gcg taaagcgcgg gcctgctggt ggc
1350

Ala Ser Arg Ala

<210> 290

<211> 409

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 290

Met Ala Pro Val Thr Gly Leu Pro Val Thr Pro Tyr Ser Gln Glu Ala
1 5 10 15

Ser Ile Gly Ala Ser Phe Pro Ala Val Asp Pro Asp Thr Lys Asp Ser
20 25 30

Ala Ala Tyr Gly His Glu Ser Gly Met Arg Glu Arg Ile Ser Asn Ala
35 40 45

Lys Arg Val Val Val Lys Ile Gly Ser Ser Ser Leu Thr Asn Asp Glu
50 55 60

Asp Gly His Thr Val Asp Pro Asn Arg Ile Asn Thr Ile Val Asn Ala
65 70 75 80

Leu Gln Ala Arg Met Glu Ala Gly Ser Asp Leu Ile Val Val Ser Ser
85 90 95

Gly Ala Val Ala Ala Gly Met Ala Pro Leu Gly Leu Ser Thr Arg Pro
100 105 110

Thr Glu Leu Ala Val Lys Gln Ala Ala Ala Ala Val Gly Gln Val His
115 120 125

Leu Met His Gln Trp Gly Arg Ser Phe Ala Arg Tyr Gly Arg Pro Ile
130 135 140

Gly Gln Val Leu Leu Thr Ala Ala Asp Ala Gly Lys Arg Asp Arg Ala
145 150 155 160

Arg Asn Ala Gln Arg Thr Ile Asp Lys Leu Arg Ile Leu Gly Ala Val
165 170 175

Pro Ile Val Asn Glu Asn Asp Thr Val Ala Thr Thr Gly Val Asn Phe
180 185 190

Gly Asp Asn Asp Arg Leu Ala Ala Ile Val Ala His Leu Val Ser Ala
195 200 205

Asp Ala Leu Val Leu Leu Ser Asp Val Asp Gly Leu Phe Asp Lys Asn
210 215 220

Pro Thr Asp Pro Thr Ala Lys Phe Ile Ser Glu Val Arg Asp Gly Asn

```
<210> 291 .
<211> 1419
<212> DNA
<213> Corynebacterium glutamicum
```

```

<400> 291
gagcagatgg ccaccgaggt cgatgtgggtg gctggctact aggcctttta tgggtgtgatc 60
cgacactgtt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
Met Ser Ser Thr Thr
1 5
cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
10 15 20
aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
25 30 35

```

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt	259
Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val	
40 45 50	
gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg	307
Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala	
55 60 65	
ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt	355
Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu	
70 75 80 85	
gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct	403
Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala	
90 95 100	
ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa	451
Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu	
105 110 115	
aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc	499
Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly	
120 125 130	
atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg	547
Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu	
135 140 145	
gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct	595
Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala	
150 155 160 165	
gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gtc ctc gag	643
Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu	
170 175 180	
cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg cct tgc caa acc	691
Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Pro Cys Gln Thr	
185 190 195	
cgc gga tcc gtc caa gat ttg atc acc gca cgc ggc ctc gtt gac gtg	739
Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg Gly Leu Val Asp Val	
200 205 210	
gtc atc cca cgc ggc ggc gca gga cta atc aac gca gtg gtc acc ggt	787
Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn Ala Val Val Thr Gly	
215 220 225	
gcg acc gtg ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac	835
Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr	
230 235 240 245	
atc gat gcc gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac	883
Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn	
250 255 260	
ggc aag acc cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt	931
Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu	
265 270 275	
ctc gac gcc gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg	979

Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala
 280 285 290

ctc cag gaa gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa
 1027

Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu
 295 300 305

gca ttc ggt gca acc gac gtg gtg gaa gca act gaa act gac tgg gat
 1075

Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp
 310 315 320 325

tct gag tac ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg
 1123

Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val
 330 335 340

gat gga gct ctg gca cac atc gct aag tac agc acc aag cac acc gaa
 1171

Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu
 345 350 355

gcg atc gcc acc caa aac att gaa acc gct cag cgc ttt gca gat cgc
 1219

Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg
 360 365 370

gtc gat gca gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat
 1267

Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp
 375 380 385

ggg gag cag tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa
 1315

Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys
 390 395 400 405

ctg cat gca cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag
 1363

Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys
 410 415 420

tgg att ctg cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca
 1416

Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro
 425 430

agc
 1419

<210> 292

<211> 432

<212> PRT

<213> Corynebacterium glutamicum

<400> 292

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
 1 5 10 15

Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val
 130 135 140
 Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg
 145 150 155 160
 Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu
 165 170 175
 Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu
 180 185 190
 Leu Pro Cys Gln Thr Arg Gly Ser Val Gln Asp Leu Ile Thr Ala Arg
 195 200 205
 Gly Leu Val Asp Val Val Ile Pro Arg Gly Gly Ala Gly Leu Ile Asn
 210 215 220
 Ala Val Val Thr Gly Ala Thr Val Pro Thr Ile Glu Thr Gly Thr Gly
 225 230 235 240
 Asn Cys His Phe Tyr Ile Asp Ala Glu Ala Lys Leu Asp Gln Ala Ile
 245 250 255
 Ala Met Val Ile Asn Gly Lys Thr Arg Arg Cys Ser Val Cys Asn Ala
 260 265 270
 Thr Glu Thr Ala Leu Leu Asp Ala Ala Leu Ser Asp Ser Asp Lys Leu
 275 280 285
 Ala Val Val Gln Ala Leu Gln Glu Ala Gly Val Thr Ile His Gly Arg
 290 295 300
 Val Ala Glu Leu Glu Ala Phe Gly Ala Thr Asp Val Val Glu Ala Thr
 305 310 315 320
 Glu Thr Asp Trp Asp Ser Glu Tyr Leu Ser Phe Asp Ile Ala Val Ala
 325 330 335
 Val Val Asp Gly Val Asp Gly Ala Leu Ala His Ile Ala Lys Tyr Ser

340	345	350
Thr Lys His Thr Glu Ala Ile Ala Thr Gln Asn Ile Glu Thr Ala Gln		
355	360	365
Arg Phe Ala Asp Arg Val Asp Ala Ala Ala Val Met Ile Asn Ala Ser		
370	375	380
Thr Ala Tyr Thr Asp Gly Glu Gln Tyr Gly Met Gly Ala Glu Ile Gly		
385	390	395
Ile Ser Thr Gln Lys Leu His Ala Arg Gly Pro Met Ala Leu Pro Glu		
405	410	415
Leu Thr Ser Thr Lys Trp Ile Leu Gln Gly Thr Gly Gln Ile Arg Pro		
420	425	430

<210> 293
 <211> 724
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(709)
 <223> FRXA02378

<400> 293
 gagcagatgg ccaccgaggt cgatgtggtg gctggctact aggcctttta tgggtgtgatc 60

cgacactggt gcttcttaag ggtctgtata gtgggcaacc atg agt tca acg acc 115
 Met Ser Ser Thr Thr
 1 5

cta act gat gac caa att cgc gac aat gag cgg acc gaa gtt cta gct 163
 Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg Thr Glu Val Leu Ala
 10 15 20

aaa gca act gca gct aag aac atc gtc ccg gat att gca gtg ttg ggc 211
 Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp Ile Ala Val Leu Gly
 25 30 35

acc gga ccg aag aac gca atc ctg cgt gcg gcg gca gat gaa ctc gtt 259
 Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala Ala Asp Glu Leu Val
 40 45 50

gca cgc agc gca gaa atc atc gaa gcc aac gct tcc gat atc gaa gcg 307
 Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala Ser Asp Ile Glu Ala
 55 60 65

ggt cgc gca aac ggc atg gaa gaa tcc atg att gat cgc ctt gcc ctt 355
 Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile Asp Arg Leu Ala Leu
 70 75 80 85

gat gaa tct cgc att gag ggc atc gct ggc ggt ttg cgc cag gtt gct 403
 Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly Leu Arg Gln Val Ala
 90 95 100

ggc ctg acc gac cca gtg ggt gaa gta ctg cgc gga cat gtc atg gaa 451
 Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg Gly His Val Met Glu
 105 110 115
 aac ggc att cag atg aag cag gtc cgt gtg cct ttg ggc gtg atg ggc 499
 Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro Leu Gly Val Met Gly
 120 125 130
 atg gtc tat gaa gcc cgc cct aac gtc acc gtc gac gcc ttc ggc ctg 547
 Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val Asp Ala Phe Gly Leu
 135 140 145
 gca ctc aag tcc gga aac gta gct ttg ctg cgc ggt tcc tcc aca gct 595
 Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg Gly Ser Ser Thr Ala
 150 155 160 165
 gtg cat tcc aac acc aag ctc gtg gaa atc ctg cag gac gta ctc gag 643
 Val His Ser Asn Thr Lys Leu Val Glu Ile Leu Gln Asp Val Leu Glu
 170 175 180
 cgt ttc gag ctg cca cgc gaa acc gtg cag ttg ctg ctt gcc aaa ccc 691
 Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu Leu Leu Ala Lys Pro
 185 190 195
 gcg gat ccg tcc aag att tgatcaccgg acgcg 724
 Ala Asp Pro Ser Lys Ile
 200

<210> 294

<211> 203

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 294

Met Ser Ser Thr Thr Leu Thr Asp Asp Gln Ile Arg Asp Asn Glu Arg
 1 5 10 15
 Thr Glu Val Leu Ala Lys Ala Thr Ala Ala Lys Asn Ile Val Pro Asp
 20 25 30
 Ile Ala Val Leu Gly Thr Gly Pro Lys Asn Ala Ile Leu Arg Ala Ala
 35 40 45
 Ala Asp Glu Leu Val Ala Arg Ser Ala Glu Ile Ile Glu Ala Asn Ala
 50 55 60
 Ser Asp Ile Glu Ala Gly Arg Ala Asn Gly Met Glu Glu Ser Met Ile
 65 70 75 80
 Asp Arg Leu Ala Leu Asp Glu Ser Arg Ile Glu Gly Ile Ala Gly Gly
 85 90 95
 Leu Arg Gln Val Ala Gly Leu Thr Asp Pro Val Gly Glu Val Leu Arg
 100 105 110
 Gly His Val Met Glu Asn Gly Ile Gln Met Lys Gln Val Arg Val Pro
 115 120 125
 Leu Gly Val Met Gly Met Val Tyr Glu Ala Arg Pro Asn Val Thr Val

130	135	140
Asp Ala Phe Gly Leu Ala Leu Lys Ser Gly Asn Val Ala Leu Leu Arg		
145	150	155 160
Gly Ser Ser Thr Ala Val His Ser Asn Thr Lys Leu Val Glu Ile Leu		
	165	170 175
Gln Asp Val Leu Glu Arg Phe Glu Leu Pro Arg Glu Thr Val Gln Leu		
	180	185 190
Leu Leu Ala Lys Pro Ala Asp Pro Ser Lys Ile		
195	200	

<210> 295

<211> 623

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(600)

<223> FRXA02382

<400> 295

ccc acc att gaa acc ggc acc ggc aac tgc cac ttc tac atc gat gcc	48
Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala	
1 5 10 15	
gaa gcc aag ctt gat cag gca atc gcc atg gtc atc aac ggc aag acc	96
Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr	
20 25 30	
cgc cgc tgc agc gtg tgc aac gct act gaa acc gcg ctt ctc gac gcc	144
Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala	
35 40 45	
gcc ctc agc gac tca gac aag ctt gca gtc gtc cag gcg ctc cag gaa	192
Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu	
50 55 60	
gca gga gtc aca att cat gga cgg gtg gcc gaa ttg gaa gca ttc ggt	240
Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly	
65 70 75 80	
gca acc gac gtg gtg gaa gca act gaa act gac tgg gat tct gag tac	288
Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr	
85 90 95	
ctg tcc ttc gat atc gct gtc gct gtg gtt gac ggt gtg gat gga gct	336
Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala	
100 105 110	
ctg gca cac atc gct aag tac agc acc aag cac acc gaa gcg atc gcc	384
Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala	
115 120 125	
acc caa aac att gaa acc gct cag cgc ttt gca gat cgc gtc gat gca	432
Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala	
130 135 140	

gca gcg gtg atg ata aac gca tcc acc gcc tac acc gat ggg gag cag 480
 Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160

tac ggc atg ggc gcg gag atc ggc att tcc acc cag aaa ctg cat gca 528
 Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175

cgt gga cca atg gcc ctg cca gag ctg acc tcc acc aag tgg att ctg 576
 Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190

cag ggc aca gga caa att agg cct taagtttgaa gaagtaatca agc 623
 Gln Gly Thr Gly Gln Ile Arg Pro
 195 200

<210> 296

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 296

Pro Thr Ile Glu Thr Gly Thr Gly Asn Cys His Phe Tyr Ile Asp Ala
 1 5 10 15

Glu Ala Lys Leu Asp Gln Ala Ile Ala Met Val Ile Asn Gly Lys Thr
 20 25 30

Arg Arg Cys Ser Val Cys Asn Ala Thr Glu Thr Ala Leu Leu Asp Ala
 35 40 45

Ala Leu Ser Asp Ser Asp Lys Leu Ala Val Val Gln Ala Leu Gln Glu
 50 55 60

Ala Gly Val Thr Ile His Gly Arg Val Ala Glu Leu Glu Ala Phe Gly
 65 70 75 80

Ala Thr Asp Val Val Glu Ala Thr Glu Thr Asp Trp Asp Ser Glu Tyr
 85 90 95

Leu Ser Phe Asp Ile Ala Val Ala Val Val Asp Gly Val Asp Gly Ala
 100 105 110

Leu Ala His Ile Ala Lys Tyr Ser Thr Lys His Thr Glu Ala Ile Ala
 115 120 125

Thr Gln Asn Ile Glu Thr Ala Gln Arg Phe Ala Asp Arg Val Asp Ala
 130 135 140

Ala Ala Val Met Ile Asn Ala Ser Thr Ala Tyr Thr Asp Gly Glu Gln
 145 150 155 160

Tyr Gly Met Gly Ala Glu Ile Gly Ile Ser Thr Gln Lys Leu His Ala
 165 170 175

Arg Gly Pro Met Ala Leu Pro Glu Leu Thr Ser Thr Lys Trp Ile Leu
 180 185 190

Gln Gly Thr Gly Gln Ile Arg Pro

195

200

```
<210> 297
<211> 933
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(910)  
<223> RXA02499
```

<400> 297

cctgggtcatg acgttcgggc cgctggcaat cgtcatgtaa tttgtcgttt tgggcccccg 60

ctgctgcaaa acaggggtgg ttagtggcag tgtgggaacc atg aca aca att gct 115
Met Thr Thr Ile Ala
1 5

gta atc ggc ggc gga caa atc ggc gag gct tta gtc tca ggt ttg atc 163
Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu Val Ser Gly Leu Ile
10 15 20

gcg gcc aac atg aat cca caa aat att cgc gtc acc aac cgt tcg gaa 211
Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val Thr Asn Arg Ser Glu
25 30 35

gag cgc ggc caa gag ctg cgt gac cgc tac ggc atc ctc aac atg acg 259
Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly Ile Leu Asn Met Thr
40 45 50

gat aat tcc caa gcc gca gac gaa gcc gac gtg gtg ttc ctg tgc gtg 307
Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val Val Phe Leu Cys Val
55 60 65

aag ccg aaa ttt atc gtc gaa gtg ctc tcc gaa atc acc ggc act ttg 355
Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu Ile Thr Gly Thr Leu
70 75 80 85

gat aac aac tcc gca caa agt gtt gtg gtc agc atg gcc gca ggc atc 403
Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser Met Ala Ala Gly Ile
90 95 100

agc atc gct gcc atg gaa gaa agc gcc tct gcg ggg ctc ccc gtc gtg 451
 Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala Gly Leu Pro Val Val
 105 110 115

cgc gtc atg ccg aac act cca atg ctc gtg ggc aag ggc atg tcg act 499
 Arg Val Met Pro Asn Thr Pro Met Leu Val Gly Lys Gly Met Ser Thr
 120 125 130

gtc acc aaa ggc cgc tac gtt gac gcg gaa cag ttg gaa caa gtc aag 547
Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln Leu Glu Gln Val Lys
135 140 145

gac ttg ttg agc acc gtt gga gac gtc ctc gaa gtc gcg gaa tca gac 595
Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu Val Ala Glu Ser Asp
150 155 160 165

atc gac gca gtc acc gcg atg tcc gga tcc tcc cct gca tac ctg ttc 643

Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser Pro Ala Tyr Leu Phe
 170 175 180
 ctt gtg acc gaa gcg ctc att gag gca gga gtt aat cta ggc ctg ccc 691
 Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val Asn Leu Gly Leu Pro
 185 190 195
 cgc gcg acc gct aaa aag ctc gct gtg gcc tca ttc gaa ggt gct gca 739
 Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser Phe Glu Gly Ala Ala
 200 205 210
 acc atg atg aag gaa acc ggc aaa gaa ccc tca gaa ttg cgc gca ggc 787
 Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser Glu Leu Arg Ala Gly
 215 220 225
 gtt tcc tca ccc gca ggc acc acc gtc gca gcc atc cga gaa ctc gaa 835
 Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala Ile Arg Glu Leu Glu
 230 235 240 245
 gaa agc gga atc cga ggc gct ttc tac cgc gca gcc caa gct tgc gcc 883
 Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala Ala Gln Ala Cys Ala
 250 255 260
 gac cga tct gaa gaa ctc gga aag cgc tagaaaccgt tatttccccg 930
 Asp Arg Ser Glu Glu Leu Gly Lys Arg
 265 270
 tta 933

 <210> 298
 <211> 270
 <212> PRT
 <213> Corynebacterium glutamicum

 <400> 298
 Met Thr Thr Ile Ala Val Ile Gly Gly Gly Gln Ile Gly Glu Ala Leu
 1 5 10 15
 Val Ser Gly Leu Ile Ala Ala Asn Met Asn Pro Gln Asn Ile Arg Val
 20 25 30
 Thr Asn Arg Ser Glu Glu Arg Gly Gln Glu Leu Arg Asp Arg Tyr Gly
 35 40 45
 Ile Leu Asn Met Thr Asp Asn Ser Gln Ala Ala Asp Glu Ala Asp Val
 50 55 60
 Val Phe Leu Cys Val Lys Pro Lys Phe Ile Val Glu Val Leu Ser Glu
 65 70 75 80
 Ile Thr Gly Thr Leu Asp Asn Asn Ser Ala Gln Ser Val Val Val Ser
 85 90 95
 Met Ala Ala Gly Ile Ser Ile Ala Ala Met Glu Glu Ser Ala Ser Ala
 100 105 110
 Gly Leu Pro Val Val Arg Val Met Pro Asn Thr Pro Met Leu Val Gly
 115 120 125
 Lys Gly Met Ser Thr Val Thr Lys Gly Arg Tyr Val Asp Ala Glu Gln

130	135	140
Leu Glu Gln Val Lys Asp Leu Leu Ser Thr Val Gly Asp Val Leu Glu 145 150 155 160		
Val Ala Glu Ser Asp Ile Asp Ala Val Thr Ala Met Ser Gly Ser Ser 165 170 175		
Pro Ala Tyr Leu Phe Leu Val Thr Glu Ala Leu Ile Glu Ala Gly Val 180 185 190		
Asn Leu Gly Leu Pro Arg Ala Thr Ala Lys Lys Leu Ala Val Ala Ser 195 200 205		
Phe Glu Gly Ala Ala Thr Met Met Lys Glu Thr Gly Lys Glu Pro Ser 210 215 220		
Glu Leu Arg Ala Gly Val Ser Ser Pro Ala Gly Thr Thr Val Ala Ala 225 230 235 240		
Ile Arg Glu Leu Glu Glu Ser Gly Ile Arg Gly Ala Phe Tyr Arg Ala 245 250 255		
Ala Gln Ala Cys Ala Asp Arg Ser Glu Glu Leu Gly Lys Arg 260 265 270		

<210> 299
 <211> 1296
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1273)
 <223> RXS02157

<400> 299
 ggggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60
 caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
 Met Ser Thr Leu Glu
 1 5
 act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163
 Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
 10 15 20
 ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
 Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
 25 30 35
 tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259
 Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
 40 45 50
 cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307
 His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
 55 60 65
 cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355

His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu	
70 75 80 85	
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa	403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln	
90 95 100	
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct	451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala	
105 110 115	
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt	499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val	
120 125 130	
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag	547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln	
135 140 145	
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc	595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe	
150 155 160 165	
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac	643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn	
170 175 180	
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg	691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr	
185 190 195	
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg	739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu	
200 205 210	
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc	787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly	
215 220 225	
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt	835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val	
230 235 240 245	
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc	883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile	
250 255 260	
ggc gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc	931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly	
265 270 275	
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc	979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala	
280 285 290	
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc	1027
Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala	
295 300 305	

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
1075

Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
1123

Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
1171

Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
1219

Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
1267

Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
375 380 385

atc gca taaaggactc aaacttatga ctt

1296

Ile Ala

390

<210> 300

<211> 391

<212> PRT

<213> Corynebacterium glutamicum

<400> 300

Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
20 25 30

Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
35 40 45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
50 55 60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
65 70 75 80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
85 90 95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
100 105 110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
115 120 125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
 130 135 140
 Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
 145 150 155 160
 Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
 165 170 175
 Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
 180 185 190
 Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
 195 200 205
 Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
 210 215 220
 Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
 225 230 235 240
 His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
 245 250 255
 Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
 260 265 270
 Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
 275 280 285
 Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
 290 295 300
 Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
 305 310 315 320
 Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
 325 330 335
 Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
 340 345 350
 Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
 355 360 365
 Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
 370 375 380
 Ala Ile Ala Glu Thr Ile Ala
 385 390

<210> 301
 <211> 1269
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1246)
 <223> RXS02262

<400> 301
gcaccaatttt cggacctgaa atccccgagg aaaccgtgcc cgacgccgtg caggtgggcg 60
tcgataagca aaaaatcgct gataactcgaa aggcctcaaa atg acc gca acc tac 115
Met Thr Ala Thr Tyr
1 5
acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg 163
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met
10 15 20
atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag 211
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu
25 30 35
gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg 259
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu
40 45 50
aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa 307
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu
55 60 65
ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg 355
Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met
70 75 80 85
ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac 403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr
90 95 100
gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac 451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His
105 110 115
acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg 499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met
120 125 130
tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg 547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val
135 140 145
ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc 595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val
150 155 160 165
gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag 643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu
170 175 180
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc 691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly
185 190 195
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa 739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu
200 205 210
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc 787

Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile
 215 220 225
 gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca 835
 Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro
 230 235 240 245
 tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca 883
 Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro
 250 255 260
 gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc 931
 Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu
 265 270 275
 gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc 979
 Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly
 280 285 290
 cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac
 1027
 Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp
 295 300 305
 ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc
 1075
 Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly
 310 315 320 325
 gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc
 1123
 Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile
 330 335 340
 atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca
 1171
 Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala
 345 350 355
 acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg
 1219
 Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu
 360 365 370
 aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg
 1266
 Asn Leu Trp Glu Ser Pro Ala Leu Ala
 375 380
 aaa
 1269
 <210> 302
 <211> 382
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 302
 Met Thr Ala Thr Tyr Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu
 1 5 10 15

Ser Glu Pro Asp Met Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys
 20 25 30
 Val Asp Val Met Glu Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr
 35 40 45
 Lys Met Ala Gly Leu Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe
 50 55 60
 Pro Glu Asn Pro Glu Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg
 65 70 75 80
 Arg Phe Met Ala Met Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr
 85 90 95
 Gly Val Lys Trp Tyr Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu
 100 105 110
 Pro Arg Ser Ile His Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala
 115 120 125
 Pro Lys Ala Ile Met Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly
 130 135 140
 Ala Val Pro Gly Val Gly Val Lys His Leu Ala Val Ala Asp Ala Thr
 145 150 155 160
 Thr Leu Ala Val Val Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu
 165 170 175
 Ala Cys Ile Ala Glu Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly
 180 185 190
 Arg Ser Glu Arg Gly Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys
 195 200 205
 Phe Pro Glu Ile Glu Val Val Ala Val Gly Ser Glu Glu Asp Val Val
 210 215 220
 Lys Asp Ala Asp Ile Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly
 225 230 235 240
 Ser Ser Ala Phe Pro Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala
 245 250 255
 Leu Leu Leu Leu Pro Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu
 260 265 270
 Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335

Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350

Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365

Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
 370 375 380

<210> 303
 <211> 1491
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1468)
 <223> RXS02970

<400> 303
 aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttatttaaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly

135	140	145	
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly 150 155 160 165			595
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr 170 175 180			643
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser 185 190 195			691
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys 200 205 210			739
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala 215 220 225			787
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro 230 235 240 245			835
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile 250 255 260			883
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys 265 270 275			931
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile 280 285 290			979
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile 295 300 305			
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser 310 315 320 325			
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys 330 335 340			
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala 345 350 355			
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu			

360 365 370
 gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385
 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405
 ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420
 atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
 1411
 Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
 425 430 435
 gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
 1459
 Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
 440 445 450
 gcg ttg ttc taagttttct agataacaag gcc
 1491
 Ala Leu Phe
 455
 <210> 304
 <211> 456
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 304
 Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 5 10 15
 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe

115	120	125
Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala 130 135 140		
Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr 145 150 155 160		
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg 165 170 175		
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro 180 185 190		
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys 195 200 205		
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala 210 215 220		
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly 225 230 235 240		
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys 245 250 255		
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe 260 265 270		
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe 275 280 285		
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala 290 295 300		
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly 305 310 315 320		
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala 325 330 335		
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile 340 345 350		
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu 355 360 365		
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile 370 375 380		
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala 385 390 395 400		
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser 405 410 415		
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu 420 425 430		
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu 435 440 445		

Leu Thr Phe Ala Gly Ala Leu Phe
450 455

<210> 305
<211> 1330
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1330)
<223> FRXA01009

<400> 305
aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
ttattttaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027	
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075	
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123	
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171	
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219	
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267	
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	

375 380 385
 gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

 ttc aag gaa cgc ggc
 1330
 Phe Lys Glu Arg Gly
 410

 <210> 306
 <211> 410
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 306
 Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 5 10 15
 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

<210> 307
 <211> 3579
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(3556)
 <223> RXN00023

<400> 307
 gggattatgt tgggggccac atctgaaaat agttgctggg atccatcaca cctacgatgc 60
 gaaacggcac ccacaccgct gatcttgaag gagaaccacc atg acg tcg atg aat 115
 Met Thr Ser Met Asn
 1 5
 ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg 163
 Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val
 10 15 20
 cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat 211
 Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp
 25 30 35

gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gag gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcc atc	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Ile	
170 175 180	
aag gtc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag gcc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Ala	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883
Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr	
250 255 260	
ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc	931
Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg	
265 270 275	

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys
 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
 1027
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag
 1075
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg
 1219
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt
 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg
 1315
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc
 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
 1459
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
 440 445 450

ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc
 1507
 Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
 455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
 1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
 470 475 480 485
 gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
 1603
 Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
 490 495 500
 gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
 1651
 Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
 505 510 515
 gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
 1699
 Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
 520 525 530
 gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
 1747
 Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
 535 540 545
 att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
 1795
 Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
 550 555 560 565
 atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
 1843
 Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
 570 575 580
 ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
 1891
 Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
 585 590 595
 gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
 1939
 Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
 600 605 610
 gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
 1987
 Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
 615 620 625
 gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
 2035
 Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
 630 635 640 645
 ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
 2083
 Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
 650 655 660
 tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
 2131
 Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala

665	670	675
aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc 2179		
Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg 680	685	690
gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg 2227		
Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp 695	700	705
cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc 2275		
Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile 710	715	720 725
gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg 2323		
Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val 730	735	740
aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc 2371		
Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu 745	750	755
ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag 2419		
Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln 760	765	770
ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc 2467		
Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro 775	780	785
tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac 2515		
Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His 790	795	800 805
cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc 2563		
His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro 810	815	820
cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa 2611		
Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu 825	830	835
ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca 2659		
Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro 840	845	850
gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc 2707		
Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe 855	860	865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca gag gta gta ctc cga
3139

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala Glu Val Val Leu Arg
1000 1005 1010

ctc gac gat tcc gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca
3187

Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala
1015 1020 1025

gcc cgt cgc gcc ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt
3235

Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val
1030 1035 1040 1045

tca gag caa gtc cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa
3283

Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu
1050 1055 1060

aca gtc gat gat tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac
3331

Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr
1065 1070 1075

gac gag aac tcc agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac
3379

Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp
1080 1085 1090

act gtc cgt gaa cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac
3427

Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp
1095 1100 1105

gat gca gta act gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa
3475

Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys
1110 1115 1120 1125

gaa caa gca att tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg
3523

Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala
1130 1135 1140

gcc ttc cac gag ttg gcg gag gaa ctt aaa cgt tgatcggtttt gcgcattgggt
3576

Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
1145 1150

cgc
3579

<210> 308

<211> 1152

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 308

Met Thr Ser Met Asn Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln
1 5 10 15

Ala Val Asp Lys Val Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser
20 25 30

Val Pro Asn Ala Asp Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro
35 40 45

Asn Gly Leu Glu Phe Thr Val Gly Phe Val Asp Arg Val Val Arg Thr
50 55 60

Glu Asp Arg Glu Ala Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile
65 70 75 80

Ala Pro Ser Thr Met Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly
85 90 95

Ser Leu Val Gly Arg Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg
100 105 110

Ala Arg Ile Arg Gln Met Val Gly His Met Ile Val Asp Ala Arg Asp
 115 120 125
 Lys Gln Phe Ala Lys Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg
 130 135 140
 Leu Asn Ile Asn Leu Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala
 145 150 155 160
 Ala Lys His Leu Asp Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val
 165 170 175
 Glu Tyr Val Ser Ile Lys Val Ser Ser Val Ala Ser Gln Ile Ser Met
 180 185 190
 Trp Gly Phe Glu Asp Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro
 195 200 205
 Leu Tyr Ile Glu Ala Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn
 210 215 220
 Leu Asp Met Glu Glu Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe
 225 230 235 240
 Lys Arg Leu Leu Ser Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile
 245 250 255
 Val Leu Gln Ala Tyr Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu
 260 265 270
 Ala Gln Phe Gly Arg Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys
 275 280 285
 Val Arg Leu Val Lys Gly Ala Asn Leu Pro Met Glu His Val His Ala
 290 295 300
 Gln Ile Thr Gly Trp Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr
 305 310 315 320
 Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
 405 410 415
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile

435					440					445					
Ser	Asp	Leu	Ala	Thr	Leu	Ile	Asp	Val	Pro	Ala	Pro	Gly	Pro	Asn	His
450					455					460					
Thr	Gln	Asp	Arg	Ser	Lys	Glu	Thr	Leu	Leu	Asp	Ala	Pro	Leu	Val	Pro
465					470					475					480
Phe	Ile	Asn	Glu	Pro	Asp	Thr	Asn	Pro	Ala	Leu	Ile	Gln	Asn	Gln	Gln
				485					490					495	
Trp	Ala	Thr	Lys	Ala	Val	Ala	Thr	Ala	Ala	Glu	Pro	Gly	Trp	Leu	Glu
			500					505					510		
Lys	Gln	Thr	Lys	Pro	Glu	Val	Leu	Glu	Glu	Gly	Asp	Val	Asp	Lys	Leu
		515					520					525			
Ile	Asn	Asp	Val	Arg	Asp	Ala	Ala	Glu	Ala	Trp	Ala	Ala	Arg	Pro	Ala
		530				535					540				
Arg	Glu	Arg	Ala	Glu	Ile	Leu	Tyr	Lys	Thr	Ala	Glu	Ile	Leu	Arg	Val
545					550					555					560
Arg	Arg	Gly	His	Leu	Ile	Ser	Val	Thr	Ala	Ala	Glu	Val	Gly	Lys	Ala
				565					570					575	
Val	Glu	Gln	Thr	Asp	Pro	Glu	Ile	Ser	Glu	Ala	Ile	Asp	Phe	Ala	Arg
			580					585					590		
Tyr	Tyr	Ala	His	Leu	Ala	Leu	Glu	Leu	Asp	Asp	Val	Asp	Asn	Ala	Glu
		595					600					605			
Phe	Thr	Pro	Asp	Arg	Val	Val	Val	Val	Thr	Pro	Pro	Trp	Asn	Phe	Pro
		610					615					620			
Ile	Ala	Ile	Pro	Ala	Gly	Ser	Thr	Phe	Ala	Ala	Leu	Ala	Ala	Gly	Ala
625					630					635					640
Gly	Val	Ile	His	Lys	Pro	Ser	Lys	Pro	Ser	Gln	His	Cys	Ser	Ala	Ala
				645					650					655	
Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His
			660					665					670		
Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His
		675					680					685			
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala
		690				695					700				
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser
705					710					715					720
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala
				725					730					735	
Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys
			740					745					750		
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu
		755					760					765			

Arg Phe Arg Lys Gln Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp
 770 775 780
 Trp Pro Thr Asn Pro Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro
 785 790 795 800
 Ser Asp Lys Leu His His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser
 805 810 815
 Trp Leu Leu Lys Pro Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser
 820 825 830
 Pro Gly Ile Lys Glu Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr
 835 840 845
 Glu Val Phe Gly Pro Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn
 850 855 860
 Glu Ala Ile Glu Phe Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly
 865 870 875 880
 Leu Gln Ser Leu Asp Ala Asp Glu Val Arg Thr Trp Leu Asp His Val
 885 890 895
 Asp Val Gly Asn Ala Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val
 900 905 910
 Gln Arg Gln Ser Phe Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly
 915 920 925
 Ser Lys Ala Gly Gly Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala
 930 935 940
 Asp Ala Pro Ser His His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser
 945 950 955 960
 Lys Leu Asp Leu Pro Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn
 965 970 975
 Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990
 Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005
 Glu Val Val Leu Arg Leu Asp Asp Ser Ala Thr Pro Arg Glu Thr Ala
 1010 1015 1020
 Arg Ala Leu Leu Ala Ala Arg Arg Ala Gly Val Thr Pro Arg Val Leu
 1025 1030 1035 1040
 Gln Thr Pro Gly Val Ser Glu Gln Val Arg Glu Val Leu Ser Ala Ala
 1045 1050 1055
 Gly Val Ser Ala Glu Thr Val Asp Asp Ser Val Phe Ile Ser Asn Val
 1060 1065 1070
 Leu Arg Gly Glu Tyr Asp Glu Asn Ser Ser Val Arg Val Arg Tyr Leu
 1075 1080 1085

Gly Lys Val Ser Asp Thr Val Arg Glu Arg Leu Ser Val Arg Pro Glu
 1090 1095 1100

Val Val Leu Leu Asp Asp Ala Val Thr Ala Ser Gly Arg Val Glu Leu
 1105 1110 1115 1120

Arg Tyr Trp Leu Lys Glu Gln Ala Ile Ser Met Thr Leu His Arg Phe
 1125 1130 1135

Gly Asn Pro Val Ala Ala Phe His Glu Leu Ala Glu Glu Leu Lys Arg
 1140 1145 1150

<210> 309

<211> 476

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(453)

<223> FRXA00023

<400> 309

cat ttt ccg ctc cga cca gca gag gta gta ctc cga ctc gac gat tcc 48
 His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser
 1 5 10 15

gcc aca ccc cga gaa act gcc cgc gca ttg ttg gca gcc cgt cgc gcc 96
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
 20 25 30

ggg gtt act ccg cga gtt ctt caa aca cca ggt gtt tca gag caa gtc 144
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45

cgc gaa gta ttg tcc gct gct gga gtg agt gca gaa aca gtc gat gat 192
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60

tcg gta ttt att tcc aac gtg ttg cgc ggc gaa tac gac gag aac tcc 240
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80

agc gtc cga gtc cgc tac ctg ggc aaa gtt agc gac act gtc cgt gaa 288
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95

cgc cta tct gta cgg ccc gaa gtt gtt ctg ctt gac gat gca gta act 336
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110

gcc tcc ggt cga gtt gaa tta cgt tac tgg ctc aaa gaa caa gca att 384
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
 115 120 125

tcc atg acg ttg cac cgt ttt gga aac cca gtt gcg gcc ttc cac gag 432
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu

130 135 140 476
 ttg gcg gag gaa ctt aaa cgt tgatcgtttt gcgcatgggt cgc
 Leu Ala Glu Glu Leu Lys Arg
 145 150

<210> 310
 <211> 151
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 310
 His Phe Pro Leu Arg Pro Ala Glu Val Val Leu Arg Leu Asp Asp Ser
 1 5 10 15
 Ala Thr Pro Arg Glu Thr Ala Arg Ala Leu Leu Ala Ala Arg Arg Ala
 20 25 30
 Gly Val Thr Pro Arg Val Leu Gln Thr Pro Gly Val Ser Glu Gln Val
 35 40 45
 Arg Glu Val Leu Ser Ala Ala Gly Val Ser Ala Glu Thr Val Asp Asp
 50 55 60
 Ser Val Phe Ile Ser Asn Val Leu Arg Gly Glu Tyr Asp Glu Asn Ser
 65 70 75 80
 Ser Val Arg Val Arg Tyr Leu Gly Lys Val Ser Asp Thr Val Arg Glu
 85 90 95
 Arg Leu Ser Val Arg Pro Glu Val Val Leu Leu Asp Asp Ala Val Thr
 100 105 110
 Ala Ser Gly Arg Val Glu Leu Arg Tyr Trp Leu Lys Glu Gln Ala Ile
 115 120 125
 Ser Met Thr Leu His Arg Phe Gly Asn Pro Val Ala Ala Phe His Glu
 130 135 140
 Leu Ala Glu Glu Leu Lys Arg
 145 150

<210> 311
 <211> 3124
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(3124)
 <223> FRXA02284

<400> 311
 gggattatgt tggggggccac atctgaaaat agttgctggg atccatcaca cctacgatgc 60
 gaaacggcac ccacaccgct gatcttgaag gagaaccacc atg acg tcg atg aat 115
 Met Thr Ser Met Asn
 1 5

ctg cct att gag ttg gct acg ctg tct gac cag gct gtg gac aag gtg	163
Leu Pro Ile Glu Leu Ala Thr Leu Ser Asp Gln Ala Val Asp Lys Val	
10 15 20	
cgc tcc tgg ctg gag tac agc aaa aag gaa agc gtg ccc aat gcc gat	211
Arg Ser Trp Leu Glu Tyr Ser Lys Lys Glu Ser Val Pro Asn Ala Asp	
25 30 35	
gcg aag cgt cta gct gca gtg ttg cag gat cct aat ggt ttg gaa ttc	259
Ala Lys Arg Leu Ala Ala Val Leu Gln Asp Pro Asn Gly Leu Glu Phe	
40 45 50	
acg gtt ggt ttc gtg gat cga gtg gtt cga act gag gat cgt gaa gcg	307
Thr Val Gly Phe Val Asp Arg Val Val Arg Thr Glu Asp Arg Glu Ala	
55 60 65	
gca gcg cat gcg ttg tat gag ttg ggc aag att gct ccg tcg acg atg	355
Ala Ala His Ala Leu Tyr Glu Leu Gly Lys Ile Ala Pro Ser Thr Met	
70 75 80 85	
tcc ttt ttg gat cgg gcg cag att cag gcc ggt tct ttg gtg ggg cgg	403
Ser Phe Leu Asp Arg Ala Gln Ile Gln Ala Gly Ser Leu Val Gly Arg	
90 95 100	
gcg ttg ccg cag gtt gtg gtt cct gcg gcg cgg gct cga atc cgg cag	451
Ala Leu Pro Gln Val Val Val Pro Ala Ala Arg Ala Arg Ile Arg Gln	
105 110 115	
atg gtt ggg cac atg att gtg gat gcc cgc gac aag cag ttc gcc aag	499
Met Val Gly His Met Ile Val Asp Ala Arg Asp Lys Gln Phe Ala Lys	
120 125 130	
gct gtc gct gag att cag tcg gat ggg cac cgc ctg aac atc aat ttg	547
Ala Val Ala Glu Ile Gln Ser Asp Gly His Arg Leu Asn Ile Asn Leu	
135 140 145	
cta ggt gaa gcg gtg ttg ggc cga aag gaa gca gcg aag cat ttg gat	595
Leu Gly Glu Ala Val Leu Gly Arg Lys Glu Ala Ala Lys His Leu Asp	
150 155 160 165	
gac acg gtg cgg ttg ttg cgc cgt ccg gat gtg gaa tat gtg tcn nnn	643
Asp Thr Val Arg Leu Leu Arg Arg Pro Asp Val Glu Tyr Val Ser Xaa	
170 175 180	
nnn ntc tct tcg gtg gca tcg cag att tcg atg tgg ggt ttc gaa gac	691
Xaa Xaa Ser Ser Val Ala Ser Gln Ile Ser Met Trp Gly Phe Glu Asp	
185 190 195	
acc gtt aat tat gtt gtg gaa cag ctg aca cct tta tat ata gag ccc	739
Thr Val Asn Tyr Val Val Glu Gln Leu Thr Pro Leu Tyr Ile Glu Pro	
200 205 210	
gcg cgg gcg ccg aaa ggc acg aag ttc atc aac ctg gac atg gag gaa	787
Ala Arg Ala Pro Lys Gly Thr Lys Phe Ile Asn Leu Asp Met Glu Glu	
215 220 225	
tac cgc gat ctg cgc ctg act atg gag gtg ttc aag cgg ctg ctc tcc	835
Tyr Arg Asp Leu Arg Leu Thr Met Glu Val Phe Lys Arg Leu Leu Ser	
230 235 240 245	
aat cca gag ctg cat gaa cta gaa gcc gga att gtg ttg cag gcg tac	883

Asn Pro Glu Leu His Glu Leu Glu Ala Gly Ile Val Leu Gln Ala Tyr
 250 255 260

ctt ccc gat gcc ctc ggt gca atc cag gac ttg gcg cag ttc ggc cgc 931
 Leu Pro Asp Ala Leu Gly Ala Ile Gln Asp Leu Ala Gln Phe Gly Arg
 265 270 275

gag cgc gtc aac aca ggc ggg gcg ggc gtt aag gtt cgc ctg gtc aag 979
 Glu Arg Val Asn Thr Gly Gly Ala Gly Val Lys Val Arg Leu Val Lys
 280 285 290

ggt gct aat ttg cct atg gag cac gtc cac gcg cag atc acc ggc tgg
 1027
 Gly Ala Asn Leu Pro Met Glu His Val His Ala Gln Ile Thr Gly Trp
 295 300 305

cca gtt gcc aca gaa cct tcc aaa caa gcc acc gat gcc aat tac aag
 1075
 Pro Val Ala Thr Glu Pro Ser Lys Gln Ala Thr Asp Ala Asn Tyr Lys
 310 315 320 325

cgc gtc ctc tat tgg acg atg cgc aaa gaa aac atg gag ggc ctg cgc
 1123
 Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn Met Glu Gly Leu Arg
 330 335 340

ctg ggc gtt gcc ggc cac aac ctt ttc gac ata gca ttc gca cat ttg
 1171
 Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile Ala Phe Ala His Leu
 345 350 355

ctc tct gtg gag cgt ggg gta gcg gac cgt gtg gag ttc gaa atg ctg
 1219
 Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val Glu Phe Glu Met Leu
 360 365 370

cag ggc atg gcg tcc gat cag gcg cgc gcc gtc agc gtt gac gtc ggt
 1267
 Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val Ser Val Asp Val Gly
 375 380 385

gag ctg ctg ctt tac gta cca gcc gtg cgc cca caa gaa ttc gac gtg
 1315
 Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro Gln Glu Phe Asp Val
 390 395 400 405

gcc att tct tac ctc gtg cgc cgc ctc gag gaa aac gcc gcg agc gaa
 1363
 Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu Asn Ala Ala Ser Glu
 410 415 420

aac ttc atg tcc gcc atc ttc gac ctc gac gcc gac aac ccg tcc ttc
 1411
 Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala Asp Asn Pro Ser Phe
 425 430 435

aag cga gag gag agc cgc ttc cgc gcc tcc ata tct gac ctc gcc acg
 1459
 Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile Ser Asp Leu Ala Thr
 440 445 450

ctc atc gac gtg ccc gcg ccc ggc ccc aac cac aca caa gac cgc agc
1507

Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His Thr Gln Asp Arg Ser
455 460 465

aaa gag acg ctt ctc gac gcc ccc ctc gtc cca ttt atc aac gag ccc
1555

Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro Phe Ile Asn Glu Pro
470 475 480 485

gac acc aac cca gcg ctc atc caa aac caa cag tgg gcc aca aaa gcc
1603

Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln Trp Ala Thr Lys Ala
490 495 500

gtc gcc acc gca gca gag ccc ggt tgg ttg gaa aaa caa aca aag ccg
1651

Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu Lys Gln Thr Lys Pro
505 510 515

gag gtg ttg gaa gag ggg gac gtc gac aag cta att aac gat gtg cgc
1699

Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu Ile Asn Asp Val Arg
520 525 530

gac gct gct gaa gcg tgg gca gcg cgc cca gcc cgt gaa cgc gct gag
1747

Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala Arg Glu Arg Ala Glu
535 540 545

att ttg tac aag acc gcc gag att ttg cgc gtg cga cgc gga cac ctg
1795

Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val Arg Arg Gly His Leu
550 555 560 565

atc tca gtg acg gcc gcg gag gtg ggc aaa gct gtg gaa caa acc gac
1843

Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala Val Glu Gln Thr Asp
570 575 580

ccg gaa atc tct gaa gcc att gat ttc gcc cgc tac tac gcg cat ttg
1891

Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg Tyr Tyr Ala His Leu
585 590 595

gcc ctg gaa ttg gac gac gta gac aat gcg gaa ttc acc cca gat cgc
1939

Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu Phe Thr Pro Asp Arg
600 605 610

gtc gtt gtg gtg acc ccg ccc tgg aat ttc ccc atc gcg atc ccc gct
1987

Val Val Val Val Thr Pro Pro Trp Asn Phe Pro Ile Ala Ile Pro Ala
615 620 625

gga tcg act ttc gca gca ctc gcg gcg ggc gct ggc gtg atc cac aaa
2035

Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala Gly Val Ile His Lys
630 635 640 645

ccc tca aag cct agc caa cat tgc tcc gct gca gtg gtc gaa gcc ctc
2083

Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala Val Val Glu Ala Leu
650 655 660

tgg gaa gcc ggc gtt ccc cgc gag gtt ctg cat tgc att tac cca gct
2131

Trp Glu Ala Gly Val Pro Arg Glu Val Leu His Cys Ile Tyr Pro Ala
665 670 675

aat cgc gat gtt gga tgt gcg ttg atc agc cat gaa cac gtc gac cgc
2179

Asn Arg Asp Val Gly Cys Ala Leu Ile Ser His Glu His Val Asp Arg
680 685 690

gtc att ttg acc ggc tcc tcc gag acc gcc gcg atg ttc tcc tcc tgg
2227

Val Ile Leu Thr Gly Ser Ser Glu Thr Ala Ala Met Phe Ser Ser Trp
695 700 705

cga cca gaa ctc acc atc aac ggc gaa acc tcc ggc aaa aac gcc atc
2275

Arg Pro Glu Leu Thr Ile Asn Gly Glu Thr Ser Gly Lys Asn Ala Ile
710 715 720 725

gtg gtc acc cca tct gcc gac cgc gac ctc gcc gtc gcc gac ctg gtg
2323

Val Val Thr Pro Ser Ala Asp Arg Asp Leu Ala Val Ala Asp Leu Val
730 735 740

aaa tcc gcc ttc ggc cat gca gga caa aaa tgt tcc gca gcc tcc ctc
2371

Lys Ser Ala Phe Gly His Ala Gly Gln Lys Cys Ser Ala Ala Ser Leu
745 750 755

ggc atc ttg gta ggc agc gtc tac gaa tca gaa cgc ttc cgg aaa cag
2419

Gly Ile Leu Val Gly Ser Val Tyr Glu Ser Glu Arg Phe Arg Lys Gln
760 765 770

ctg gta gac gcc gca tcc tca ctc atc gtc gac tgg cct acc aac ccc
2467

Leu Val Asp Ala Ala Ser Ser Leu Ile Val Asp Trp Pro Thr Asn Pro
775 780 785

tcc gca acc gtc gga cca ctc acc gaa ctc ccc agc gat aaa ctc cac
2515

Ser Ala Thr Val Gly Pro Leu Thr Glu Leu Pro Ser Asp Lys Leu His
790 795 800 805

cac gcc cta acc acc ctc gaa gaa gga gaa agc tgg ctg ctg aaa ccc
2563

His Ala Leu Thr Thr Leu Glu Glu Gly Glu Ser Trp Leu Leu Lys Pro
810 815 820

cga caa ctc gac gac acc ggc cga ctc tgg tca ccc ggc atc aaa gaa
2611

Arg Gln Leu Asp Asp Thr Gly Arg Leu Trp Ser Pro Gly Ile Lys Glu
825 830 835

ggc gtc aaa cca gga acc ttc ttc cac ctc aca gaa gta ttc gga cca
2659

Gly Val Lys Pro Gly Thr Phe Phe His Leu Thr Glu Val Phe Gly Pro
840 845 850

gtc ctc ggc ctg atg aaa gcc acc gac ctc aat gaa gcc atc gaa ttc
2707

Val Leu Gly Leu Met Lys Ala Thr Asp Leu Asn Glu Ala Ile Glu Phe
855 860 865

caa aac ggc aac gac ttc gga ctc acc ggc gga ctc caa tcc ctc gac
2755

Gln Asn Gly Asn Asp Phe Gly Leu Thr Gly Gly Leu Gln Ser Leu Asp
870 875 880 885

gcc gac gaa gtc cgc acc tgg ctt gac cac gtc gat gtc gga aac gcc
2803

Ala Asp Glu Val Arg Thr Trp Leu Asp His Val Asp Val Gly Asn Ala
890 895 900

tac gtc aac cgc ggc atc acc ggc gcc att gtc caa cgc caa tcc ttc
2851

Tyr Val Asn Arg Gly Ile Thr Gly Ala Ile Val Gln Arg Gln Ser Phe
905 910 915

gga ggc tgg aaa aaa tcc tcc gtc ggc ctc gga tcc aaa gcc gga gga
2899

Gly Gly Trp Lys Lys Ser Ser Val Gly Leu Gly Ser Lys Ala Gly Gly
920 925 930

ccc aac tat gtc atg ctc atg gga acc tgg gcc gac gcg cca agc cac
2947

Pro Asn Tyr Val Met Leu Met Gly Thr Trp Ala Asp Ala Pro Ser His
935 940 945

cac gcc cca cgc gaa aca aac ccg ctg atc agc aaa ctg gat ctc ccc
2995

His Ala Pro Arg Glu Thr Asn Pro Leu Ile Ser Lys Leu Asp Leu Pro
950 955 960 965

gga gaa gag ctc gaa tgg ctc gaa aaa gcc aac gcc agc gat gaa aca
3043

Gly Glu Glu Leu Glu Trp Leu Glu Lys Ala Asn Ala Ser Asp Glu Thr
970 975 980

gca tgg aac acg gaa ttc ggc agc cca cgc gac ccc tcc ggc ctc gat
3091

Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp Pro Ser Gly Leu Asp
985 990 995

gta gaa gcc aac att ttc cgc tac cga cca gca
3124

Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
1000 1005

<210> 312

<211> 1008

<212> PRT

<213> Corynebacterium glutamicum

<400> 312

Met	Thr	Ser	Met	Asn	Leu	Pro	Ile	Glu	Leu	Ala	Thr	Leu	Ser	Asp	Gln
1				5					10					15	
Ala	Val	Asp	Lys	Val	Arg	Ser	Trp	Leu	Glu	Tyr	Ser	Lys	Lys	Glu	Ser
			20					25					30		
Val	Pro	Asn	Ala	Asp	Ala	Lys	Arg	Leu	Ala	Ala	Val	Leu	Gln	Asp	Pro
		35					40					45			
Asn	Gly	Leu	Glu	Phe	Thr	Val	Gly	Phe	Val	Asp	Arg	Val	Val	Arg	Thr
	50					55					60				
Glu	Asp	Arg	Glu	Ala	Ala	Ala	His	Ala	Leu	Tyr	Glu	Leu	Gly	Lys	Ile
65					70					75					80
Ala	Pro	Ser	Thr	Met	Ser	Phe	Leu	Asp	Arg	Ala	Gln	Ile	Gln	Ala	Gly
				85					90					95	
Ser	Leu	Val	Gly	Arg	Ala	Leu	Pro	Gln	Val	Val	Val	Pro	Ala	Ala	Arg
			100					105					110		
Ala	Arg	Ile	Arg	Gln	Met	Val	Gly	His	Met	Ile	Val	Asp	Ala	Arg	Asp
		115					120					125			
Lys	Gln	Phe	Ala	Lys	Ala	Val	Ala	Glu	Ile	Gln	Ser	Asp	Gly	His	Arg
	130					135					140				
Leu	Asn	Ile	Asn	Leu	Leu	Gly	Glu	Ala	Val	Leu	Gly	Arg	Lys	Glu	Ala
145					150					155					160
Ala	Lys	His	Leu	Asp	Asp	Thr	Val	Arg	Leu	Leu	Arg	Arg	Pro	Asp	Val
				165					170					175	
Glu	Tyr	Val	Ser	Xaa	Xaa	Xaa	Ser	Ser	Val	Ala	Ser	Gln	Ile	Ser	Met
			180					185					190		
Trp	Gly	Phe	Glu	Asp	Thr	Val	Asn	Tyr	Val	Val	Glu	Gln	Leu	Thr	Pro
		195					200					205			
Leu	Tyr	Ile	Glu	Pro	Ala	Arg	Ala	Pro	Lys	Gly	Thr	Lys	Phe	Ile	Asn
	210					215					220				
Leu	Asp	Met	Glu	Glu	Tyr	Arg	Asp	Leu	Arg	Leu	Thr	Met	Glu	Val	Phe
225					230					235					240
Lys	Arg	Leu	Leu	Ser	Asn	Pro	Glu	Leu	His	Glu	Leu	Glu	Ala	Gly	Ile
				245					250					255	
Val	Leu	Gln	Ala	Tyr	Leu	Pro	Asp	Ala	Leu	Gly	Ala	Ile	Gln	Asp	Leu
			260					265					270		
Ala	Gln	Phe	Gly	Arg	Glu	Arg	Val	Asn	Thr	Gly	Gly	Ala	Gly	Val	Lys
		275					280					285			
Val	Arg	Leu	Val	Lys	Gly	Ala	Asn	Leu	Pro	Met	Glu	His	Val	His	Ala
	290					295					300				
Gln	Ile	Thr	Gly	Trp	Pro	Val	Ala	Thr	Glu	Pro	Ser	Lys	Gln	Ala	Thr
305					310					315					320

Asp Ala Asn Tyr Lys Arg Val Leu Tyr Trp Thr Met Arg Lys Glu Asn
 325 330 335
 Met Glu Gly Leu Arg Leu Gly Val Ala Gly His Asn Leu Phe Asp Ile
 340 345 350
 Ala Phe Ala His Leu Leu Ser Val Glu Arg Gly Val Ala Asp Arg Val
 355 360 365
 Glu Phe Glu Met Leu Gln Gly Met Ala Ser Asp Gln Ala Arg Ala Val
 370 375 380
 Ser Val Asp Val Gly Glu Leu Leu Leu Tyr Val Pro Ala Val Arg Pro
 385 390 395 400
 Gln Glu Phe Asp Val Ala Ile Ser Tyr Leu Val Arg Arg Leu Glu Glu
 405 410 415
 Asn Ala Ala Ser Glu Asn Phe Met Ser Ala Ile Phe Asp Leu Asp Ala
 420 425 430
 Asp Asn Pro Ser Phe Lys Arg Glu Glu Ser Arg Phe Arg Ala Ser Ile
 435 440 445
 Ser Asp Leu Ala Thr Leu Ile Asp Val Pro Ala Pro Gly Pro Asn His
 450 455 460
 Thr Gln Asp Arg Ser Lys Glu Thr Leu Leu Asp Ala Pro Leu Val Pro
 465 470 475 480
 Phe Ile Asn Glu Pro Asp Thr Asn Pro Ala Leu Ile Gln Asn Gln Gln
 485 490 495
 Trp Ala Thr Lys Ala Val Ala Thr Ala Ala Glu Pro Gly Trp Leu Glu
 500 505 510
 Lys Gln Thr Lys Pro Glu Val Leu Glu Glu Gly Asp Val Asp Lys Leu
 515 520 525
 Ile Asn Asp Val Arg Asp Ala Ala Glu Ala Trp Ala Ala Arg Pro Ala
 530 535 540
 Arg Glu Arg Ala Glu Ile Leu Tyr Lys Thr Ala Glu Ile Leu Arg Val
 545 550 555 560
 Arg Arg Gly His Leu Ile Ser Val Thr Ala Ala Glu Val Gly Lys Ala
 565 570 575
 Val Glu Gln Thr Asp Pro Glu Ile Ser Glu Ala Ile Asp Phe Ala Arg
 580 585 590
 Tyr Tyr Ala His Leu Ala Leu Glu Leu Asp Asp Val Asp Asn Ala Glu
 595 600 605
 Phe Thr Pro Asp Arg Val Val Val Val Thr Pro Pro Trp Asn Phe Pro
 610 615 620
 Ile Ala Ile Pro Ala Gly Ser Thr Phe Ala Ala Leu Ala Ala Gly Ala
 625 630 635 640
 Gly Val Ile His Lys Pro Ser Lys Pro Ser Gln His Cys Ser Ala Ala

645							650							655						
Val	Val	Glu	Ala	Leu	Trp	Glu	Ala	Gly	Val	Pro	Arg	Glu	Val	Leu	His					
			660					665						670						
Cys	Ile	Tyr	Pro	Ala	Asn	Arg	Asp	Val	Gly	Cys	Ala	Leu	Ile	Ser	His					
		675					680					685								
Glu	His	Val	Asp	Arg	Val	Ile	Leu	Thr	Gly	Ser	Ser	Glu	Thr	Ala	Ala					
	690					695					700									
Met	Phe	Ser	Ser	Trp	Arg	Pro	Glu	Leu	Thr	Ile	Asn	Gly	Glu	Thr	Ser					
705					710					715					720					
Gly	Lys	Asn	Ala	Ile	Val	Val	Thr	Pro	Ser	Ala	Asp	Arg	Asp	Leu	Ala					
				725				730						735						
Val	Ala	Asp	Leu	Val	Lys	Ser	Ala	Phe	Gly	His	Ala	Gly	Gln	Lys	Cys					
			740					745					750							
Ser	Ala	Ala	Ser	Leu	Gly	Ile	Leu	Val	Gly	Ser	Val	Tyr	Glu	Ser	Glu					
		755					760					765								
Arg	Phe	Arg	Lys	Gln	Leu	Val	Asp	Ala	Ala	Ser	Ser	Leu	Ile	Val	Asp					
	770					775					780									
Trp	Pro	Thr	Asn	Pro	Ser	Ala	Thr	Val	Gly	Pro	Leu	Thr	Glu	Leu	Pro					
785					790					795					800					
Ser	Asp	Lys	Leu	His	His	Ala	Leu	Thr	Thr	Leu	Glu	Glu	Gly	Glu	Ser					
				805					810					815						
Trp	Leu	Leu	Lys	Pro	Arg	Gln	Leu	Asp	Asp	Thr	Gly	Arg	Leu	Trp	Ser					
			820					825					830							
Pro	Gly	Ile	Lys	Glu	Gly	Val	Lys	Pro	Gly	Thr	Phe	Phe	His	Leu	Thr					
		835					840					845								
Glu	Val	Phe	Gly	Pro	Val	Leu	Gly	Leu	Met	Lys	Ala	Thr	Asp	Leu	Asn					
	850					855					860									
Glu	Ala	Ile	Glu	Phe	Gln	Asn	Gly	Asn	Asp	Phe	Gly	Leu	Thr	Gly	Gly					
865					870					875					880					
Leu	Gln	Ser	Leu	Asp	Ala	Asp	Glu	Val	Arg	Thr	Trp	Leu	Asp	His	Val					
				885					890					895						
Asp	Val	Gly	Asn	Ala	Tyr	Val	Asn	Arg	Gly	Ile	Thr	Gly	Ala	Ile	Val					
			900					905					910							
Gln	Arg	Gln	Ser	Phe	Gly	Gly	Trp	Lys	Lys	Ser	Ser	Val	Gly	Leu	Gly					
		915					920					925								
Ser	Lys	Ala	Gly	Gly	Pro	Asn	Tyr	Val	Met	Leu	Met	Gly	Thr	Trp	Ala					
	930					935					940									
Asp	Ala	Pro	Ser																	

Ala Ser Asp Glu Thr Ala Trp Asn Thr Glu Phe Gly Ser Pro Arg Asp
 980 985 990

Pro Ser Gly Leu Asp Val Glu Ala Asn Ile Phe Arg Tyr Arg Pro Ala
 995 1000 1005

<210> 313

<211> 927

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(904)

<223> RXC02498

<400> 313

caaggtagaa atttgtccgt gggcacttcg tgaaggtgtg atcctcacca ggatcgacaa 60

aggactcgag taacatttac ccggaaagga gttggcgaaa atg agt gaa gag aaa 115
 Met Ser Glu Glu Lys
 1 5

ctc aca gtc gct gag ctg atg gcg cgt gcc gcg aaa gag gga cgc tcc 163
 Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala Lys Glu Gly Arg Ser
 10 15 20

acc gat gct ccc cga cga cgc agg cgc cgc agc atc gaa gac ggt ggc 211
 Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser Ile Glu Asp Gly Gly
 25 30 35

gta tcc gtt gct gag ctg acc ggc tcc att cct gcc gtt aag gaa aag 259
 Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro Ala Val Lys Glu Lys
 40 45 50

ccc gcg gag tcc aag cac tcc agc gtg ccc atc gat gca cca gca gaa 307
 Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile Asp Ala Pro Ala Glu
 55 60 65

cct gag gtt gtt gag gcc ccc aag cct gag ccc gcc gaa gaa gta gaa 355
 Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro Ala Glu Glu Val Glu
 70 75 80 85

gtg gct tcg gtg gag ggc gac gtc gat aag cag gaa acc cct gag cgt 403
 Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln Glu Thr Pro Glu Arg
 90 95 100

ccg gcg ccg agc aac gaa gaa acc atg gtg ctg cgc atc gtg gat gaa 451
 Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu Arg Ile Val Asp Glu
 105 110 115

aaa gat cca att agc ttg acg acg ggc gcg ttc ccc gtg gtt ccg gca 499
 Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe Pro Val Val Pro Ala
 120 125 130

gtt gcc gcc aag ccg gcg ccc gta gtg cgc gcg gag aag gac gcc gat 547

Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala Glu Lys Asp Ala Asp
 135 140 145

gtg gag act gcc gta aag gca gat ttc gca gag gtg gaa gtc gat aac 595
 Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu Val Glu Val Asp Asn
 150 155 160 165

act gac acc acg cag atg gct gtg gtg gaa gaa gtt gac gag gag cca 643
 Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu Val Asp Glu Glu Pro
 170 175 180

gag caa gaa aac aaa atg tcc gta ttc gcg atc atc atg atg gcg atc 691
 Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile Ile Met Met Ala Ile
 185 190 195

gtc gga gtt gtt ctc ggt gtc gtt gta ttc ctc ggc ttt gaa atg ctg 739
 Val Gly Val Val Leu Gly Val Val Val Phe Leu Gly Phe Glu Met Leu
 200 205 210

tgg gag cgc ctg aac aag tgg atc gtc gct gtt ctg gca gtc ggc gtg 787
 Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val Leu Ala Val Gly Val
 215 220 225

acc ttg gga atg gtg ggc atc atc cac gct ttg cgc acc tca cgt gat 835
 Thr Leu Gly Met Val Gly Ile Ile His Ala Leu Arg Thr Ser Arg Asp
 230 235 240 245

ggt ttc agc atg gtt ctc gca gga atc gtg ggc ctg gtc atg acg ttc 883
 Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly Leu Val Met Thr Phe
 250 255 260

ggg ccg ctg gca atc gtc atg taatttgtcg ttttgggccc ccg 927
 Gly Pro Leu Ala Ile Val Met
 265

<210> 314

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 314

Met Ser Glu Glu Lys Leu Thr Val Ala Glu Leu Met Ala Arg Ala Ala
 1 5 10 15

Lys Glu Gly Arg Ser Thr Asp Ala Pro Arg Arg Arg Arg Arg Arg Ser
 20 25 30

Ile Glu Asp Gly Gly Val Ser Val Ala Glu Leu Thr Gly Ser Ile Pro
 35 40 45

Ala Val Lys Glu Lys Pro Ala Glu Ser Lys His Ser Ser Val Pro Ile
 50 55 60

Asp Ala Pro Ala Glu Pro Glu Val Val Glu Ala Pro Lys Pro Glu Pro
 65 70 75 80

Ala Glu Glu Val Glu Val Ala Ser Val Glu Gly Asp Val Asp Lys Gln
 85 90 95

Glu Thr Pro Glu Arg Pro Ala Pro Ser Asn Glu Glu Thr Met Val Leu

100	105	110
Arg Ile Val Asp Glu Lys Asp Pro Ile Ser Leu Thr Thr Gly Ala Phe 115 120 125		
Pro Val Val Pro Ala Val Ala Ala Lys Pro Ala Pro Val Val Arg Ala 130 135 140		
Glu Lys Asp Ala Asp Val Glu Thr Ala Val Lys Ala Asp Phe Ala Glu 145 150 155 160		
Val Glu Val Asp Asn Thr Asp Thr Thr Gln Met Ala Val Val Glu Glu 165 170 175		
Val Asp Glu Glu Pro Glu Gln Glu Asn Lys Met Ser Val Phe Ala Ile 180 185 190		
Ile Met Met Ala Ile Val Gly Val Val Leu Gly Val Val Val Phe Leu 195 200 205		
Gly Phe Glu Met Leu Trp Glu Arg Leu Asn Lys Trp Ile Val Ala Val 210 215 220		
Leu Ala Val Gly Val Thr Leu Gly Met Val Gly Ile Ile His Ala Leu 225 230 235 240		
Arg Thr Ser Arg Asp Gly Phe Ser Met Val Leu Ala Gly Ile Val Gly 245 250 255		
Leu Val Met Thr Phe Gly Pro Leu Ala Ile Val Met 260 265		

<210> 315

<211> 774

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(751)

<223> RXA01491

<400> 315

aacggtgtga aacacattga agtgtcgttg gggtatccgc gcgaatggga gcattggtct 60

gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct	115
Met Leu Asp Glu Ser	
1 5	

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct	163
Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala	
10 15 20	

gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg	211
Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu	
25 30 35	

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg	259
Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg	
40 45 50	

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat 307
 Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
 55 60 65
 ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg 355
 Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
 70 75 80 85
 tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg 403
 Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
 90 95 100
 cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag 451
 Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
 105 110 115
 ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att 499
 Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
 120 125 130
 cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc 547
 Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
 135 140 145
 ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg 595
 Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
 150 155 160 165
 acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat 643
 Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
 170 175 180
 gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg 691
 Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
 185 190 195
 ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg 739
 Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
 200 205 210
 act gca gtg act tgaactggat ggagaggata cct 774
 Thr Ala Val Thr
 215

<210> 316

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile
 1 5 10 15

Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
 20 25 30

Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
 35 40 45

Phe	Gly	Asp	Ala	Arg	Trp	Cys	Ala	His	Gln	Ala	Leu	Gln	Ala	Leu	Gly
50						55					60				
Arg	Asp	Ser	Gly	Asp	Pro	Ile	Leu	Arg	Gly	Glu	Arg	Gly	Met	Pro	Leu
65					70					75					80
Trp	Pro	Ser	Ser	Val	Ser	Gly	Ser	Leu	Thr	His	Thr	Asp	Gly	Phe	Arg
				85					90					95	
Ala	Ala	Val	Val	Ala	Pro	Arg	Leu	Leu	Val	Arg	Ser	Met	Gly	Leu	Asp
			100					105					110		
Ala	Glu	Pro	Ala	Glu	Pro	Leu	Pro	Lys	Asp	Val	Leu	Gly	Ser	Ile	Ala
		115					120					125			
Arg	Val	Gly	Glu	Ile	Pro	Gln	Leu	Lys	Arg	Leu	Glu	Glu	Gln	Gly	Val
	130					135					140				
His	Cys	Ala	Asp	Arg	Leu	Leu	Phe	Cys	Ala	Lys	Glu	Ala	Thr	Tyr	Lys
145					150					155					160
Ala	Trp	Phe	Pro	Leu	Thr	His	Arg	Trp	Leu	Gly	Phe	Glu	Gln	Ala	Glu
				165					170					175	
Ile	Asp	Leu	Arg	Asp	Asp	Gly	Thr	Phe	Val	Ser	Tyr	Leu	Leu	Val	Arg
			180				185						190		
Pro	Thr	Pro	Val	Pro	Phe	Ile	Ser	Gly	Lys	Trp	Val	Leu	Arg	Asp	Gly
		195					200					205			
Tyr	Val	Ile	Ala	Ala	Thr	Ala	Val	Thr							
	210					215									

```
<210> 317
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1264)
<223> RXA02155
```

```

<400> 317
tcggcgctcgc accttaaagt agcgccttaa agcggcgctt caaaccaagc gccctaacca 60

gcaaacacaa caaacacatc taattcagta ggagttccac atg gca gaa aaa ggc 115
Met Ala Glu Lys Gly
1 5

att acc gcg ccg aaa ggc ttc gtt gct tct gca acg acc gcg ggt att 163
Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala Thr Thr Ala Gly Ile
10 15 20

aaa gct tct ggc aat cct gac atg gcg ttg gtg gtt aac cag ggt cca 211
Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val Val Asn Gln Gly Pro
25 30 35

gag ttt tcc gca gcg gcc gtg ttt aca cgt aac cga gtt ttc gca gcg 259
Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn Arg Val Phe Ala Ala

```

40	45	50	
cct gtg aag gtg agc cga gag aac gtt gct gat ggc cag atc agg gct Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp Gly Gln Ile Arg Ala 55 60 65			307
gtt ttg tac aac gct ggt aat gct aat gcg tgt aat ggt ctg cag ggt Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys Asn Gly Leu Gln Gly 70 75 80 85			355
gag aag gat gct cgt gag tct gtt tct cat cta gct caa aat ttg ggc Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu Ala Gln Asn Leu Gly 90 95 100			403
ttg gag gat tcc gat att ggt gtg tgt tcc act ggt ctt att ggt gag Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr Gly Leu Ile Gly Glu 105 110 115			451
ttg ctt ccg atg gat aag ctc aat gca ggt att gat cag ctg acc gct Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile Asp Gln Leu Thr Ala 120 125 130			499
gag ggc gct ttg ggt gac aat ggt gca gct gct gcc aag gcg atc atg Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala Ala Lys Ala Ile Met 135 140 145			547
acc act gac acg gtg gat aag gaa acc gtc gtg ttt gct gat ggt tgg Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val Phe Ala Asp Gly Trp 150 155 160 165			595
act gtc ggc gga atg ggc aag ggc gtg ggc atg atg gcg ccg tct ctt Thr Val Gly Gly Met Gly Lys Gly Val Gly Met Met Ala Pro Ser Leu 170 175 180			643
gcc acc atg ctg gtc tgc ttg acc act gat gca tcc gtt act cag gaa Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala Ser Val Thr Gln Glu 185 190 195			691
atg gct cag atc gcg ctg gct aat gct acg gcc gtt acg ttt gac acc Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala Val Thr Phe Asp Thr 200 205 210			739
ctg gat att gat gga tca acc tcc acc aat gac acc gtg ttc ctg ctg Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp Thr Val Phe Leu Leu 215 220 225			787
gca tct ggc gct agc gga atc acc cca act cag gat gaa ctc aac gat Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln Asp Glu Leu Asn Asp 230 235 240 245			835
gcg gtg tac gca gct tgt tct gat atc gca gcg aag ctt cag gct gat Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala Lys Leu Gln Ala Asp 250 255 260			883
gca gag ggt gtg acc aag cgc gtt gct gtg aca gtg gtg gga acc acc Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr Val Val Gly Thr Thr 265 270 275			931
aac aac gag cag gcg att aat gcg gct cgc act gtt gct cgt gac aat Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr Val Ala Arg Asp Asn 280 285 290			979

ttg ttc aag tgc gca atg ttt gga tct gat cca aac tgg ggt cgc gtg
1027

Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro Asn Trp Gly Arg Val
295 300 305

ttg gct gca gtc ggc atg gct gat gct gat atg gaa cca gag aag att
1075

Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met Glu Pro Glu Lys Ile
310 315 320 325

tct gtg ttc ttc aat ggt caa gca gta tgc ctt gat tcc act ggc gct
1123

Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu Asp Ser Thr Gly Ala
330 335 340

cct ggt gct cgt gag gtg gat ctt tcc ggc gct gac att gat gtc cga
1171

Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala Asp Ile Asp Val Arg
345 350 355

att gat ttg ggc acc agt ggg gaa ggc cag gca aca gtt cga acc act
1219

Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala Thr Val Arg Thr Thr
360 365 370

gac ctg agc ttc tcc tac gtg gag atc aac tcc gcg tac agc tct
1264

Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser Ala Tyr Ser Ser
375 380 385

taaaaagaaa cagcactcca act
1287

<210> 318

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

Met Ala Glu Lys Gly Ile Thr Ala Pro Lys Gly Phe Val Ala Ser Ala
1 5 10 15

Thr Thr Ala Gly Ile Lys Ala Ser Gly Asn Pro Asp Met Ala Leu Val
20 25 30

Val Asn Gln Gly Pro Glu Phe Ser Ala Ala Ala Val Phe Thr Arg Asn
35 40 45

Arg Val Phe Ala Ala Pro Val Lys Val Ser Arg Glu Asn Val Ala Asp
50 55 60

Gly Gln Ile Arg Ala Val Leu Tyr Asn Ala Gly Asn Ala Asn Ala Cys
65 70 75 80

Asn Gly Leu Gln Gly Glu Lys Asp Ala Arg Glu Ser Val Ser His Leu
85 90 95

Ala Gln Asn Leu Gly Leu Glu Asp Ser Asp Ile Gly Val Cys Ser Thr
100 105 110

Gly Leu Ile Gly Glu Leu Leu Pro Met Asp Lys Leu Asn Ala Gly Ile
 115 120 125
 Asp Gln Leu Thr Ala Glu Gly Ala Leu Gly Asp Asn Gly Ala Ala Ala
 130 135 140
 Ala Lys Ala Ile Met Thr Thr Asp Thr Val Asp Lys Glu Thr Val Val
 145 150 155 160
 Phe Ala Asp Gly Trp Thr Val Gly Gly Met Gly Lys Gly Val Gly Met
 165 170 175
 Met Ala Pro Ser Leu Ala Thr Met Leu Val Cys Leu Thr Thr Asp Ala
 180 185 190
 Ser Val Thr Gln Glu Met Ala Gln Ile Ala Leu Ala Asn Ala Thr Ala
 195 200 205
 Val Thr Phe Asp Thr Leu Asp Ile Asp Gly Ser Thr Ser Thr Asn Asp
 210 215 220
 Thr Val Phe Leu Leu Ala Ser Gly Ala Ser Gly Ile Thr Pro Thr Gln
 225 230 235 240
 Asp Glu Leu Asn Asp Ala Val Tyr Ala Ala Cys Ser Asp Ile Ala Ala
 245 250 255
 Lys Leu Gln Ala Asp Ala Glu Gly Val Thr Lys Arg Val Ala Val Thr
 260 265 270
 Val Val Gly Thr Thr Asn Asn Glu Gln Ala Ile Asn Ala Ala Arg Thr
 275 280 285
 Val Ala Arg Asp Asn Leu Phe Lys Cys Ala Met Phe Gly Ser Asp Pro
 290 295 300
 Asn Trp Gly Arg Val Leu Ala Ala Val Gly Met Ala Asp Ala Asp Met
 305 310 315 320
 Glu Pro Glu Lys Ile Ser Val Phe Phe Asn Gly Gln Ala Val Cys Leu
 325 330 335
 Asp Ser Thr Gly Ala Pro Gly Ala Arg Glu Val Asp Leu Ser Gly Ala
 340 345 350
 Asp Ile Asp Val Arg Ile Asp Leu Gly Thr Ser Gly Glu Gly Gln Ala
 355 360 365
 Thr Val Arg Thr Thr Asp Leu Ser Phe Ser Tyr Val Glu Ile Asn Ser
 370 375 380
 Ala Tyr Ser Ser
 385

<210> 319

<211> 1074

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1051)

<223> RXA02156

<400> 319

```

aaccactgac ctgagcttct cctacgtgga gatcaactcc gcgtacagct cttaaaaaga 60

aacagcactc caactaacaa gcagggaaaa gggcacaggc atg aat gac ttg atc 115
                                         Met Asn Asp Leu Ile
                                           1           5

aaa gat tta ggc tct gag gtg cgc gca aat gtc ctc gct gag gcg ttg 163
Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val Leu Ala Glu Ala Leu
                        10                        15                        20

cca tgg ttg cag cac ttc cgc gac aag att gtt gtc gtg aaa tat ggc 211
Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val Val Val Lys Tyr Gly
                        25                        30                        35

gga aac gcc atg gtg gat gat gat ctc aag gct gct ttt gct gcc gac 259
Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala Ala Phe Ala Ala Asp
                        40                        45                        50

atg gtc ttc ttg cgc acc gtg ggc gca aaa cca gtg gtg gtg cac ggt 307
Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro Val Val Val His Gly
                        55                        60                        65

ggg gga cct cag att tct gag atg cta aac cgt gtg ggt ctc cag ggc 355
Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg Val Gly Leu Gln Gly
                        70                        75                        80                        85

gag ttc aag ggt ggt ttc cgt gtg acc act cct gag gtc atg gac att 403
Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro Glu Val Met Asp Ile
                        90                        95                        100

gtg cgc atg gtg ctc ttt ggt cag gtc ggt cgc gat tta gtt ggt ttg 451
Val Arg Met Val Leu Phe Gly Gln Val Gly Arg Asp Leu Val Gly Leu
                        105                        110                        115

atc aac tct cat ggc cct tac gct gtg gga acc tcc ggt gag gat gcc 499
Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr Ser Gly Glu Asp Ala
                        120                        125                        130

ggc ctg ttt acc gcg cag aag cgc atg gtc aac atc gat ggc gta ccc 547
Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn Ile Asp Gly Val Pro
                        135                        140                        145

act gat att ggt ttg gtc gga gac atc att aat gtc gat gcc tct tcc 595
Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn Val Asp Ala Ser Ser
                        150                        155                        160                        165

ttg atg gat atc atc gag gcc ggt cgc att cct gtg gtc tct acg att 643
Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro Val Val Ser Thr Ile
                        170                        175                        180

gct cca ggc gaa gac ggc cag att tac aac att aac gcc gat acc gca 691
Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile Asn Ala Asp Thr Ala
                        185                        190                        195

gca ggt gct ttg gct gca gcg att ggt gca gaa cgc ctg ctg gtt ctc 739

```


Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu Arg Leu Leu Val Leu
 200 205 210

acc aat gtg gaa ggt ctg tac acc gat tgg cct gat aag agc tca ctg 787
 Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro Asp Lys Ser Ser Leu
 215 220 225

gtg tcc aag atc aag gcc acc gag ctg gag gcc att ctt ccg gga ctt 835
 Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala Ile Leu Pro Gly Leu
 230 235 240 245

gat tcc ggc atg att cca aag atg gag tct tgc ttg aac gcg gtg cgt 883
 Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys Leu Asn Ala Val Arg
 250 255 260

ggg gga gta agc gct gct cat gtc att gac ggc cgc atc gcg cac tcg 931
 Gly Gly Val Ser Ala Ala His Val Ile Asp Gly Arg Ile Ala His Ser
 265 270 275

gtg ttg ctg gag ctt ttg acc atg ggt gga att ggc acg atg gtg ctg 979
 Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile Gly Thr Met Val Leu
 280 285 290

ccg gat gtt ttt gat cgg gag aat tat cct gaa ggc acc gtt ttt aga
 1027
 Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu Gly Thr Val Phe Arg
 295 300 305

aaa gac gac aag gat ggg gaa ctg taaatgagca cgctggaaac ttg
 1074
 Lys Asp Asp Lys Asp Gly Glu Leu
 310 315

<210> 320
 <211> 317
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 320
 Met Asn Asp Leu Ile Lys Asp Leu Gly Ser Glu Val Arg Ala Asn Val
 1 5 10 15

Leu Ala Glu Ala Leu Pro Trp Leu Gln His Phe Arg Asp Lys Ile Val
 20 25 30

Val Val Lys Tyr Gly Gly Asn Ala Met Val Asp Asp Asp Leu Lys Ala
 35 40 45

Ala Phe Ala Ala Asp Met Val Phe Leu Arg Thr Val Gly Ala Lys Pro
 50 55 60

Val Val Val His Gly Gly Gly Pro Gln Ile Ser Glu Met Leu Asn Arg
 65 70 75 80

Val Gly Leu Gln Gly Glu Phe Lys Gly Gly Phe Arg Val Thr Thr Pro
 85 90 95

Glu Val Met Asp Ile Val Arg Met Val Leu Phe Gly Gln Val Gly Arg
 100 105 110

Asp Leu Val Gly Leu Ile Asn Ser His Gly Pro Tyr Ala Val Gly Thr
 115 120 125
 Ser Gly Glu Asp Ala Gly Leu Phe Thr Ala Gln Lys Arg Met Val Asn
 130 135 140
 Ile Asp Gly Val Pro Thr Asp Ile Gly Leu Val Gly Asp Ile Ile Asn
 145 150 155 160
 Val Asp Ala Ser Ser Leu Met Asp Ile Ile Glu Ala Gly Arg Ile Pro
 165 170 175
 Val Val Ser Thr Ile Ala Pro Gly Glu Asp Gly Gln Ile Tyr Asn Ile
 180 185 190
 Asn Ala Asp Thr Ala Ala Gly Ala Leu Ala Ala Ala Ile Gly Ala Glu
 195 200 205
 Arg Leu Leu Val Leu Thr Asn Val Glu Gly Leu Tyr Thr Asp Trp Pro
 210 215 220
 Asp Lys Ser Ser Leu Val Ser Lys Ile Lys Ala Thr Glu Leu Glu Ala
 225 230 235 240
 Ile Leu Pro Gly Leu Asp Ser Gly Met Ile Pro Lys Met Glu Ser Cys
 245 250 255
 Leu Asn Ala Val Arg Gly Gly Val Ser Ala Ala His Val Ile Asp Gly
 260 265 270
 Arg Ile Ala His Ser Val Leu Leu Glu Leu Leu Thr Met Gly Gly Ile
 275 280 285
 Gly Thr Met Val Leu Pro Asp Val Phe Asp Arg Glu Asn Tyr Pro Glu
 290 295 300
 Gly Thr Val Phe Arg Lys Asp Asp Lys Asp Gly Glu Leu
 305 310 315

<210> 321

<211> 903

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(880)

<223> RXN02153

<400> 321

cccacttgca gttttagctg taggtggggtt tttgcatgtc taaccctgtct tttatgcaca 60

cccccgcaat gaatcaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115
 Met Ile Met His Asn
 1 5

gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163
 Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser
 10 15 20

gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct	211
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala	
25 30 35	
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc	259
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr	
40 45 50	
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg	307
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala	
55 60 65	
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat	355
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp	
70 75 80 85	
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt	403
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu	
90 95 100	
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt	451
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg	
105 110 115	
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag	499
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln	
120 125 130	
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct	547
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala	
135 140 145	
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt	595
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly	
150 155 160 165	
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca	643
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro	
170 175 180	
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa	691
Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys	
185 190 195	
gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg	739
Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala	
200 205 210	
tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac	787
Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn	
215 220 225	
ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg	835
Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val	
230 235 240 245	
ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt	880
Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu	
250 255 260	
tgaaagaagg cgttaccgca gaa	903

<210> 322

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 322

```

Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
 1             5             10             15

Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
      20             25             30

Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
      35             40             45

Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
      50             55             60

Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
      65             70             75             80

Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
      85             90             95

Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
      100            105            110

Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
      115            120            125

Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
      130            135            140

Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
      145            150            155            160

Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
      165            170            175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
      180            185            190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
      195            200            205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
      210            215            220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
      225            230            235            240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
      245            250            255

Gln Pro His Leu
      260

```

<210> 323

```
<211> 903
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (880)  
<223> FRXA02153
```

<400> 323																
cccacttgca gtttttagctg taggtggggtt tttgcatgtc taaccctgtct tttatgcaca 60																
cccccgcaat gaatcaaaaaa tttatgcatg aataatttgc atg atc atg cat aac 115																
Met Ile Met His Asn 1 5																
gtg tat ggt gta act atg aca atc aag gtt gca atc gca gga gcc agt 163																
Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala Ile Ala Gly Ala Ser 10 15 20																
gga tat gcc ggc gga gaa atc ctt cgt ctc ctt tta ggc cat cca gct 211																
Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu Leu Gly His Pro Ala 25 30 35																
tat gca tct ggt gaa cta gaa atc gga gca ctc acc gcg gca tca acc 259																
Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu Thr Ala Ala Ser Thr 40 45 50																
gca ggc agc acg ctc ggt gaa ttg atg cca cac att ccg cag ttg gcg 307																
Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His Ile Pro Gln Leu Ala 55 60 65																
gat cgt gtt att caa gac acc aca gct gaa act cta gcc ggt cat gat 355																
Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr Leu Ala Gly His Asp 70 75 80 85																
gtc gta ttt cta gga ctt cca cac gga ttc tct gca gaa att gca ctt 403																
Val Val Phe Leu Gly Leu Pro His Gly Phe Ser Ala Glu Ile Ala Leu 90 95 100																
cag ctc gga cca gat gtc aca gtg att gac tgt gca gct gac ttt cgt 451																
Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys Ala Ala Asp Phe Arg 105 110 115																
ctg caa aat gct gca gat tgg gag aag ttc tac ggc tca gag cac cag 499																
Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr Gly Ser Glu His Gln 120 125 130																
gga aca tgg cct tat ggc att cca gaa atg cca gga cac cgc gag gct 547																
Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro Gly His Arg Glu Ala 135 140 145																
ctt cgt ggt gct aag cgt gta gca gtg cca gga tgt ttc cca acc ggt 595																
Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly Cys Phe Pro Thr Gly 150 155 160 165																
gca acc ttg gct ctt ctt cct gcg gtt caa gcg gga ctt atc gag cca 643																
Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala Gly Leu Ile Glu Pro 170 175 180																
gat gtt tcc gta gtg tcc atc acc ggc gta tca ggt gca ggt aag aaa 691																

Asp Val Ser Val Val Ser Ile Thr Gly Val Ser Gly Ala Gly Lys Lys
 185 190 195
 gca tct gtt gca cta ctt ggc tcg gaa acc atg ggt tca ctc aag gcg 739
 Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met Gly Ser Leu Lys Ala
 200 205 210
 tac aac acc tcc gga aag cac cgc cac acc ccg gaa att gcc cag aac 787
 Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro Glu Ile Ala Gln Asn
 215 220 225
 ctc ggc gaa gtc agc gac aag cca gtc aag gtg agc ttc acc cca gtg 835
 Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val Ser Phe Thr Pro Val
 230 235 240 245
 ctt gca ccg tta cct cgc gaa ttc tca cca ctg caa ccg cac ctt 880
 Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu Gln Pro His Leu
 250 255 260
 tgaaagaagg cgttaccgca gaa 903

<210> 324
 <211> 260
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 324
 Met Ile Met His Asn Val Tyr Gly Val Thr Met Thr Ile Lys Val Ala
 1 5 10 15
 Ile Ala Gly Ala Ser Gly Tyr Ala Gly Gly Glu Ile Leu Arg Leu Leu
 20 25 30
 Leu Gly His Pro Ala Tyr Ala Ser Gly Glu Leu Glu Ile Gly Ala Leu
 35 40 45
 Thr Ala Ala Ser Thr Ala Gly Ser Thr Leu Gly Glu Leu Met Pro His
 50 55 60
 Ile Pro Gln Leu Ala Asp Arg Val Ile Gln Asp Thr Thr Ala Glu Thr
 65 70 75 80
 Leu Ala Gly His Asp Val Val Phe Leu Gly Leu Pro His Gly Phe Ser
 85 90 95
 Ala Glu Ile Ala Leu Gln Leu Gly Pro Asp Val Thr Val Ile Asp Cys
 100 105 110
 Ala Ala Asp Phe Arg Leu Gln Asn Ala Ala Asp Trp Glu Lys Phe Tyr
 115 120 125
 Gly Ser Glu His Gln Gly Thr Trp Pro Tyr Gly Ile Pro Glu Met Pro
 130 135 140
 Gly His Arg Glu Ala Leu Arg Gly Ala Lys Arg Val Ala Val Pro Gly
 145 150 155 160
 Cys Phe Pro Thr Gly Ala Thr Leu Ala Leu Leu Pro Ala Val Gln Ala
 165 170 175

Gly Leu Ile Glu Pro Asp Val Ser Val Val Ser Ile Thr Gly Val Ser
 180 185 190

Gly Ala Gly Lys Lys Ala Ser Val Ala Leu Leu Gly Ser Glu Thr Met
 195 200 205

Gly Ser Leu Lys Ala Tyr Asn Thr Ser Gly Lys His Arg His Thr Pro
 210 215 220

Glu Ile Ala Gln Asn Leu Gly Glu Val Ser Asp Lys Pro Val Lys Val
 225 230 235 240

Ser Phe Thr Pro Val Leu Ala Pro Leu Pro Arg Glu Phe Ser Pro Leu
 245 250 255

Gln Pro His Leu
 260

<210> 325
 <211> 414
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(391)
 <223> RXA02154

<400> 325
 cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60

caccgttacc tcgcgaattc tcaccactgc aaccgcacct ttg aaa gaa ggc gtt 115
 Leu Lys Glu Gly Val
 1 5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa 163
 Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu
 10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca 211
 Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala
 25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa 259
 Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu
 40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307
 Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
 55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
 Thr Ala Gly Ala Ala Gln Cys Met Asn Leu Ser Val Gly Phe Asp
 70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401
 Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro
 90 95

ccttaaagcg gcg 414

```
<210> 326
<211> 97
<212> PRT
<213> Corynebacterium glutamicum
```

```

<400> 326
Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
  1                      5                      10                      15

Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
                20                      25                      30

Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
      35                      40                      45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
  50                      55                      60

Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
  65                      70                      75                      80

Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
                85                      90                      95

Pro

```

```
<210> 327
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1273)
<223> RXA02157
```

<400> 327																
gggtggaatt	ggcacgatgg	tgctgccgga	tgtttttgat	cgggagaatt	atcctgaagg	60										
caccgttttt	agaaaagacg	acaaggatgg	ggaactgtaa	atg	agc	acg	ctg	gaa	115							
				Met	Ser	Thr	Leu	Glu								
				1				5								
act	tgg	cca	cag	gtc	att	att	aat	acg	tac	ggc	acc	cca	cca	gtt	gag	163
Thr	Trp	Pro	Gln	Val	Ile	Ile	Asn	Thr	Tyr	Gly	Thr	Pro	Pro	Val	Glu	
				10					15					20		
ctg	gtg	tcc	ggc	aag	ggc	gca	acc	gtc	act	gat	gac	cag	ggc	aat	gtc	211
Leu	Val	Ser	Gly	Lys	Gly	Ala	Thr	Val	Thr	Asp	Asp	Gln	Gly	Asn	Val	
			25					30					35			
tac	atc	gac	ttg	ctc	gcg	ggc	atc	gca	gtc	aac	gcg	ttg	ggc	cac	gcc	259
Tyr	Ile	Asp	Leu	Leu	Ala	Gly	Ile	Ala	Val	Asn	Ala	Leu	Gly	His	Ala	
		40					45					50				
cac	ccg	gcg	atc	atc	gag	gcg	gtc	acc	aac	cag	atc	ggc	caa	ctt	ggc	307
His	Pro	Ala	Ile	Ile	Glu	Ala	Val	Thr	Asn	Gln	Ile	Gly	Gln	Leu	Gly	

55	60	65	
cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu 70 75 80 85			355
gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln 90 95 100			403
acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala 105 110 115			451
ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val 120 125 130			499
cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln 135 140 145			547
cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe 150 155 160 165			595
tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn 170 175 180			643
cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr 185 190 195			691
ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu 200 205 210			739
tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly 215 220 225			787
gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val 230 235 240 245			835
ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile 250 255 260			883
ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly 265 270 275			931
aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala 280 285 290			979
aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027 Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala			

295 300 305
 cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt
 1075
 Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
 310 315 320 325
 gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc
 1123
 Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
 330 335 340
 gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att
 1171
 Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
 345 350 355
 ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg
 1219
 Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
 360 365 370
 atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca
 1267
 Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
 375 380 385
 atc gca taaaggactc aaacttatga ctt
 1296
 Ile Ala
 390
 <210> 328
 <211> 391
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 328
 Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
 1 5 10 15
 Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
 20 25 30
 Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
 35 40 45
 Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
 50 55 60
 Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
 65 70 75 80
 Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
 85 90 95
 Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
 100 105 110
 Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg

115	120	125
Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu 130 135 140		
Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro 145 150 155 160		
Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys 165 170 175		
Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro 180 185 190		
Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys 195 200 205		
Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp 210 215 220		
Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln 225 230 235 240		
His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly 245 250 255		
Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu 260 265 270		
Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val 275 280 285		
Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe 290 295 300		
Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala 305 310 315 320		
Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly 325 330 335		
Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe 340 345 350		
Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu 355 360 365		
Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys 370 375 380		
Ala Ile Ala Glu Thr Ile Ala 385 390		

<210> 329

<211> 1491

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1468)

<223> RXS02970

<400> 329

```

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttattttaag acttcataat attttgggga gtgaactggg ttg gca ttg aag ggt 115
                                   Leu Ala Leu Lys Gly
                                   1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
              10              15              20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
              25              30              35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
              40              45              50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
              55              60              65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
              70              75              80              85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
              90              95              100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
              105              110              115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
              120              125              130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
              135              140              145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
              150              155              160              165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
              170              175              180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
              185              190              195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
              200              205              210

```

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
 His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
 215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
 Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
 230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
 Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
 250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
 Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
 265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
 Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
 280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
 1027
 Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
 295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
 1075
 Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
 310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
 1123
 Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
 330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
 1171
 Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
 345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
 1219
 Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
 360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
 1267
 Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
 375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
 1315
 Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
 390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
 1363
 Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
 410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

gcg ttg ttc taagttttct agataacaag gcc
1491

Ala Leu Phe
455

<210> 330

<211> 456

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 330

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
 405 410 415
 Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
 420 425 430
 Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
 435 440 445
 Leu Thr Phe Ala Gly Ala Leu Phe
 450 455

<210> 331

<211> 1330

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> FRXA01009

<400> 331

aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttattttaag acttcataat attttgggga gtgaactggt	ttg gca ttg aag ggt	115
	Leu Ala Leu Lys Gly	
	1 5	
tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca	163	
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala		
10 15 20		
aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc	211	
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe		
25 30 35		
cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct	259	
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala		
40 45 50		
gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac	307	
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp		
55 60 65		
atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga	355	
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg		
70 75 80 85		
tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac	403	
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn		
90 95 100		
ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg	451	
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val		
105 110 115		
tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc	499	
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly		
120 125 130		
gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga	547	
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly		
135 140 145		
cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga	595	
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly		
150 155 160 165		
tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643	
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr		
170 175 180		
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691	
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser		
185 190 195		
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739	
Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys Glu Arg Ala Leu Lys		
200 205 210		
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787	
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala		
215 220 225		


```

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230                235                240                245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
                250                255                260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
                265                270                275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
                280                285                290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc
1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
295                300                305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc
1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310                315                320                325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag
1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
330                335                340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct
1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
345                350                355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa
1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
360                365                370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca
1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
375                380                385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390                395                400                405

ttc aag gaa cgc ggc
1330
Phe Lys Glu Arg Gly
410

```

<210> 332

<211> 410

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 5 10 15
 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255
 Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

<210> 333
 <211> 1080
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1057)
 <223> RXA02158

<400> 333
 aacattatcc gtttgacccc gccgctggtg atcaccgacg aagaaatcgc agacgcagtc 60

aaggctattg ccgagacaat cgcataaagg actcaaactt atg act tca caa cca 115
 Met Thr Ser Gln Pro
 1 5

cag gtt cgc cat ttt ctg gct gat gat gat ctc acc cct gca gag cag 163
 Gln Val Arg His Phe Leu Ala Asp Asp Asp Leu Thr Pro Ala Glu Gln
 10 15 20

gca gag gtt ttg acc cta gcc gca aag ctc aag gca gcg ccg ttt tcg 211
 Ala Glu Val Leu Thr Leu Ala Ala Lys Leu Lys Ala Ala Pro Phe Ser
 25 30 35

gag cgt cca ctc gag gga cca aag tcc gtt gca gtt ctt ttt gat aag 259
 Glu Arg Pro Leu Glu Gly Pro Lys Ser Val Ala Val Leu Phe Asp Lys
 40 45 50

act tca act cgt act cgc ttc tcc ttc gac gcg ggc atc gct cat ttg 307
 Thr Ser Thr Arg Thr Arg Phe Ser Phe Asp Ala Gly Ile Ala His Leu
 55 60 65

ggg gga cac gcc atc gtc gtg gat tcc ggt agc tca cag atg ggt aag 355
 Gly Gly His Ala Ile Val Val Asp Ser Gly Ser Ser Gln Met Gly Lys
 70 75 80 85

ggc gag tcc ctg cag gac acc gca gct gta ttg tcc cgc tac gtg gaa 403
 Gly Glu Ser Leu Gln Asp Thr Ala Ala Val Leu Ser Arg Tyr Val Glu
 90 95 100

gca att gtg tgg cgc acc tac gca cac agc aat ttc cac gcc atg gcg 451
 Ala Ile Val Trp Arg Thr Tyr Ala His Ser Asn Phe His Ala Met Ala
 105 110 115

gag acg tcc act gtg ccg ctg gtg aac tcc ttg tcc gat gat ctg cac 499
 Glu Thr Ser Thr Val Pro Leu Val Asn Ser Leu Ser Asp Asp Leu His
 120 125 130

cca tgc cag att ctg gct gat ctg cag act atc gtg gaa aac ctc agc 547
 Pro Cys Gln Ile Leu Ala Asp Leu Gln Thr Ile Val Glu Asn Leu Ser
 135 140 145

cct gaa gaa ggc cca gca ggc ctt aag ggt aag aag gct gtg tac ctg 595
 Pro Glu Glu Gly Pro Ala Gly Leu Lys Gly Lys Lys Ala Val Tyr Leu
 150 155 160 165

ggc gat ggc gac aac aac atg gcc aac tcc tac atg att ggc ttt gcc 643
 Gly Asp Gly Asp Asn Asn Met Ala Asn Ser Tyr Met Ile Gly Phe Ala
 170 175 180

acc gcg ggc atg gat att tcc atc atc gct cct gaa ggg ttc cag cct 691
 Thr Ala Gly Met Asp Ile Ser Ile Ile Ala Pro Glu Gly Phe Gln Pro
 185 190 195

cgt gcg gaa ttc gtg gag cgc gcg gaa aag cgt ggc cag gaa acc ggc 739
 Arg Ala Glu Phe Val Glu Arg Ala Glu Lys Arg Gly Gln Glu Thr Gly
 200 205 210

gcg aag gtt gtt gtc acc gac agc ctc gac gag gtt gcc ggc gcc gat 787
 Ala Lys Val Val Val Thr Asp Ser Leu Asp Glu Val Ala Gly Ala Asp
 215 220 225

gtt gtc atc acc gat acc tgg gta tcc atg ggt atg gaa aac gac ggc 835
 Val Val Ile Thr Asp Thr Trp Val Ser Met Gly Met Glu Asn Asp Gly
 230 235 240 245

atc gat cgc acc aca cct ttc gtt cct tac cag gtc aac gat gag gtc 883
 Ile Asp Arg Thr Thr Pro Phe Val Pro Tyr Gln Val Asn Asp Glu Val
 250 255 260

atg gcg aaa gct aac gac ggc gcc atc ttc ctg cac tgc ctt cct gcc 931
 Met Ala Lys Ala Asn Asp Gly Ala Ile Phe Leu His Cys Leu Pro Ala
 265 270 275

tac cgt ggc aaa gaa gtg gca gcc tcc gtg att gat gga cca gcg tcc 979
 Tyr Arg Gly Lys Glu Val Ala Ala Ser Val Ile Asp Gly Pro Ala Ser
 280 285 290

aaa gtt ttc gat gaa gca gaa aac cgc ctc cac gct cag aaa gca ctg
 1027
 Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His Ala Gln Lys Ala Leu
 295 300 305

ctg gtg tgg ctg ctg gcc aac cag ccg agg taagacatgt cccttggtc
 1077
 Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 310 315

aac
 1080

<210> 334

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Met	Thr	Ser	Gln	Pro	Gln	Val	Arg	His	Phe	Leu	Ala	Asp	Asp	Asp	Leu
1				5					10					15	
Thr	Pro	Ala	Glu	Gln	Ala	Glu	Val	Leu	Thr	Leu	Ala	Ala	Lys	Leu	Lys
			20					25					30		
Ala	Ala	Pro	Phe	Ser	Glu	Arg	Pro	Leu	Glu	Gly	Pro	Lys	Ser	Val	Ala
		35					40					45			
Val	Leu	Phe	Asp	Lys	Thr	Ser	Thr	Arg	Thr	Arg	Phe	Ser	Phe	Asp	Ala
	50					55					60				
Gly	Ile	Ala	His	Leu	Gly	Gly	His	Ala	Ile	Val	Val	Asp	Ser	Gly	Ser
65					70					75					80
Ser	Gln	Met	Gly	Lys	Gly	Glu	Ser	Leu	Gln	Asp	Thr	Ala	Ala	Val	Leu
				85					90					95	
Ser	Arg	Tyr	Val	Glu	Ala	Ile	Val	Trp	Arg	Thr	Tyr	Ala	His	Ser	Asn
			100					105					110		
Phe	His	Ala	Met	Ala	Glu	Thr	Ser	Thr	Val	Pro	Leu	Val	Asn	Ser	Leu
		115					120					125			
Ser	Asp	Asp	Leu	His	Pro	Cys	Gln	Ile	Leu	Ala	Asp	Leu	Gln	Thr	Ile
	130					135					140				
Val	Glu	Asn	Leu	Ser	Pro	Glu	Glu	Gly	Pro	Ala	Gly	Leu	Lys	Gly	Lys
145					150					155					160
Lys	Ala	Val	Tyr	Leu	Gly	Asp	Gly	Asp	Asn	Asn	Met	Ala	Asn	Ser	Tyr
				165					170					175	
Met	Ile	Gly	Phe	Ala	Thr	Ala	Gly	Met	Asp	Ile	Ser	Ile	Ile	Ala	Pro
			180					185					190		
Glu	Gly	Phe	Gln	Pro	Arg	Ala	Glu	Phe	Val	Glu	Arg	Ala	Glu	Lys	Arg
		195					200					205			
Gly	Gln	Glu	Thr	Gly	Ala	Lys	Val	Val	Val	Thr	Asp	Ser	Leu	Asp	Glu
	210					215					220				
Val	Ala	Gly	Ala	Asp	Val	Val	Ile	Thr	Asp	Thr	Trp	Val	Ser	Met	Gly
225					230					235					240
Met	Glu	Asn	Asp	Gly	Ile	Asp	Arg	Thr	Thr	Pro	Phe	Val	Pro	Tyr	Gln
				245					250					255	
Val	Asn	Asp	Glu	Val	Met	Ala	Lys	Ala	Asn	Asp	Gly	Ala	Ile	Phe	Leu
			260					265					270		
His	Cys	Leu	Pro	Ala	Tyr	Arg	Gly	Lys	Glu	Val	Ala	Ala	Ser	Val	Ile
		275					280					285			

Asp Gly Pro Ala Ser Lys Val Phe Asp Glu Ala Glu Asn Arg Leu His
 290 295 300

Ala Gln Lys Ala Leu Leu Val Trp Leu Leu Ala Asn Gln Pro Arg
 305 310 315

<210> 335

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1303)

<223> RXA02160

<400> 335

ttttcgagga ataccaaccc tttcaacaca ataattttct ttaaacaatcc ttgctgtcca 60

ccacggctgg caaggaactt aaaatgaagg agcacacctc atg act aac cgc atc 115
 Met Thr Asn Arg Ile
 1 5

gtt ctt gca tac tcc ggc ggt ctg gac acc act gtg gca att cca tac 163
 Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr Val Ala Ile Pro Tyr
 10 15 20

ctg aag aag atg att gat ggt gaa gtc atc gca gtt tcc ctc gac ctg 211
 Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala Val Ser Leu Asp Leu
 25 30 35

ggc cag ggt gga gag aac atg gac aac gtt cgc cag cgt gca ttg gat 259
 Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg Gln Arg Ala Leu Asp
 40 45 50

gcc ggt gca gct gag tcc atc gtt gtt gat gca aag gat gag ttc gct 307
 Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala Lys Asp Glu Phe Ala
 55 60 65

gag gag tac tgc ctg cca acc atc aag gca aac ggc atg tac atg aag 355
 Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn Gly Met Tyr Met Lys
 70 75 80 85

cag tac cca ctg gtt tct gca atc tcc cgc cca ctg atc gtc aag cac 403
 Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro Leu Ile Val Lys His
 90 95 100

ctc gtt gag gct ggc aag cag ttc aac ggt acc cac gtt gca cac ggc 451
 Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr His Val Ala His Gly
 105 110 115

tgc act ggt aag ggc aac gac cag gtt cgt ttc gag gtc ggc ttc atg 499
 Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe Glu Val Gly Phe Met
 120 125 130

gac acc gat cca aac ctg gag atc att gca cct gct cgt gac ttc gca 547
 Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro Ala Arg Asp Phe Ala
 135 140 145

tgg acc cgc gac aag gct atc gcc ttc gcc gag gag aac aac gtt cca 595

Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu Glu Asn Asn Val Pro	
150 155 160 165	
atc gag cag tcc gtg aag tcc cca ttc tcc atc gac cag aac gtc tgg	643
Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile Asp Gln Asn Val Trp	
170 175 180	
ggc cgc gct att gag acc ggt tac ctg gaa gat ctg tgg aat gct cca	691
Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp Leu Trp Asn Ala Pro	
185 190 195	
acc aag gac atc tac gca tac acc gag gat cca gct ctg ggt aac gct	739
Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro Ala Leu Gly Asn Ala	
200 205 210	
cca gat gag gtc atc atc tcc ttc gag ggt ggc aag cca gtc tcc atc	787
Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly Lys Pro Val Ser Ile	
215 220 225	
gat ggc cgt cca gtc tcc gta ctg cag gct att gaa gag ctg aac cgt	835
Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile Glu Glu Leu Asn Arg	
230 235 240 245	
cgt gca ggc gca cag ggc gtt ggc cgc ctt gac atg gtt gag gac cgt	883
Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp Met Val Glu Asp Arg	
250 255 260	
ctc gtg ggc atc aag tcc cgc gaa atc tac gaa gca cca ggc gca atc	931
Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu Ala Pro Gly Ala Ile	
265 270 275	
gca ctg att aag gct cac gag gct ttg gaa gat gtc acc atc gag cgc	979
Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp Val Thr Ile Glu Arg	
280 285 290	
gaa ctg gct cgc tac aag cgc ggc gtt gac gca cgt tgg gct gag gaa	
1027	
Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala Arg Trp Ala Glu Glu	
295 300 305	
gta tac gac ggc ctg tgg ttc gga cct ctg aag cgc tcc ctg gac gcg	
1075	
Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys Arg Ser Leu Asp Ala	
310 315 320 325	
ttc att gat tcc acc cag gag cac gtc acc ggc gat atc cgc atg gtt	
1123	
Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly Asp Ile Arg Met Val	
330 335 340	
ctg cac gca ggt tcc atc acc atc aat ggt cgt cgt tcc agc cac tcc	
1171	
Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg Arg Ser Ser His Ser	
345 350 355	
ctg tac gac ttc aac ctg gct acc tac gac acc ggc gac acc ttc gac	
1219	
Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr Gly Asp Thr Phe Asp	
360 365 370	

cag acc ctg gct aag ggc ttt gtc cag ctg cac ggt ctg tcc tcc aag
1267

Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His Gly Leu Ser Ser Lys
375 380 385

atc gct aac aag cgc gat cgc gaa gct ggc aac aac taagccacct
1313

Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn Asn
390 395 400

tttcaagcat cca
1326

<210> 336

<211> 401

<212> PRT

<213> Corynebacterium glutamicum

<400> 336

Met Thr Asn Arg Ile Val Leu Ala Tyr Ser Gly Gly Leu Asp Thr Thr
1 5 10 15

Val Ala Ile Pro Tyr Leu Lys Lys Met Ile Asp Gly Glu Val Ile Ala
20 25 30

Val Ser Leu Asp Leu Gly Gln Gly Gly Glu Asn Met Asp Asn Val Arg
35 40 45

Gln Arg Ala Leu Asp Ala Gly Ala Ala Glu Ser Ile Val Val Asp Ala
50 55 60

Lys Asp Glu Phe Ala Glu Glu Tyr Cys Leu Pro Thr Ile Lys Ala Asn
65 70 75 80

Gly Met Tyr Met Lys Gln Tyr Pro Leu Val Ser Ala Ile Ser Arg Pro
85 90 95

Leu Ile Val Lys His Leu Val Glu Ala Gly Lys Gln Phe Asn Gly Thr
100 105 110

His Val Ala His Gly Cys Thr Gly Lys Gly Asn Asp Gln Val Arg Phe
115 120 125

Glu Val Gly Phe Met Asp Thr Asp Pro Asn Leu Glu Ile Ile Ala Pro
130 135 140

Ala Arg Asp Phe Ala Trp Thr Arg Asp Lys Ala Ile Ala Phe Ala Glu
145 150 155 160

Glu Asn Asn Val Pro Ile Glu Gln Ser Val Lys Ser Pro Phe Ser Ile
165 170 175

Asp Gln Asn Val Trp Gly Arg Ala Ile Glu Thr Gly Tyr Leu Glu Asp
180 185 190

Leu Trp Asn Ala Pro Thr Lys Asp Ile Tyr Ala Tyr Thr Glu Asp Pro
195 200 205

Ala Leu Gly Asn Ala Pro Asp Glu Val Ile Ile Ser Phe Glu Gly Gly
210 215 220

Lys Pro Val Ser Ile Asp Gly Arg Pro Val Ser Val Leu Gln Ala Ile
 225 230 235 240
 Glu Glu Leu Asn Arg Arg Ala Gly Ala Gln Gly Val Gly Arg Leu Asp
 245 250 255
 Met Val Glu Asp Arg Leu Val Gly Ile Lys Ser Arg Glu Ile Tyr Glu
 260 265 270
 Ala Pro Gly Ala Ile Ala Leu Ile Lys Ala His Glu Ala Leu Glu Asp
 275 280 285
 Val Thr Ile Glu Arg Glu Leu Ala Arg Tyr Lys Arg Gly Val Asp Ala
 290 295 300
 Arg Trp Ala Glu Glu Val Tyr Asp Gly Leu Trp Phe Gly Pro Leu Lys
 305 310 315 320
 Arg Ser Leu Asp Ala Phe Ile Asp Ser Thr Gln Glu His Val Thr Gly
 325 330 335
 Asp Ile Arg Met Val Leu His Ala Gly Ser Ile Thr Ile Asn Gly Arg
 340 345 350
 Arg Ser Ser His Ser Leu Tyr Asp Phe Asn Leu Ala Thr Tyr Asp Thr
 355 360 365
 Gly Asp Thr Phe Asp Gln Thr Leu Ala Lys Gly Phe Val Gln Leu His
 370 375 380
 Gly Leu Ser Ser Lys Ile Ala Asn Lys Arg Asp Arg Glu Ala Gly Asn
 385 390 395 400
 Asn

<210> 337
 <211> 1554
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1531)
 <223> RXN02162

<400> 337
 gatcgctaac aagcgcgatc gcgaagctgg caacaactaa gccacctttt caagcatcca 60
 gactagaact tcaagtattt agaaagtaga agaacaccac atg gaa cag cac gga 115
 Met Glu Gln His Gly
 1 5
 acc aat gaa ggt gcg ctg tgg ggc ggc cgc ttc tcc ggt gga ccc tcc 163
 Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe Ser Gly Gly Pro Ser
 10 15 20
 gag gcc atg ttc gcc ttg agt gtc tcc act cat ttc gac tgg gtt ttg 211
 Glu Ala Met Phe Ala Leu Ser Val Ser Thr His Phe Asp Trp Val Leu

25						30						35						
gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac	259		
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His			
		40					45					50						
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307		
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly			
		55				60					65							
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg	355		
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu			
		70			75					80					85			
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac	403		
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp			
				90					95					100				
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc	451		
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg			
			105					110					115					
aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg	499		
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val			
		120					125					130						
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547		
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala			
		135				140					145							
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595		
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe			
		150			155					160					165			
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643		
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala			
				170					175					180				
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691		
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg			
			185					190					195					
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg	739		
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu			
		200					205					210						
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787		
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala			
		215				220					225							
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835		
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu			
		230			235					240					245			
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	gtg	gat	atg	tcc	cgc	ttg	gct	883		
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Val	Asp	Met	Ser	Arg	Leu	Ala			
			250					255						260				
gaa	gaa	atc	atc	gca	tgg	tgc	acc	cca	gaa	ttt	ggg	tac	atc	acc	ttg	931		
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu			
			265					270					275					

```

tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac 979
Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met Pro Gln Lys Lys Asn
280 285 290

cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt
1027
Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser Gly Arg Leu Ile Gly
295 300 305

aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac
1075
Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala Gln Pro Leu Ala Tyr
310 315 320 325

aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg
1123
Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile Val Asp Ser Val Ala
330 335 340

cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg
1171
Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly Leu Val Ser Thr Leu
345 350 355

acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc
1219
Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala Pro Ala Gly Phe Thr
360 365 370

ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc
1267
Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg Gln Gly Val Pro Phe
375 380 385

cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc
1315
Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val Arg Ile Ala Glu Ser
390 395 400 405

agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt
1363
Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu Glu Leu Ser Gly Val
410 415 420

gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt
1411
Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val Leu Thr Ile Asp Gly
425 430 435

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt
1459
Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
440 445 450

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag
1507
Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
455 460 465

```

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg

1554

Trp Ala Arg Ala Gly Val Arg Arg

470

475

<210> 338

<211> 477

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 338

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
1 5 10 15

Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Val Asp
245 250 255

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe

```
<210> 339
<211> 906
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(883)  
<223> FRXA02161
```

506

				10				15				20							
gag	gcc	atg	ttc	gcc	ttg	agt	gtc	tcc	act	cat	ttc	gac	tgg	gtt	ttg	211			
Glu	Ala	Met	Phe	Ala	Leu	Ser	Val	Ser	Thr	His	Phe	Asp	Trp	Val	Leu				
25								30				35							
gcc	cct	tat	gat	gtg	ttg	gcc	tcc	aag	gca	cac	gcc	aag	gtt	ttg	cac	259			
Ala	Pro	Tyr	Asp	Val	Leu	Ala	Ser	Lys	Ala	His	Ala	Lys	Val	Leu	His				
40								45				50							
caa	gca	gat	cta	ctt	tct	gat	gaa	gat	cta	gcc	acc	atg	ctg	gct	ggg	307			
Gln	Ala	Asp	Leu	Leu	Ser	Asp	Glu	Asp	Leu	Ala	Thr	Met	Leu	Ala	Gly				
55								60				65							
ctt	gat	cag	ctg	ggc	aag	gat	gtc	gcc	gac	gga	acc	ttc	ggg	ccg	ctg	355			
Leu	Asp	Gln	Leu	Gly	Lys	Asp	Val	Ala	Asp	Gly	Thr	Phe	Gly	Pro	Leu				
70								75				80				85			
cct	tct	gat	gag	gat	gtg	cac	ggc	gcg	atg	gaa	cgc	ggg	gtg	att	gac	403			
Pro	Ser	Asp	Glu	Asp	Val	His	Gly	Ala	Met	Glu	Arg	Gly	Val	Ile	Asp				
90								95				100							
cgc	gtt	ggg	cct	gag	gtg	ggc	ggc	cgt	ctg	cgc	gct	ggg	cgt	tcc	cgc	451			
Arg	Val	Gly	Pro	Glu	Val	Gly	Gly	Arg	Leu	Arg	Ala	Gly	Arg	Ser	Arg				
105								110				115							
aac	gac	cag	gtg	gca	acc	ctg	ttc	cgc	atg	tgg	gtc	cgc	gac	gca	gtg	499			
Asn	Asp	Gln	Val	Ala	Thr	Leu	Phe	Arg	Met	Trp	Val	Arg	Asp	Ala	Val				
120								125				130							
cgc	gac	atc	gcg	ctg	gga	aca	acc	gag	ctt	gtc	gac	gcc	ctc	agc	gcc	547			
Arg	Asp	Ile	Ala	Leu	Gly	Thr	Thr	Glu	Leu	Val	Asp	Ala	Leu	Ser	Ala				
135								140				145							
caa	gct	aag	gca	cat	gca	ggc	gcg	atc	atg	cca	ggc	aag	acc	cac	ttc	595			
Gln	Ala	Lys	Ala	His	Ala	Gly	Ala	Ile	Met	Pro	Gly	Lys	Thr	His	Phe				
150								155				160				165			
cag	gca	gct	cag	ccg	gtc	ctt	ctg	gca	cac	cag	ctg	ctg	gca	cac	gca	643			
Gln	Ala	Ala	Gln	Pro	Val	Leu	Leu	Ala	His	Gln	Leu	Leu	Ala	His	Ala				
170								175				180							
cag	cct	ttg	ctg	cgc	gat	att	gat	cgt	atc	cgt	gac	ctg	gac	aag	cgt	691			
Gln	Pro	Leu	Leu	Arg	Asp	Ile	Asp	Arg	Ile	Arg	Asp	Leu	Asp	Lys	Arg				
185								190				195							
ctt	gcg	gtg	tct	cct	tac	ggg	tcc	ggc	gca	ctt	gct	ggg	tcc	tct	ttg	739			
Leu	Ala	Val	Ser	Pro	Tyr	Gly	Ser	Gly	Ala	Leu	Ala	Gly	Ser	Ser	Leu				
200								205				210							
aag	ctc	aac	cct	gaa	gca	atc	gct	gaa	gaa	ctc	ggc	ttt	gat	tcc	gca	787			
Lys	Leu	Asn	Pro	Glu	Ala	Ile	Ala	Glu	Glu	Leu	Gly	Phe	Asp	Ser	Ala				
215								220				225							
gca	gat	aac	tcc	att	gat	gcc	acc	agc	tcc	cgc	gat	ttc	gca	tct	gaa	835			
Ala	Asp	Asn	Ser	Ile	Asp	Ala	Thr	Ser	Ser	Arg	Asp	Phe	Ala	Ser	Glu				
230								235				240				245			
acc	gcc	ttc	gtg	ctg	gcg	cag	ctt	gca	ngt	gga	tat	gtc	ccg	ctt	ggc	883			
Thr	Ala	Phe	Val	Leu	Ala	Gln	Leu	Ala	Xaa	Gly	Tyr	Val	Pro	Leu	Gly				
250								255				260							

tgaagaaatc atcgcatggt gca

906

<210> 340

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Glu Gln His Gly Thr Asn Glu Gly Ala Leu Trp Gly Gly Arg Phe
1 5 10 15

Ser Gly Gly Pro Ser Glu Ala Met Phe Ala Leu Ser Val Ser Thr His
20 25 30

Phe Asp Trp Val Leu Ala Pro Tyr Asp Val Leu Ala Ser Lys Ala His
35 40 45

Ala Lys Val Leu His Gln Ala Asp Leu Leu Ser Asp Glu Asp Leu Ala
50 55 60

Thr Met Leu Ala Gly Leu Asp Gln Leu Gly Lys Asp Val Ala Asp Gly
65 70 75 80

Thr Phe Gly Pro Leu Pro Ser Asp Glu Asp Val His Gly Ala Met Glu
85 90 95

Arg Gly Val Ile Asp Arg Val Gly Pro Glu Val Gly Gly Arg Leu Arg
100 105 110

Ala Gly Arg Ser Arg Asn Asp Gln Val Ala Thr Leu Phe Arg Met Trp
115 120 125

Val Arg Asp Ala Val Arg Asp Ile Ala Leu Gly Thr Thr Glu Leu Val
130 135 140

Asp Ala Leu Ser Ala Gln Ala Lys Ala His Ala Gly Ala Ile Met Pro
145 150 155 160

Gly Lys Thr His Phe Gln Ala Ala Gln Pro Val Leu Leu Ala His Gln
165 170 175

Leu Leu Ala His Ala Gln Pro Leu Leu Arg Asp Ile Asp Arg Ile Arg
180 185 190

Asp Leu Asp Lys Arg Leu Ala Val Ser Pro Tyr Gly Ser Gly Ala Leu
195 200 205

Ala Gly Ser Ser Leu Lys Leu Asn Pro Glu Ala Ile Ala Glu Glu Leu
210 215 220

Gly Phe Asp Ser Ala Ala Asp Asn Ser Ile Asp Ala Thr Ser Ser Arg
225 230 235 240

Asp Phe Ala Ser Glu Thr Ala Phe Val Leu Ala Gln Leu Ala Xaa Gly
245 250 255

Tyr Val Pro Leu Gly
260

```
<210> 341
<211> 786
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(763)  
<223> FRXA02162
```

<400> 341																
ctcgcgcttttg attccgcagc agataactcc attgatgcca ccagctccccg cgatttcgca																60
tctgaaaccg ccttcgtgct ggcgcagctt gcangtggat																
											atg	tcc	cgc	ttg	gct	115
											Met	Ser	Arg	Leu	Ala	
											1				5	
gaa gaa atc atc gca tgg tgc acc cca gaa ttt ggt tac atc acc ttg																163
Glu	Glu	Ile	Ile	Ala	Trp	Cys	Thr	Pro	Glu	Phe	Gly	Tyr	Ile	Thr	Leu	
				10					15					20		
tct gat tcc tgg tcc aca ggc agc tca atc atg ccg cag aag aag aac																211
Ser	Asp	Ser	Trp	Ser	Thr	Gly	Ser	Ser	Ile	Met	Pro	Gln	Lys	Lys	Asn	
			25					30					35			
cct gac gtg gca gag ctg acc cgt ggc aag tct ggt cgc ttg atc ggt																259
Pro	Asp	Val	Ala	Glu	Leu	Thr	Arg	Gly	Lys	Ser	Gly	Arg	Leu	Ile	Gly	
		40					45					50				
aac ctc acc ggt ctg ctg gct acc ctg aag gca cag cct tta gcg tac																307
Asn	Leu	Thr	Gly	Leu	Leu	Ala	Thr	Leu	Lys	Ala	Gln	Pro	Leu	Ala	Tyr	
	55					60					65					
aac cgc gac ctg cag gaa gat aag gaa cca atc gta gat tcc gtg gcg																355
Asn	Arg	Asp	Leu	Gln	Glu	Asp	Lys	Glu	Pro	Ile	Val	Asp	Ser	Val	Ala	
70				75					80						85	
cag ctc aac ctg ctg ctc cct gca atg act ggt ttg gtt tcc acc ttg																403
Gln	Leu	Asn	Leu	Leu	Leu	Pro	Ala	Met	Thr	Gly	Leu	Val	Ser	Thr	Leu	
			90						95					100		
acc ttc aac acc gag cgc atg cgt gaa ctt gca cca gca ggt ttc acc																451
Thr	Phe	Asn	Thr	Glu	Arg	Met	Arg	Glu	Leu	Ala	Pro	Ala	Gly	Phe	Thr	
			105					110					115			
ctt gcc acc gac ttg gct gag tgg atg gtg cgc cag ggc gtt cca ttc																499
Leu	Ala	Thr	Asp	Leu	Ala	Glu	Trp	Met	Val	Arg	Gln	Gly	Val	Pro	Phe	
		120				125					130					
cgt gag gca cac gaa gca tcc ggc gct tgc gtg cgg atc gcg gag tcc																547
Arg	Glu	Ala	His	Glu	Ala	Ser	Gly	Ala	Cys	Val	Arg	Ile	Ala	Glu	Ser	
	135					140				145						
agg gga gtg gac ctt atc gat ctc act gat gaa gaa ctc agt ggc gtt																595
Arg	Gly	Val	Asp	Leu	Ile	Asp	Leu	Thr	Asp	Glu	Glu	Leu	Ser	Gly	Val	
150					155					160					165	
gat gca cgt ctg acc cca gag gta cgg gaa gtg ctc acc att gat ggt																643
Asp	Ala	Arg	Leu	Thr	Pro	Glu	Val	Arg	Glu	Val	Leu	Thr	Ile	Asp	Gly	
			170						175					180		

gca gtg gct tcc cgt gca acg cgc ggt gga acc gcg ggc gtg cgg gtt 691
 Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr Ala Gly Val Arg Val
 185 190 195

gcg gag caa cgc gca cgt gtc gat gcc gca agt acc gct cac gcg gag 739
 Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser Thr Ala His Ala Glu
 200 205 210

tgg gca cgt gcg ggg gta cgt cga taagcattag tttatggcct gtg 786
 Trp Ala Arg Ala Gly Val Arg Arg
 215 220

<210> 342

<211> 221

<212> PRT

<213> Corynebacterium glutamicum

<400> 342

Met Ser Arg Leu Ala Glu Glu Ile Ile Ala Trp Cys Thr Pro Glu Phe
 1 5 10 15

Gly Tyr Ile Thr Leu Ser Asp Ser Trp Ser Thr Gly Ser Ser Ile Met
 20 25 30

Pro Gln Lys Lys Asn Pro Asp Val Ala Glu Leu Thr Arg Gly Lys Ser
 35 40 45

Gly Arg Leu Ile Gly Asn Leu Thr Gly Leu Leu Ala Thr Leu Lys Ala
 50 55 60

Gln Pro Leu Ala Tyr Asn Arg Asp Leu Gln Glu Asp Lys Glu Pro Ile
 65 70 75 80

Val Asp Ser Val Ala Gln Leu Asn Leu Leu Leu Pro Ala Met Thr Gly
 85 90 95

Leu Val Ser Thr Leu Thr Phe Asn Thr Glu Arg Met Arg Glu Leu Ala
 100 105 110

Pro Ala Gly Phe Thr Leu Ala Thr Asp Leu Ala Glu Trp Met Val Arg
 115 120 125

Gln Gly Val Pro Phe Arg Glu Ala His Glu Ala Ser Gly Ala Cys Val
 130 135 140

Arg Ile Ala Glu Ser Arg Gly Val Asp Leu Ile Asp Leu Thr Asp Glu
 145 150 155 160

Glu Leu Ser Gly Val Asp Ala Arg Leu Thr Pro Glu Val Arg Glu Val
 165 170 175

Leu Thr Ile Asp Gly Ala Val Ala Ser Arg Ala Thr Arg Gly Gly Thr
 180 185 190

Ala Gly Val Arg Val Ala Glu Gln Arg Ala Arg Val Asp Ala Ala Ser
 195 200 205

Thr Ala His Ala Glu Trp Ala Arg Ala Gly Val Arg Arg
 210 215 220

```
<210> 343
<211> 1269
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1246)
<223> RXA02262
```

<400> 343																	
gcaccaattt cggacctgaa atccccgagg aaaccgtgcc cgacgccgtg caggtgggcg																	60
tcgataagca aaaaatcgct gatactcgaa aggcctcaaa atg acc gca acc tac																	115
Met Thr Ala Thr Tyr																	5
1																	
acc act gaa acc gcc atc aat ttc ttg ttc ttg agc gaa ccg gac atg																	163
Thr Thr Glu Thr Ala Ile Asn Phe Leu Phe Leu Ser Glu Pro Asp Met																	
10 15 20																	
atc gcg gcc gga gtc aaa gac gtc gcg caa tgc gtc gat gtc atg gag																	211
Ile Ala Ala Gly Val Lys Asp Val Ala Gln Cys Val Asp Val Met Glu																	
25 30 35																	
gaa acg ctc gtg ctc ttg gcg cag ggc gac tac aaa atg gcc ggt ttg																	259
Glu Thr Leu Val Leu Leu Ala Gln Gly Asp Tyr Lys Met Ala Gly Leu																	
40 45 50																	
aac tcc aac tcg cat ggc gcg atg atc acc ttc ccg gaa aac cca gaa																	307
Asn Ser Asn Ser His Gly Ala Met Ile Thr Phe Pro Glu Asn Pro Glu																	
55 60 65																	
ttt gaa ggc atg ccc aag gac ggc ccc gac cgc cga ttc atg gcg atg																	355
Phe Glu Gly Met Pro Lys Asp Gly Pro Asp Arg Arg Phe Met Ala Met																	
70 75 80 85																	
ccc gca tac ctc ggc ggg cga ttc aaa aac acc ggc gtg aag tgg tac																	403
Pro Ala Tyr Leu Gly Gly Arg Phe Lys Asn Thr Gly Val Lys Trp Tyr																	
90 95 100																	
gga tcc aac gcg gaa aac aag gcc tca ggc ttg cct cgc tcg atc cac																	451
Gly Ser Asn Ala Glu Asn Lys Ala Ser Gly Leu Pro Arg Ser Ile His																	
105 110 115																	
acc ttc gtc ctc aac gac acg gtc acc ggt gca ccg aag gcc atc atg																	499
Thr Phe Val Leu Asn Asp Thr Val Thr Gly Ala Pro Lys Ala Ile Met																	
120 125 130																	
tcc gcg aac ctg ctg tcc gcc tac cgc acc ggc gcg gtt ccc ggc gtg																	547
Ser Ala Asn Leu Leu Ser Ala Tyr Arg Thr Gly Ala Val Pro Gly Val																	
135 140 145																	
ggc gtg aag cac tta gcg gtc gcc gac gcg aca acc ttg gct gtc gtc																	595
Gly Val Lys His Leu Ala Val Ala Asp Ala Thr Thr Leu Ala Val Val																	
150 155 160 165																	
gga cct ggt gtc atg gcg aaa acc atc acc gaa gcg tgc atc gca gag																	643
Gly Pro Gly Val Met Ala Lys Thr Ile Thr Glu Ala Cys Ile Ala Glu																	

	170	175	180	
cgc cca gga atc acc acc atc aag atc aag gga cgc agc gaa cgc ggc				691
Arg Pro Gly Ile Thr Thr Ile Lys Ile Lys Gly Arg Ser Glu Arg Gly				
	185	190	195	
atc aac gcc ttt gca aca tgg gcg ttg gaa aaa ttc ccc gag atc gaa				739
Ile Asn Ala Phe Ala Thr Trp Ala Leu Glu Lys Phe Pro Glu Ile Glu				
	200	205	210	
gtg gtc gcc gtc gga tct gaa gaa gac gtg gtc aaa gac gcc gac atc				787
Val Val Ala Val Gly Ser Glu Glu Asp Val Val Lys Asp Ala Asp Ile				
	215	220	225	
gtc atc gcc gcc acc acc acg gac gcc gcc ggc tcc tcc gcc ttc cca				835
Val Ile Ala Ala Thr Thr Thr Asp Ala Ala Gly Ser Ser Ala Phe Pro				
	230	235	240	245
tac ttc aaa aaa gaa tgg ctc aag ccg ggc gca ttg ctg ctg ctt cca				883
Tyr Phe Lys Lys Glu Trp Leu Lys Pro Gly Ala Leu Leu Leu Leu Pro				
	250	255	260	
gcc gcc ggt cgc ttc gac gac gct tat ttg ctt gac gac gcc cgc ctc				931
Ala Ala Gly Arg Phe Asp Asp Ala Tyr Leu Leu Asp Asp Ala Arg Leu				
	265	270	275	
gtt gtt gac tac atg ggg ctc tac gaa gcc tgg gca gaa gaa tac ggc				979
Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp Ala Glu Glu Tyr Gly				
	280	285	290	
cca cag gcc tac caa cta ctc ggc att cca gga acc cac tgg tac gac				
1027				
Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly Thr His Trp Tyr Asp				
	295	300	305	
ctg gcg ctg caa gga aaa ctc gac ctt gca aag att tcc cag att ggc				
1075				
Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys Ile Ser Gln Ile Gly				
	310	315	320	325
gat atc tgc tcc ggc aag cta ccc gga cgc acc aac gat gag gaa atc				
1123				
Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr Asn Asp Glu Glu Ile				
	330	335	340	
atc ctc tat tcc gtc ggc ggc atg cca gta gaa gac gtc gcc tgg gca				
1171				
Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu Asp Val Ala Trp Ala				
	345	350	355	
acc caa gtg tat gaa aac gcc ctg gaa aaa ggc gtc ggc acc aca ttg				
1219				
Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly Val Gly Thr Thr Leu				
	360	365	370	
aac ctg tgg gaa tca ccc gca ctg gct tgagagaaga aacaacaatg				
1266				
Asn Leu Trp Glu Ser Pro Ala Leu Ala				
	375	380		

aaa
1269

<210> 344
<211> 382
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 344

Met	Thr	Ala	Thr	Tyr	Thr	Thr	Glu	Thr	Ala	Ile	Asn	Phe	Leu	Phe	Leu	1	5	10	15
Ser	Glu	Pro	Asp	Met	Ile	Ala	Ala	Gly	Val	Lys	Asp	Val	Ala	Gln	Cys	20	25	30	
Val	Asp	Val	Met	Glu	Glu	Thr	Leu	Val	Leu	Leu	Ala	Gln	Gly	Asp	Tyr	35	40	45	
Lys	Met	Ala	Gly	Leu	Asn	Ser	Asn	Ser	His	Gly	Ala	Met	Ile	Thr	Phe	50	55	60	
Pro	Glu	Asn	Pro	Glu	Phe	Glu	Gly	Met	Pro	Lys	Asp	Gly	Pro	Asp	Arg	65	70	75	80
Arg	Phe	Met	Ala	Met	Pro	Ala	Tyr	Leu	Gly	Gly	Arg	Phe	Lys	Asn	Thr	85	90	95	
Gly	Val	Lys	Trp	Tyr	Gly	Ser	Asn	Ala	Glu	Asn	Lys	Ala	Ser	Gly	Leu	100	105	110	
Pro	Arg	Ser	Ile	His	Thr	Phe	Val	Leu	Asn	Asp	Thr	Val	Thr	Gly	Ala	115	120	125	
Pro	Lys	Ala	Ile	Met	Ser	Ala	Asn	Leu	Leu	Ser	Ala	Tyr	Arg	Thr	Gly	130	135	140	
Ala	Val	Pro	Gly	Val	Gly	Val	Lys	His	Leu	Ala	Val	Ala	Asp	Ala	Thr	145	150	155	160
Thr	Leu	Ala	Val	Val	Gly	Pro	Gly	Val	Met	Ala	Lys	Thr	Ile	Thr	Glu	165	170	175	
Ala	Cys	Ile	Ala	Glu	Arg	Pro	Gly	Ile	Thr	Thr	Ile	Lys	Ile	Lys	Gly	180	185	190	
Arg	Ser	Glu	Arg	Gly	Ile	Asn	Ala	Phe	Ala	Thr	Trp	Ala	Leu	Glu	Lys	195	200	205	
Phe	Pro	Glu	Ile	Glu	Val	Val	Ala	Val	Gly	Ser	Glu	Glu	Asp	Val	Val	210	215	220	
Lys	Asp	Ala	Asp	Ile	Val	Ile	Ala	Ala	Thr	Thr	Thr	Asp	Ala	Ala	Gly	225	230	235	240
Ser	Ser	Ala	Phe	Pro	Tyr	Phe	Lys	Lys	Glu	Trp	Leu	Lys	Pro	Gly	Ala	245	250	255	
Leu	Leu	Leu	Leu	Pro	Ala	Ala	Gly	Arg	Phe	Asp	Asp	Ala	Tyr	Leu	Leu	260	265	270	

Asp Asp Ala Arg Leu Val Val Asp Tyr Met Gly Leu Tyr Glu Ala Trp
 275 280 285
 Ala Glu Glu Tyr Gly Pro Gln Ala Tyr Gln Leu Leu Gly Ile Pro Gly
 290 295 300
 Thr His Trp Tyr Asp Leu Ala Leu Gln Gly Lys Leu Asp Leu Ala Lys
 305 310 315 320
 Ile Ser Gln Ile Gly Asp Ile Cys Ser Gly Lys Leu Pro Gly Arg Thr
 325 330 335
 Asn Asp Glu Glu Ile Ile Leu Tyr Ser Val Gly Gly Met Pro Val Glu
 340 345 350
 Asp Val Ala Trp Ala Thr Gln Val Tyr Glu Asn Ala Leu Glu Lys Gly
 355 360 365
 Val Gly Thr Thr Leu Asn Leu Trp Glu Ser Pro Ala Leu Ala
 370 375 380

<210> 345

<211> 1065

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA00219

<400> 345

tttgccgtac atgCGcgagc acctcctcaa cagcccgcac caccgaccaa tcacataaga 60

cacaagcact aaaacagcat taaagaaaga aagctttttc gtg gcc cgt aag aaa 115
 Val Ala Arg Lys Lys
 1 5

aac acg tcc gat caa tcc cgc tcc caa gct gcc aac acg ccc att gct 163
 Asn Thr Ser Asp Gln Ser Arg Ser Gln Ala Ala Asn Thr Pro Ile Ala
 10 15 20

ggc acc tat gag ggt gaa tat tcc gtc atc gag ttg gag gcc gat tcc 211
 Gly Thr Tyr Glu Gly Glu Tyr Ser Val Ile Glu Leu Glu Ala Asp Ser
 25 30 35

tac acc acc gat ggc tgg ttg atc agc att aat ggc gtg ccc agc tct 259
 Tyr Thr Thr Asp Gly Trp Leu Ile Ser Ile Asn Gly Val Pro Ser Ser
 40 45 50

cat att gtc ctg ggg caa ccg cag gca ctg gaa ttt gag tac atg cgg 307
 His Ile Val Leu Gly Gln Pro Gln Ala Leu Glu Phe Glu Tyr Met Arg
 55 60 65

tgg atc gct acc ggc gct cgg gcg ttc atc gat gcg cat cag gat gca 355
 Trp Ile Ala Thr Gly Ala Arg Ala Phe Ile Asp Ala His Gln Asp Ala
 70 75 80 85

tcc aag ctg cgg att act cac ctc ggc ggc ggt gcg tgc acg atg gcc 403
 Ser Lys Leu Arg Ile Thr His Leu Gly Gly Gly Ala Cys Thr Met Ala

90										95					100					
agg	tat	ttc	gcg	gat	gtt	tac	ccg	cag	tca	cgc	aac	act	gtc	gtg	gaa	451				
Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	Asn	Thr	Val	Val	Glu					
			105							110				115						
ttg	gat	gca	gag	ctt	gcc	cgc	ctg	tcg	cgt	gaa	tgg	ttc	gac	att	ccg	499				
Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	Trp	Phe	Asp	Ile	Pro					
			120							125				130						
cgc	gcg	cca	cgg	gta	aag	att	cgt	gtg	gat	gat	gcc	cga	atg	gtg	gca	547				
Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	Ala	Arg	Met	Val	Ala					
			135							140				145						
gaa	tct	ttc	act	ccc	gca	agc	cgc	gat	gtg	atc	atc	cgt	gac	gtt	ttt	595				
Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	Ile	Arg	Asp	Val	Phe					
			150							155				160						
gcc	gga	gct	atc	acg	ccg	cag	aac	ttc	acc	acc	gtg	gag	ttc	ttt	gag	643				
Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	Val	Glu	Phe	Phe	Glu					
			170							175				180						
cac	tgt	cac	cgt	ggc	ctt	gct	ccc	ggc	gga	ttg	tac	gtt	gcc	aac	tgt	691				
His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	Tyr	Val	Ala	Asn	Cys					
			185							190				195						
ggc	gat	cat	tcg	gat	ctg	cgc	gga	gct	aaa	tct	gag	ctc	gcg	gga	atg	739				
Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	Glu	Leu	Ala	Gly	Met					
			200							205				210						
atg	gag	gtg	ttc	gag	cac	gtc	gcg	gtc	atc	gcc	gat	ccc	ccg	atg	ctt	787				
Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	Asp	Pro	Pro	Met	Leu					
			215							220				225						
aaa	ggg	cgc	cgt	tac	ggc	aac	atc	att	ttg	atg	ggg	tca	gac	acc	gag	835				
Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	Gly	Ser	Asp	Thr	Glu					
			230							235				240						
ttc	ttt	agc	tcc	aac	agc	acg	gaa	gcg	tcc	gcg	att	acc	cgt	gag	ctt	883				
Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	Ile	Thr	Arg	Glu	Leu					
			250							255				260						
ctt	ggc	ggc	ggc	gtt	cca	gcg	cag	tac	aag	gat	gaa	tcc	tgg	gtg	cgg	931				
Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	Glu	Ser	Trp	Val	Arg					
			265							270				275						
aaa	ttc	gcc	tcg	gga	gcc	cag	gcc	cgc	cac	gat	ggg	gtc	tct	acc	ctc	979				
Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	Gly	Val	Ser	Thr	Leu					
			280							285				290						
caa	atg	ccg	agt	gat	act	cca	caa	cac	cct	gcg	gaa	acg	ccg	gag	cat					
1027																				
Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala	Glu	Thr	Pro	Glu	His					
			295							300				305						
tca	aac	aca	cag	cca	taaaaaattc	cgctggcgcg	tcc													
1065																				
Ser	Asn	Thr	Gln	Pro																
310																				

<210> 346

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 346

Val	Ala	Arg	Lys	Lys	Asn	Thr	Ser	Asp	Gln	Ser	Arg	Ser	Gln	Ala	Ala	1	5	10	15
Asn	Thr	Pro	Ile	Ala	Gly	Thr	Tyr	Glu	Gly	Glu	Tyr	Ser	Val	Ile	Glu	20	25	30	
Leu	Glu	Ala	Asp	Ser	Tyr	Thr	Thr	Asp	Gly	Trp	Leu	Ile	Ser	Ile	Asn	35	40	45	
Gly	Val	Pro	Ser	Ser	His	Ile	Val	Leu	Gly	Gln	Pro	Gln	Ala	Leu	Glu	50	55	60	
Phe	Glu	Tyr	Met	Arg	Trp	Ile	Ala	Thr	Gly	Ala	Arg	Ala	Phe	Ile	Asp	65	70	75	80
Ala	His	Gln	Asp	Ala	Ser	Lys	Leu	Arg	Ile	Thr	His	Leu	Gly	Gly	Gly	85	90	95	
Ala	Cys	Thr	Met	Ala	Arg	Tyr	Phe	Ala	Asp	Val	Tyr	Pro	Gln	Ser	Arg	100	105	110	
Asn	Thr	Val	Val	Glu	Leu	Asp	Ala	Glu	Leu	Ala	Arg	Leu	Ser	Arg	Glu	115	120	125	
Trp	Phe	Asp	Ile	Pro	Arg	Ala	Pro	Arg	Val	Lys	Ile	Arg	Val	Asp	Asp	130	135	140	
Ala	Arg	Met	Val	Ala	Glu	Ser	Phe	Thr	Pro	Ala	Ser	Arg	Asp	Val	Ile	145	150	155	160
Ile	Arg	Asp	Val	Phe	Ala	Gly	Ala	Ile	Thr	Pro	Gln	Asn	Phe	Thr	Thr	165	170	175	
Val	Glu	Phe	Phe	Glu	His	Cys	His	Arg	Gly	Leu	Ala	Pro	Gly	Gly	Leu	180	185	190	
Tyr	Val	Ala	Asn	Cys	Gly	Asp	His	Ser	Asp	Leu	Arg	Gly	Ala	Lys	Ser	195	200	205	
Glu	Leu	Ala	Gly	Met	Met	Glu	Val	Phe	Glu	His	Val	Ala	Val	Ile	Ala	210	215	220	
Asp	Pro	Pro	Met	Leu	Lys	Gly	Arg	Arg	Tyr	Gly	Asn	Ile	Ile	Leu	Met	225	230	235	240
Gly	Ser	Asp	Thr	Glu	Phe	Phe	Ser	Ser	Asn	Ser	Thr	Glu	Ala	Ser	Ala	245	250	255	
Ile	Thr	Arg	Glu	Leu	Leu	Gly	Gly	Gly	Val	Pro	Ala	Gln	Tyr	Lys	Asp	260	265	270	
Glu	Ser	Trp	Val	Arg	Lys	Phe	Ala	Ser	Gly	Ala	Gln	Ala	Arg	His	Asp	275	280	285	
Gly	Val	Ser	Thr	Leu	Gln	Met	Pro	Ser	Asp	Thr	Pro	Gln	His	Pro	Ala				

290 295 300

Glu Thr Pro Glu His Ser Asn Thr Gln Pro
305 310

<210> 347
<211> 1662
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1639)
<223> RXA01508

<400> 347
ttccgggacg tttccgtgat ctctgtggaag atcccaaaact ccgttccggg gccgtcgtgg 60
ccgccgtcat cttgatcgtg gtgggaaccg taaacgctgc atg tct gat tta gga 115
Met Ser Asp Leu Gly
1 5
ccc atc tgg cgc tgg ctg tta tta gtt tcc gtc tcc att tgt gcg gca 163
Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val Ser Ile Cys Ala Ala
10 15 20
tcg ggg ctg gtc tat gag cta gcc ctg gta tcg ctt tcc acc agc ttg 211
Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser Leu Ser Thr Ser Leu
25 30 35
aac ggt ggc gga att gta gaa acc tcc ctc atc gtc gca ggt tat gta 259
Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile Val Ala Gly Tyr Val
40 45 50
gct gcc ctt gga ctt ggt gca ctg ctg gtc aag ccg ttt ctc aac tgg 307
Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys Pro Phe Leu Asn Trp
55 60 65
cct gcg caa acc ttc ctc ggt gtg gaa acc ctc ctt gga ctt att ggt 355
Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu Leu Gly Leu Ile Gly
70 75 80 85
ggt tgt tcc gcg ctg gtg ctg tat ttc acc ttc gcg acc atc ggc caa 403
Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe Ala Thr Ile Gly Gln
90 95 100
tcc ctg tgg att ctg gtg att gcc acc gct gca att ggc atc ctg gtc 451
Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala Ile Gly Ile Leu Val
105 110 115
ggc gct gaa ctt cca ctg ctg atg acc atg atc cag caa ggc cgc ctc 499
Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile Gln Gln Gly Arg Leu
120 125 130
gcc gac gcc aaa acc aca gga tct ctg gtt gcc acc ttg aat gct gct 547
Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala Thr Leu Asn Ala Ala
135 140 145
gat tac ctt ggc gca ctt tta ggt ggc ctg gcc tgg cct ttt gtg ttg 595
Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala Trp Pro Phe Val Leu

150	155	160	165	
ctg ccg tgg ctt ggc atg atg cgc ggt gcc gca gca gcc gga atg atc				643
Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala Ala Ala Gly Met Ile	170	175	180	
aac ctc gtt gca gca cta ttc gtg ggc tgt gtg ctg ctg cga cat ttg				691
Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val Leu Leu Arg His Leu	185	190	195	
ctt ccg cgc acc cac ttc ttc gta tcc gtg gtg gcg ctt ctt ctc gcg				739
Leu Pro Arg Thr His Phe Phe Val Ser Val Val Ala Leu Leu Leu Ala	200	205	210	
atc gca gcg cta gcc acc gtg ttg gtg aaa tcc gac ggg atc gtt gcc				787
Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser Asp Gly Ile Val Ala	215	220	225	
acc gcc cgc gca cag ctc tac cgc gac ccc gtg atc tat tca cac caa				835
Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val Ile Tyr Ser His Gln	230	235	240	245
tct gac tac caa gac atc gta gtg aca gaa cga ggc aaa gac cga cgc				883
Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg Gly Lys Asp Arg Arg	250	255	260	
ctc tac ctc aat ggc ggt ttg cag tat tcc act cgt gac cag cat aga				931
Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr Arg Asp Gln His Arg	265	270	275	
tat aca gaa tca ctg gtg tat cca agc ctt aat cca gag gca gaa tcg				979
Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn Pro Glu Ala Glu Ser	280	285	290	
gtg tta atc atc ggc ggt ggc gat ggc ctc gca gca cgg gaa ctc ctc				
1027				
Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala Ala Arg Glu Leu Leu	295	300	305	
cga ttc cca tca atg cag atc acc caa gtt gaa tta gac cca gaa gtc				
1075				
Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu Leu Asp Pro Glu Val	310	315	320	325
atc gaa gta gcc aac aca gtg ctg cgc tct gac aat ggg gga gcg atg				
1123				
Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp Asn Gly Gly Ala Met	330	335	340	
gaa gat ccc cgc gtc tcc atc atc gtt gac gac gct ttc acc tgg ctg				
1171				
Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp Ala Phe Thr Trp Leu	345	350	355	
cgc tcc ggc gga aat aat ggc gaa act tac gat tcc atc atc atc gat				
1219				
Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp Ser Ile Ile Ile Asp	360	365	370	
ctt ccc gac cca aac aac gac acc atg gcc agg ctg tat tca gaa gag				
1267				

Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg Leu Tyr Ser Glu Glu
 375 380 385

ttc tac acc ttg gcc cga gca cga ctg aac gaa caa ggc cgc atg gtg
 1315

Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu Gln Gly Arg Met Val
 390 395 400 405

gtg caa tcc tcc agc gcc tac acc act cca gat gtg ttc tgg cga gtt
 1363

Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp Val Phe Trp Arg Val
 410 415 420

gga gca acc ttg aaa tcg gcg ggc tgt gaa caa gtc atc cca tat cac
 1411

Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln Val Ile Pro Tyr His
 425 430 435

gtg cat gtt ccc aca ttt ggc gac tgg ggc ttc caa ctg tgt ggc cct
 1459

Val His Val Pro Thr Phe Gly Asp Trp Gly Phe Gln Leu Cys Gly Pro
 440 445 450

gcc gac atg gaa tta gag ctt cgg gaa gac acc ccg cca ctg act ttc
 1507

Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr Pro Pro Leu Thr Phe
 455 460 465

ctt aat gat gaa gtt ctg gtg gct gct ggg gtg ttt ggg ttg gat aat
 1555

Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val Phe Gly Leu Asp Asn
 470 475 480 485

cag cct cgt gaa ttg gaa cct tcc acg ctg gat cat ccc cgc gtg gtg
 1603

Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp His Pro Arg Val Val
 490 495 500

gag gat ctg cgc aag gga tac cgc gaa tca ggc gac tagctgcaac
 1649

Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly Asp
 505 510

gatgcgctgt gtg
 1662

<210> 348

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met Ser Asp Leu Gly Pro Ile Trp Arg Trp Leu Leu Leu Val Ser Val
 1 5 10 15

Ser Ile Cys Ala Ala Ser Gly Leu Val Tyr Glu Leu Ala Leu Val Ser
 20 25 30

Leu Ser Thr Ser Leu Asn Gly Gly Gly Ile Val Glu Thr Ser Leu Ile
 35 40 45

Val Ala Gly Tyr Val Ala Ala Leu Gly Leu Gly Ala Leu Leu Val Lys
 50 55 60
 Pro Phe Leu Asn Trp Pro Ala Gln Thr Phe Leu Gly Val Glu Thr Leu
 65 70 75 80
 Leu Gly Leu Ile Gly Gly Cys Ser Ala Leu Val Leu Tyr Phe Thr Phe
 85 90 95
 Ala Thr Ile Gly Gln Ser Leu Trp Ile Leu Val Ile Ala Thr Ala Ala
 100 105 110
 Ile Gly Ile Leu Val Gly Ala Glu Leu Pro Leu Leu Met Thr Met Ile
 115 120 125
 Gln Gln Gly Arg Leu Ala Asp Ala Lys Thr Thr Gly Ser Leu Val Ala
 130 135 140
 Thr Leu Asn Ala Ala Asp Tyr Leu Gly Ala Leu Leu Gly Gly Leu Ala
 145 150 155 160
 Trp Pro Phe Val Leu Leu Pro Trp Leu Gly Met Met Arg Gly Ala Ala
 165 170 175
 Ala Ala Gly Met Ile Asn Leu Val Ala Ala Leu Phe Val Gly Cys Val
 180 185 190
 Leu Leu Arg His Leu Leu Pro Arg Thr His Phe Phe Val Ser Val Val
 195 200 205
 Ala Leu Leu Leu Ala Ile Ala Ala Leu Ala Thr Val Leu Val Lys Ser
 210 215 220
 Asp Gly Ile Val Ala Thr Ala Arg Ala Gln Leu Tyr Arg Asp Pro Val
 225 230 235 240
 Ile Tyr Ser His Gln Ser Asp Tyr Gln Asp Ile Val Val Thr Glu Arg
 245 250 255
 Gly Lys Asp Arg Arg Leu Tyr Leu Asn Gly Gly Leu Gln Tyr Ser Thr
 260 265 270
 Arg Asp Gln His Arg Tyr Thr Glu Ser Leu Val Tyr Pro Ser Leu Asn
 275 280 285
 Pro Glu Ala Glu Ser Val Leu Ile Ile Gly Gly Gly Asp Gly Leu Ala
 290 295 300
 Ala Arg Glu Leu Leu Arg Phe Pro Ser Met Gln Ile Thr Gln Val Glu
 305 310 315 320
 Leu Asp Pro Glu Val Ile Glu Val Ala Asn Thr Val Leu Arg Ser Asp
 325 330 335
 Asn Gly Gly Ala Met Glu Asp Pro Arg Val Ser Ile Ile Val Asp Asp
 340 345 350
 Ala Phe Thr Trp Leu Arg Ser Gly Gly Asn Asn Gly Glu Thr Tyr Asp
 355 360 365

Ser Ile Ile Ile Asp Leu Pro Asp Pro Asn Asn Asp Thr Met Ala Arg
 370 375 380

Leu Tyr Ser Glu Glu Phe Tyr Thr Leu Ala Arg Ala Arg Leu Asn Glu
 385 390 395 400

Gln Gly Arg Met Val Val Gln Ser Ser Ser Ala Tyr Thr Thr Pro Asp
 405 410 415

Val Phe Trp Arg Val Gly Ala Thr Leu Lys Ser Ala Gly Cys Glu Gln
 420 425 430

Val Ile Pro Tyr His Val His Val Pro Thr Phe Gly Asp Trp Gly Phe
 435 440 445

Gln Leu Cys Gly Pro Ala Asp Met Glu Leu Glu Leu Arg Glu Asp Thr
 450 455 460

Pro Pro Leu Thr Phe Leu Asn Asp Glu Val Leu Val Ala Ala Gly Val
 465 470 475 480

Phe Gly Leu Asp Asn Gln Pro Arg Glu Leu Glu Pro Ser Thr Leu Asp
 485 490 495

His Pro Arg Val Val Glu Asp Leu Arg Lys Gly Tyr Arg Glu Ser Gly
 500 505 510

Asp

<210> 349
 <211> 924
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(901)
 <223> RXA01757

<400> 349
 cgcttattga acggatgcct ctcgatcaag ccaacgaggc tattgcacgt atttcagctg 60

gtaaaccacg tttccgtatt gtcttggagc cgaattcata atg cca aca gca agc 115
 Met Pro Thr Ala Ser
 1 5

cca att tat gat gtc gtt gtc gtc gga gcc ggc att tct ggc ctc atc 163
 Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly Ile Ser Gly Leu Ile
 10 15 20

gcc acg caa ctg ttg gac cgc gca ggt cta aac atc aaa tgc ttc gaa 211
 Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn Ile Lys Cys Phe Glu
 25 30 35

gcc tgc tca aga gtt ggc ggc cga gca gtg tct gtc caa cag tcc gat 259
 Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser Val Gln Gln Ser Asp
 40 45 50

ttg ttc ctg gac ctc ggc gca aca tgg ttc tgg ctc aac gaa cca ctt 307

Leu	Phe	Leu	Asp	Leu	Gly	Ala	Thr	Trp	Phe	Trp	Leu	Asn	Glu	Pro	Leu		
55						60					65						
gtg	cag	caa	ctc	gtc	aat	aat	ctc	ggc	ctc	ggc	aca	ttc	cct	cag	gcc	355	
Val	Gln	Gln	Leu	Val	Asn	Asn	Leu	Gly	Leu	Gly	Thr	Phe	Pro	Gln	Ala	85	
70					75					80							
atc	gag	ggg	gat	gcg	ctt	ttt	gag	acg	ctt	gtc	gac	gcc	ccg	agc	cgc	403	
Ile	Glu	Gly	Asp	Ala	Leu	Phe	Glu	Thr	Leu	Val	Asp	Ala	Pro	Ser	Arg	100	
				90					95								
ctg	cgg	ggg	aac	ccc	ata	gac	gct	gct	tca	ggc	agg	ttc	caa	gca	ggg	451	
Leu	Arg	Gly	Asn	Pro	Ile	Asp	Ala	Ala	Ser	Gly	Arg	Phe	Gln	Ala	Gly	115	
			105					110									
gcc	tcc	tcg	ctt	gcg	ctc	ggg	ctt	gca	gcc	cag	ctc	aag	cca	gga	gtt	499	
Ala	Ser	Ser	Leu	Ala	Leu	Gly	Leu	Ala	Ala	Gln	Leu	Lys	Pro	Gly	Val	130	
			120				125										
tta	gaa	ctc	ggg	gac	ccc	gtc	cat	tct	ctc	agt	gag	gaa	gat	ggg	gaa	547	
Leu	Glu	Leu	Gly	Asp	Pro	Val	His	Ser	Leu	Ser	Glu	Glu	Asp	Gly	Glu	145	
	135					140											
atc	gtt	gtg	aag	tct	tcc	aaa	cag	att	gtg	agg	gca	aag	cac	gtc	atc	595	
Ile	Val	Val	Lys	Ser	Ser	Lys	Gln	Ile	Val	Arg	Ala	Lys	His	Val	Ile	165	
	150					155				160							
att	gcg	gtt	cca	ccg	gca	ctc	gct	gcc	gag	ttg	att	ggg	ttc	acc	cta	643	
Ile	Ala	Val	Pro	Pro	Ala	Leu	Ala	Ala	Glu	Leu	Ile	Gly	Phe	Thr	Leu	180	
				170					175								
gat	tta	cca	gct	gac	gtg	cga	aaa	gca	gcg	cat	cca	caa	cat	ata	gct	691	
Asp	Leu	Pro	Ala	Asp	Val	Arg	Lys	Ala	Ala	His	Pro	Gln	His	Ile	Ala	195	
			185					190									
gtg	atg	aat	tgg	gca	aag	gag	aaa	tac	acc	tta	ccc	aca	caa	gcc	gca	739	
Val	Met	Asn	Trp	Ala	Lys	Glu	Lys	Tyr	Thr	Leu	Pro	Thr	Gln	Ala	Ala	210	
		200					205										
tcg	gct	ggg	ggg	ttt	ggg	cat	gag	ctg	ttc	caa	caa	cca	ctc	gga	cat	787	
Ser	Ala	Gly	Gly	Phe	Gly	His	Glu	Leu	Phe	Gln	Gln	Pro	Leu	Gly	His	225	
	215					220											
ggg	cga	att	cat	tgg	gca	tca	acg	gaa	gtt	gcc	act	gag	ttt	ggg	gga	835	
Gly	Arg	Ile	His	Trp	Ala	Ser	Thr	Glu	Val	Ala	Thr	Glu	Phe	Gly	Gly	245	
	230				235					240							
cac	ctt	gaa	ggc	gca	gtt	cgt	gca	gga	att	cag	gct	gcg	ctt	caa	aca	883	
His	Leu	Glu	Gly	Ala	Val	Arg	Ala	Gly	Ile	Gln	Ala	Ala	Leu	Gln	Thr	260	
				250					255								
gga	ttt	aat	cta	aaa	tct	taa	ac	ctc	gt	att	ttc	cc	tg	ata		924	
Gly	Phe	Asn	Leu	Lys	Ser											265	

<210> 350

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

Met Pro Thr Ala Ser Pro Ile Tyr Asp Val Val Val Val Gly Ala Gly
 1 5 10 15

Ile Ser Gly Leu Ile Ala Thr Gln Leu Leu Asp Arg Ala Gly Leu Asn
 20 25 30

Ile Lys Cys Phe Glu Ala Cys Ser Arg Val Gly Gly Arg Ala Val Ser
 35 40 45

Val Gln Gln Ser Asp Leu Phe Leu Asp Leu Gly Ala Thr Trp Phe Trp
 50 55 60

Leu Asn Glu Pro Leu Val Gln Gln Leu Val Asn Asn Leu Gly Leu Gly
 65 70 75 80

Thr Phe Pro Gln Ala Ile Glu Gly Asp Ala Leu Phe Glu Thr Leu Val
 85 90 95

Asp Ala Pro Ser Arg Leu Arg Gly Asn Pro Ile Asp Ala Ala Ser Gly
 100 105 110

Arg Phe Gln Ala Gly Ala Ser Ser Leu Ala Leu Gly Leu Ala Ala Gln
 115 120 125

Leu Lys Pro Gly Val Leu Glu Leu Gly Asp Pro Val His Ser Leu Ser
 130 135 140

Glu Glu Asp Gly Glu Ile Val Val Lys Ser Ser Lys Gln Ile Val Arg
 145 150 155 160

Ala Lys His Val Ile Ile Ala Val Pro Pro Ala Leu Ala Ala Glu Leu
 165 170 175

Ile Gly Phe Thr Leu Asp Leu Pro Ala Asp Val Arg Lys Ala Ala His
 180 185 190

Pro Gln His Ile Ala Val Met Asn Trp Ala Lys Glu Lys Tyr Thr Leu
 195 200 205

Pro Thr Gln Ala Ala Ser Ala Gly Gly Phe Gly His Glu Leu Phe Gln
 210 215 220

Gln Pro Leu Gly His Gly Arg Ile His Trp Ala Ser Thr Glu Val Ala
 225 230 235 240

Thr Glu Phe Gly Gly His Leu Glu Gly Ala Val Arg Ala Gly Ile Gln
 245 250 255

Ala Ala Leu Gln Thr Gly Phe Asn Leu Lys Ser
 260 265

<210> 351

<211> 636

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(613)

<223> RXA02159

<400> 351

tgatggacca	gcgtccaaag	ttttcgatga	agcagaaaac	cgctctccacg	ctcagaaagc	60										
actgctggtg	tggctgctgg	ccaaccagcc	gaggtaagac	atg Met 1	tcc Ser 5	ctt Leu 5	ggc Gly 5	tca Ser 5	115							
acc Thr	ccg Pro	tca Ser	aca Thr	ccg Pro 10	gaa Glu	aac Asn	tta Leu	aat Asn	ccc Pro 15	gtg Val	act Thr	cg Arg	act Thr	gca Ala 20	cg Arg	163
caa Gln	gct Ala	ctc Leu	att Ile 25	ttg Leu	cag Gln	att Ile	ttg Leu	gac Asp 30	aaa Lys	caa Gln	aaa Lys	gtc Val	acc Thr 35	agc Ser	cag Gln	211
gta Val	caa Gln	ctg Leu	tct Ser	gaa Glu	ttg Leu	ctg Leu	ctg Leu	gat Asp 45	gaa Glu	ggc Gly	atc Ile 50	gat Asp	atc Ile	acc Thr	cag Gln	259
gcc Ala	acc Thr 55	ttg Leu	tcc Ser	cga Arg	gat Asp	ctc Leu 60	gat Asp	gaa Glu	ctc Leu	ggt Gly	gca Ala 65	cg Arg	aag Lys	gtt Val	cg Arg	307
ccc Pro 70	gat Asp	ggg Gly	gga Gly	cg Arg	gcc Ala 75	tac Tyr	tac Tyr	gcg Ala	gtc Val	ggc Gly 80	cca Pro	gta Val	gat Asp	agc Ser	atc Ile 85	355
gcc Ala	cg Arg	gaa Glu	gat Asp	ctc Leu 90	cg Arg	ggt Gly	ccg Pro	tcg Ser	gag Glu 95	aag Lys	ctg Leu	cg Arg	cg Arg	atg Met 100	ctt Leu	403
gat Asp	gaa Glu	ctg Leu	ctg Leu	gtt Val	tct Ser	aca Thr	gat Asp	cat His 110	tcc Ser	ggc Gly	aac Asn	atc Ile	gcg Ala 115	atg Met	ctg Leu	451
cg Arg	acc Thr	ccg Pro	ccg Pro	gga Gly	gct Ala	gcc Ala	cag Gln	tac Tyr	ctg Leu	gca Ala	agt Ser	ttc Phe 130	atc Ile	gat Asp	agg Arg	499
gtg Val	ggg Gly 135	ctg Leu	aaa Lys	gaa Glu	gtc Val	gtt Val	ggc Gly	acc Thr	atc Ile	gct Ala	ggt Gly 145	gat Asp	gac Asp	acc Thr	gtt Val	547
ttc Phe 150	gtt Val	ctc Leu	gcc Ala	cg Arg	gat Asp 155	ccg Pro	ctc Leu	aca Thr	ggt Gly	aaa Lys 160	gaa Glu	cta Leu	ggt Gly	gaa Glu	tta Leu 165	595
ctc Leu	agc Ser	ggg Gly	cg Arg	acc Thr 170	act Thr	taaagcgccc	ctagttcaag	gct								636

<210> 352

<211> 171

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 352

Met Ser Leu Gly Ser Thr Pro Ser Thr Pro Glu Asn Leu Asn Pro Val

1	5	10	15
Thr Arg Thr	Ala Arg Gln Ala Leu	Ile Leu Gln Ile Leu	Asp Lys Gln
	20	25	30
Lys Val Thr	Ser Gln Val Gln Leu	Ser Glu Leu Leu Leu	Asp Glu Gly
	35	40	45
Ile Asp Ile	Thr Gln Ala Thr Leu	Ser Arg Asp Leu	Asp Glu Leu Gly
	50	55	60
Ala Arg Lys	Val Arg Pro Asp Gly	Gly Arg Ala Tyr Tyr	Ala Val Gly
	65	70	75
Pro Val Asp	Ser Ile Ala Arg Glu	Asp Leu Arg Gly	Pro Ser Glu Lys
	85	90	95
Leu Arg Arg	Met Leu Asp Glu Leu	Leu Val Ser Thr	Asp His Ser Gly
	100	105	110
Asn Ile Ala	Met Leu Arg Thr Pro	Pro Gly Ala Ala	Gln Tyr Leu Ala
	115	120	125
Ser Phe Ile	Asp Arg Val Gly Leu	Lys Glu Val Val	Gly Thr Ile Ala
	130	135	140
Gly Asp Asp	Thr Val Phe Val Leu	Ala Arg Asp Pro	Leu Thr Gly Lys
	145	150	155
Glu Leu Gly	Glu Leu Leu Ser Gly	Arg Thr Thr	
	165	170	

<210> 353

<211> 414

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(391)

<223> RXN02154

<400> 353

cccagaacct cggcgaagtc agcgacaagc cagtcaaggt gagcttcacc ccagtgcttg 60

caccgttacc	tcgcgaattc	tcaccactgc	aaccgcacct	ttg aaa gaa ggc gtt	115
				Leu Lys Glu Gly Val	
				1	5

acc gca gaa cag gct cgc gca gta tat gaa gag ttc tat gca cag gaa	163
Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu Phe Tyr Ala Gln Glu	
	10 15 20

acc ttc gtg cat gtt ctt cca gaa ggt gca cag cca caa acc caa gca	211
Thr Phe Val His Val Leu Pro Glu Gly Ala Gln Pro Gln Thr Gln Ala	
	25 30 35

gtt ctt ggc tcc aac atg tgc cac gtg cag gta gaa att gat gag gaa	259
Val Leu Gly Ser Asn Met Cys His Val Gln Val Glu Ile Asp Glu Glu	
	40 45 50

gca ggc aaa gtc ctt gtt acc tcc gca atc gat aac ctc acc aag gga 307
Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp Asn Leu Thr Lys Gly
55 60 65

act gcc ggc gcc gct gtt cag tgc atg aac tta agc gtt ggt ttt gat 355
Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu Ser Val Gly Phe Asp
70 75 80 85

gag gca gca ggc ctg cca cag gtc ggc gtc gca cct taaagtagcg 401
Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala Pro
90 95

ccttaaagcg gcg 414

<210> 354

<211> 97

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

Leu Lys Glu Gly Val Thr Ala Glu Gln Ala Arg Ala Val Tyr Glu Glu
1 5 10 15

Phe Tyr Ala Gln Glu Thr Phe Val His Val Leu Pro Glu Gly Ala Gln
20 25 30

Pro Gln Thr Gln Ala Val Leu Gly Ser Asn Met Cys His Val Gln Val
35 40 45

Glu Ile Asp Glu Glu Ala Gly Lys Val Leu Val Thr Ser Ala Ile Asp
50 55 60

Asn Leu Thr Lys Gly Thr Ala Gly Ala Ala Val Gln Cys Met Asn Leu
65 70 75 80

Ser Val Gly Phe Asp Glu Ala Ala Gly Leu Pro Gln Val Gly Val Ala
85 90 95

Pro

<210> 355

<211> 1302

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1279)

<223> RXS00147

<400> 355

attgcatata atgcaatgaa ttgaataaac tacattcagg gttatcaacc agccaatttc 60

ttttaaaaag gcagacacac gaaaggcgac aacagtcacc gtg agt aaa gac acc 115
Val Ser Lys Asp Thr
1 5

acc acc tac cag gga gtc acc gag atc gga tcc gtt ccg gca tac ctg	163
Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser Val Pro Ala Tyr Leu	
10 15 20	
gtt ctt gca gac gga cgt acc ttc acc gga ttt ggc ttt gga gct atc	211
Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe Gly Phe Gly Ala Ile	
25 30 35	
ggc acc acc ctt ggt gag gca gtg ttc act acc gcc atg acc ggt tac	259
Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr Ala Met Thr Gly Tyr	
40 45 50	
caa gaa acc atg acc gat cct tcc tat cac cgc cag att gtt gtg gct	307
Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg Gln Ile Val Val Ala	
55 60 65	
acc gca cca cag atc ggc aac acc ggc tgg aac gat gag gac aac gag	355
Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn Asp Glu Asp Asn Glu	
70 75 80 85	
tcc cgc gac ggc aag att tgg gtt gca ggc ctt gtt atc cgc gac ctc	403
Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu Val Ile Arg Asp Leu	
90 95 100	
gca gca cgt gtg tcc aac tgg cgc gcc acc acc tcc ttg cag cag gaa	451
Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr Ser Leu Gln Gln Glu	
105 110 115	
atg gca ggc cag ggc atc gtc ggc atc ggc gga atc gac acc cgc gca	499
Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly Ile Asp Thr Arg Ala	
120 125 130	
ctg gtt cgc cac ctg cgc aat gaa ggt tcc att gca gcg ggc atc ttc	547
Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile Ala Ala Gly Ile Phe	
135 140 145	
tcc ggc gct gac gca cag cgc cca gtt gaa gaa ctc gta gag atc gtc	595
Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu Leu Val Glu Ile Val	
150 155 160 165	
aag aat cag cca gca atg acc ggc gca aac ctc tcc gtt gag gtc tct	643
Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu Ser Val Glu Val Ser	
170 175 180	
gct gat gaa acc tac gtc atc gaa gct gaa ggc gaa gag cgc cac acc	691
Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly Glu Glu Arg His Thr	
185 190 195	
gtc gtg gcc tac gac ctg ggc att aag caa aac acc cca cgt cgt ttc	739
Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn Thr Pro Arg Arg Phe	
200 205 210	
tct gca cgc ggt gtt cgc acc gtc atc gtg cct gct gaa acc cca ttc	787
Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro Ala Glu Thr Pro Phe	
215 220 225	
gag gat atc aag cag tac aac cca tca ggc gtg ttc atc tcc aac ggc	835
Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val Phe Ile Ser Asn Gly	
230 235 240 245	
cct ggc gat cct gca gca gca gac gtc atg gtt gat atc gtc cgc gaa	883

Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val Asp Ile Val Arg Glu
 250 255 260

gtt ctt gaa gcc gac att cca ttc ttt ggc atc tgc ttc ggc aac cag 931
 Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile Cys Phe Gly Asn Gln
 265 270 275

att ctt ggc cgc gca ttc ggc atg gag acc tac aag ctg aag ttc ggc 979
 Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr Lys Leu Lys Phe Gly
 280 285 290

cac cgc ggc atc aac gtt cca gtg aag aac cac atc acc ggc aag atc
 1027

His Arg Gly Ile Asn Val Pro Val Lys Asn His Ile Thr Gly Lys Ile
 295 300 305

gac atc acc gcc cag aac cac ggc ttc gca ctc aag ggt gaa gca ggc
 1075

Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu Lys Gly Glu Ala Gly
 310 315 320 325

cag gaa ttc gag acc gat ttc ggc act gca att gtc acc cac acc tgc
 1123

Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile Val Thr His Thr Cys
 330 335 340

ctc aac gac ggc gtc gtt gaa ggt att gcg ctg aag tcc gga cgc gca
 1171

Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu Lys Ser Gly Arg Ala
 345 350 355

tac tcc gtt cag tac cac cca gag gcc gct gcc ggc cca aat gat gca
 1219

Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala Gly Pro Asn Asp Ala
 360 365 370

agc ccc ctg ttt gac cag ttt gtt gag ctg atg gat gca gac gct cag
 1267

Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met Asp Ala Asp Ala Gln
 375 380 385

aag aaa ggc gca taaataacat gccaaagcgt tca
 1302

Lys Lys Gly Ala
 390

<210> 356

<211> 393

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 356

Val Ser Lys Asp Thr Thr Thr Tyr Gln Gly Val Thr Glu Ile Gly Ser
 1 5 10 15

Val Pro Ala Tyr Leu Val Leu Ala Asp Gly Arg Thr Phe Thr Gly Phe
 20 25 30

Gly Phe Gly Ala Ile Gly Thr Thr Leu Gly Glu Ala Val Phe Thr Thr
 35 40 45

Ala Met Thr Gly Tyr Gln Glu Thr Met Thr Asp Pro Ser Tyr His Arg
 50 55 60
 Gln Ile Val Val Ala Thr Ala Pro Gln Ile Gly Asn Thr Gly Trp Asn
 65 70 75 80
 Asp Glu Asp Asn Glu Ser Arg Asp Gly Lys Ile Trp Val Ala Gly Leu
 85 90 95
 Val Ile Arg Asp Leu Ala Ala Arg Val Ser Asn Trp Arg Ala Thr Thr
 100 105 110
 Ser Leu Gln Gln Glu Met Ala Gly Gln Gly Ile Val Gly Ile Gly Gly
 115 120 125
 Ile Asp Thr Arg Ala Leu Val Arg His Leu Arg Asn Glu Gly Ser Ile
 130 135 140
 Ala Ala Gly Ile Phe Ser Gly Ala Asp Ala Gln Arg Pro Val Glu Glu
 145 150 155 160
 Leu Val Glu Ile Val Lys Asn Gln Pro Ala Met Thr Gly Ala Asn Leu
 165 170 175
 Ser Val Glu Val Ser Ala Asp Glu Thr Tyr Val Ile Glu Ala Glu Gly
 180 185 190
 Glu Glu Arg His Thr Val Val Ala Tyr Asp Leu Gly Ile Lys Gln Asn
 195 200 205
 Thr Pro Arg Arg Phe Ser Ala Arg Gly Val Arg Thr Val Ile Val Pro
 210 215 220
 Ala Glu Thr Pro Phe Glu Asp Ile Lys Gln Tyr Asn Pro Ser Gly Val
 225 230 235 240
 Phe Ile Ser Asn Gly Pro Gly Asp Pro Ala Ala Ala Asp Val Met Val
 245 250 255
 Asp Ile Val Arg Glu Val Leu Glu Ala Asp Ile Pro Phe Phe Gly Ile
 260 265 270
 Cys Phe Gly Asn Gln Ile Leu Gly Arg Ala Phe Gly Met Glu Thr Tyr
 275 280 285
 Lys Leu Lys Phe Gly His Arg Gly Ile Asn Val Pro Val Lys Asn His
 290 295 300
 Ile Thr Gly Lys Ile Asp Ile Thr Ala Gln Asn His Gly Phe Ala Leu
 305 310 315 320
 Lys Gly Glu Ala Gly Gln Glu Phe Glu Thr Asp Phe Gly Thr Ala Ile
 325 330 335
 Val Thr His Thr Cys Leu Asn Asp Gly Val Val Glu Gly Ile Ala Leu
 340 345 350
 Lys Ser Gly Arg Ala Tyr Ser Val Gln Tyr His Pro Glu Ala Ala Ala
 355 360 365

Gly Pro Asn Asp Ala Ser Pro Leu Phe Asp Gln Phe Val Glu Leu Met
 370 375 380

Asp Ala Asp Ala Gln Lys Lys Gly Ala
 385 390

<210> 357

<211> 924

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(901)

<223> RXS00905

<400> 357

cgctgcccct ctatgctgct cctagttacc cctgcacaaa tagcggtttt tctcagcat 60

tctgcatcga gtcgggtcga cgtatataag gtggaaaggc atg acc caa ttc gaa 115
 Met Thr Gln Phe Glu
 1 5

aac gcg caa gta ctt aaa gag aac atc gaa aac caa cgc gag cag atc 163
 Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn Gln Arg Glu Gln Ile
 10 15 20

ttt acc cag ttg aaa gaa att gtg tct ttc aac tcc gtg cac agc gat 211
 Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn Ser Val His Ser Asp
 25 30 35

cca aac cta ctg gag gac tac gcc ggc gcg aaa gaa tgg gta aaa gaa 259
 Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys Glu Trp Val Lys Glu
 40 45 50

aca ctg acc aac gca ggt ctc acc gtc agc gaa ttc gct gcc gaa gat 307
 Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu Phe Ala Ala Glu Asp
 55 60 65

gga acc acc aac ttc atc ggc acc cgc aag ggc tcc gaa ggt gca cca 355
 Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly Ser Glu Gly Ala Pro
 70 75 80 85

aag gta ctg ctg tac agc cac ttc gac gtt gtc cca tcc ggc cct ttg 403
 Lys Val Leu Leu Tyr Ser His Phe Asp Val Val Pro Ser Gly Pro Leu
 90 95 100

gat ctc tgg gac acc aat cct ttt gaa ctc acc gag cgc gac gct ggc 451
 Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr Glu Arg Asp Ala Gly
 105 110 115

cac ggc acc cgc tgg tac ggc cgc ggc gcc gct gac tgc aag ggc aac 499
 His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala Asp Cys Lys Gly Asn
 120 125 130

ctg gtc atg cac ctc gca gca ctg cgc gcc gtc gaa gcc agc ggc gac 547
 Leu Val Met His Leu Ala Ala Leu Arg Ala Val Glu Ala Ser Gly Asp
 135 140 145

acc aca ctc aac ctc acc tac gtg gtc gag ggc tcc gag gaa atg gga 595

Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly Ser Glu Glu Met Gly
 150 155 160 165
 ggc gga gcg ctc agc gcg ctc atc aag gac aag cct gag ctt ttc gac 643
 Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys Pro Glu Leu Phe Asp
 170 175 180
 gca gat gtc atc ttg att gca gac agc gga aac gct tcc gtg ggc acc 691
 Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn Ala Ser Val Gly Thr
 185 190 195
 cca acc ttg acc act acc ctg cgc ggt ggc gga cag gtc acc gtc acc 739
 Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly Gln Val Thr Val Thr
 200 205 210
 gtg gac acc ctt gaa ggc gct gtt cac tcc ggc cag aac ggt ggc gct 787
 Val Asp Thr Leu Glu Gly Ala Val His Ser Gly Gln Asn Gly Gly Ala
 215 220 225
 gcc cca gat gct gtt gct gct ctc gtg cgc gtt ctg gat act ttg cgc 835
 Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val Leu Asp Thr Leu Arg
 230 235 240 245
 gat gaa cac gga cgc acc gtt atc gac ggc tgt caa cac cac cgc aaa 883
 Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys Gln His His Arg Lys
 250 255 260
 ctg gaa ggg cga gcc tta tgatccagag actttccgca gcg 924
 Leu Glu Gly Arg Ala Leu
 265

<210> 358

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

Met Thr Gln Phe Glu Asn Ala Gln Val Leu Lys Glu Asn Ile Glu Asn
 1 5 10 15
 Gln Arg Glu Gln Ile Phe Thr Gln Leu Lys Glu Ile Val Ser Phe Asn
 20 25 30
 Ser Val His Ser Asp Pro Asn Leu Leu Glu Asp Tyr Ala Gly Ala Lys
 35 40 45
 Glu Trp Val Lys Glu Thr Leu Thr Asn Ala Gly Leu Thr Val Ser Glu
 50 55 60
 Phe Ala Ala Glu Asp Gly Thr Thr Asn Phe Ile Gly Thr Arg Lys Gly
 65 70 75 80
 Ser Glu Gly Ala Pro Lys Val Leu Leu Tyr Ser His Phe Asp Val Val
 85 90 95
 Pro Ser Gly Pro Leu Asp Leu Trp Asp Thr Asn Pro Phe Glu Leu Thr
 100 105 110
 Glu Arg Asp Ala Gly His Gly Thr Arg Trp Tyr Gly Arg Gly Ala Ala
 115 120 125

Asp Cys Lys Gly Asn Leu Val Met His Leu Ala Ala Leu Arg Ala Val
 130 135 140

Glu Ala Ser Gly Asp Thr Thr Leu Asn Leu Thr Tyr Val Val Glu Gly
 145 150 155 160

Ser Glu Glu Met Gly Gly Gly Ala Leu Ser Ala Leu Ile Lys Asp Lys
 165 170 175

Pro Glu Leu Phe Asp Ala Asp Val Ile Leu Ile Ala Asp Ser Gly Asn
 180 185 190

Ala Ser Val Gly Thr Pro Thr Leu Thr Thr Thr Leu Arg Gly Gly Gly
 195 200 205

Gln Val Thr Val Thr Val Asp Thr Leu Glu Gly Ala Val His Ser Gly
 210 215 220

Gln Asn Gly Gly Ala Ala Pro Asp Ala Val Ala Ala Leu Val Arg Val
 225 230 235 240

Leu Asp Thr Leu Arg Asp Glu His Gly Arg Thr Val Ile Asp Gly Cys
 245 250 255

Gln His His Arg Lys Leu Glu Gly Arg Ala Leu
 260 265

<210> 359

<211> 627

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(604)

<223> RXS00906

<400> 359

accgtggaca cccttgaagg cgctgttcac tccggccaga acggtggcgc tgccccagat 60

gctgttgctg ctctcgtgcg cgttctggat actttgcgcg atg aac acg gac gca 115
 Met Asn Thr Asp Ala
 1 5

ccg tta tcg acg gct gtc aac acc acc gca aac tgg aag ggc gag cct 163
 Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn Trp Lys Gly Glu Pro
 10 15 20

tat gat cca gag act ttc cgc agc gat gcc ggc atc ctc gac ggt gta 211
 Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly Ile Leu Asp Gly Val
 25 30 35

gac atc atg ggc gac ggc gac aac cca gca agc atg ctg tgg tcc agg 259
 Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser Met Leu Trp Ser Arg
 40 45 50

cct gca atc tcc atc acc gga ttc act tcc acc cca gtg gca gaa gca 307
 Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr Pro Val Ala Glu Ala
 55 60 65

ctc aac gca gtg ccc gca acg gcg tcc gcc aag cta aac ctt cgc gtg 355
 Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys Leu Asn Leu Arg Val 85
 70 75 80

cca gca ggc ctg gaa gca aac gat gtg gcc gag aag ctg aag cag cac 403
 Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu Lys Leu Lys Gln His 100
 90 95

ctg atc aat cac aca cct tgg ggc gca aag atc acg gtg gag atc gat 451
 Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile Thr Val Glu Ile Asp 115
 105 110

gac att aac caa ccg ttc tcc acc gat att acc ggc cct gca atg tcc 499
 Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr Gly Pro Ala Met Ser 130
 120 125

acc ctg gcg tcc tgc ctg agc gct gcg tac gag ggc aag gat ctt gtc 547
 Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu Gly Lys Asp Leu Val 145
 135 140

acc gaa ggc agc ggc gga tcc att cca ctg tgt acc gaa ctg att gag 595
 Thr Glu Gly Ser Gly Gly Ser Ile Pro Leu Cys Thr Glu Leu Ile Glu 165
 150 155 160

gtc aac cca taagcagaat tggcactcta cgg 627
 Val Asn Pro

<210> 360

<211> 168

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 360

Met Asn Thr Asp Ala Pro Leu Ser Thr Ala Val Asn Thr Thr Ala Asn
 1 5 10 15

Trp Lys Gly Glu Pro Tyr Asp Pro Glu Thr Phe Arg Ser Asp Ala Gly
 20 25 30

Ile Leu Asp Gly Val Asp Ile Met Gly Asp Gly Asp Asn Pro Ala Ser
 35 40 45

Met Leu Trp Ser Arg Pro Ala Ile Ser Ile Thr Gly Phe Thr Ser Thr
 50 55 60

Pro Val Ala Glu Ala Leu Asn Ala Val Pro Ala Thr Ala Ser Ala Lys
 65 70 75 80

Leu Asn Leu Arg Val Pro Ala Gly Leu Glu Ala Asn Asp Val Ala Glu
 85 90 95

Lys Leu Lys Gln His Leu Ile Asn His Thr Pro Trp Gly Ala Lys Ile
 100 105 110

Thr Val Glu Ile Asp Asp Ile Asn Gln Pro Phe Ser Thr Asp Ile Thr
 115 120 125

Gly Pro Ala Met Ser Thr Leu Ala Ser Cys Leu Ser Ala Ala Tyr Glu

130					135					140					
Gly	Lys	Asp	Leu	Val	Thr	Glu	Gly	Ser	Gly	Gly	Ser	Ile	Pro	Leu	Cys
145					150					155					160
Thr Glu Leu Ile Glu Val Asn Pro															
165															

```
<210> 361
<211> 246
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(223)  
<223> RXS00907
```

```

<400> 361
cctgagcgcgt gcgtacgagg gcaaggatct tgtcaccgaa ggcagcggcg gatccattcc 60

actgtgtacc gaactgattg aggtcaaccc ataagcagaa ttg gca ctc tac ggt 115
Leu Ala Leu Tyr Gly
1 5

gtg gaa gaa ccc ctc acc gtt atc cac tcc gct aat gaa tct gtt gac 163
Val Glu Glu Pro Leu Thr Val Ile His Ser Ala Asn Glu Ser Val Asp
10 15 20

ccc aat gag att cgc gat atc gcc acc gca gaa gca ttg ttc ctg ctc 211
Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu Ala Leu Phe Leu Leu
25 30 35

aac tac acc aag tagaccçaaa agcaggcggtt aac 246
Asn Tyr Thr Lys
40

```

```
<210> 362
<211> 41
<212> PRT
<213> Corynebacterium glutamicum
```

```
<400> 362
Leu Ala Leu Tyr Gly Val Glu Glu Pro Leu Thr Val Ile His Ser Ala
 1             5             10             15
Asn Glu Ser Val Asp Pro Asn Glu Ile Arg Asp Ile Ala Thr Ala Glu
      20             25             30
Ala Leu Phe Leu Leu Asn Tyr Thr Lys
 35             40
```

```
<210> 363
<211> 1281
<212> DNA
<213> Corynebacterium glutamicum
```

<220>

<221> CDS

<222> (101)..(1258)

<223> RXS02001

<400> 363

```

gcggtttcgt catggataag gactgtgttc gggaccattg cgatactcgt gtcaaaaggc 60

gatagtccag catagaccgt gctttatcga aggtgaaccc atg ccc gtt atc aat 115
                               Met Pro Val Ile Asn
                               1 5

agt atc gcc agt ttt tcc gac gag atg acc cgc tgg cgg cgt cac ctg 163
Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg Trp Arg Arg His Leu
                               10 15 20

cat caa aac ccc gaa atc agc ttt gat tgt gtg gaa act gcg gcc ttc 211
His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val Glu Thr Ala Ala Phe
                               25 30 35

gtg gcc gag cag ctg cgc agc ttc ggg gtg gat gaa att cac acc ggc 259
Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp Glu Ile His Thr Gly
                               40 45 50

atc gcg aaa acc ggt atc atc gcc ctg att cac ggg cgc gag gct ggc 307
Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His Gly Arg Glu Ala Gly
                               55 60 65

ccc gtc gtc ggc ctg cgc gcc gat atg gac gcg ctg ccg ctg acc gag 355
Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala Leu Pro Leu Thr Glu
                               70 75 80 85

att acc ggc gtc gac tat gcc tcg acc acc ccc gga aaa atg cac gcc 403
Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro Gly Lys Met His Ala
                               90 95 100

tgc ggc cac gac ggc cac acg acc atg ctg ctg ggc gcc gcc aaa tat 451
Cys Gly His Asp Gly His Thr Thr Met Leu Leu Gly Ala Ala Lys Tyr
                               105 110 115

ctg gcc gag acg cgc aat ttc gca ggt acc gtc gcg ctg atc ttc cag 499
Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val Ala Leu Ile Phe Gln
                               120 125 130

cct gcg gaa gaa aac ggc ggc ggc gcg ggc gtt atg gtc gat gaa ggc 547
Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val Met Val Asp Glu Gly
                               135 140 145

gtc ctc gac cgc ttt gcc atc gcc gaa gtc tac gcc ctg cac aac cag 595
Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr Ala Leu His Asn Gln
                               150 155 160 165

ccc ggc ctg ccg ctt ggc cat ttt atg acg aca gcc ggc ccg atc atg 643
Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr Ala Gly Pro Ile Met
                               170 175 180

gcc gct gtc gac acg ttc gac atc aac att acc gga cgc ggc ggc cac 691
Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr Gly Arg Gly Gly His
                               185 190 195

ggg gcc aaa ccg cac caa acc cgc gac ccc atc gtc gca gcc gtc gga 739
Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile Val Ala Ala Val Gly

```

200	205	210	
att gtc caa gcg ttt caa acg ata gtc agc cgg aat cac aat ccg gtc I1 Val Gln Ala Phe Gln Thr Ile Val Ser Arg Asn His Asn Pro Val 215 220 225			787
gag gac ctt gtc gtg tcg gtc acg caa atc cac acc ggc agc gcc gat Glu Asp Leu Val Val Ser Val Thr Gln Ile His Thr Gly Ser Ala Asp 230 235 240 245			835
aat atc atc ccc gaa acc gcc tat atc aac ggc act gtc cgc acc ttc Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly Thr Val Arg Thr Phe 250 255 260			883
aac aaa gac gtg cag gcc atg gtc atc acg cgg atg gaa gaa atc gtc Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg Met Glu Glu Ile Val 265 270 275			931
gcg ggc caa gct gca gcc tat ggg gtc gag gcg acg ctg acc tac aac Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala Thr Leu Thr Tyr Asn 280 285 290			979
cgc aac tat ccc gcc acc att aac gac gcc gcc aaa gcc gcc atc gct 1027 Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala Lys Ala Ala Ile Ala 295 300 305			
gcc gaa gtc gcg ggc gag gtc ggc ctc ggg gtc aac ccg aac ggc tcg 1075 Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val Asn Pro Asn Gly Ser 310 315 320 325			
cgc ggg atg ggg gcc gag gat ttc tcg tat ttc ctc gaa aag cgc ccg 1123 Arg Gly Met Gly Ala Glu Asp Phe Ser Tyr Phe Leu Glu Lys Arg Pro 330 335 340			
ggt gcc tac ctg ttc gtc ggt aat ggc gac agc gcg ggc ctt cac aac 1171 Gly Ala Tyr Leu Phe Val Gly Asn Gly Asp Ser Ala Gly Leu His Asn 345 350 355			
ccc gcc tat aat ttc aac gac gag gcc gcg ccc tac ggc gca tcg ttc 1219 Pro Ala Tyr Asn Phe Asn Asp Glu Ala Ala Pro Tyr Gly Ala Ser Phe 360 365 370			
ttg gcc cgc atg gca gaa cgc ccc ttg ccg tta aag ggc tgatccatgg 1268 Leu Ala Arg Met Ala Glu Arg Pro Leu Pro Leu Lys Gly 375 380 385			
cgctcgaaga tgc 1281			
<210> 364			
<211> 386			
<212> PRT			
<213> Corynebacterium glutamicum			

<400> 364

```

Met Pro Val Ile Asn Ser Ile Ala Ser Phe Ser Asp Glu Met Thr Arg
 1           5           10           15

Trp Arg Arg His Leu His Gln Asn Pro Glu Ile Ser Phe Asp Cys Val
          20           25           30

Glu Thr Ala Ala Phe Val Ala Glu Gln Leu Arg Ser Phe Gly Val Asp
          35           40           45

Glu Ile His Thr Gly Ile Ala Lys Thr Gly Ile Ile Ala Leu Ile His
          50           55           60

Gly Arg Glu Ala Gly Pro Val Val Gly Leu Arg Ala Asp Met Asp Ala
          65           70           75           80

Leu Pro Leu Thr Glu Ile Thr Gly Val Asp Tyr Ala Ser Thr Thr Pro
          85           90           95

Gly Lys Met His Ala Cys Gly His Asp Gly His Thr Thr Met Leu Leu
          100          105          110

Gly Ala Ala Lys Tyr Leu Ala Glu Thr Arg Asn Phe Ala Gly Thr Val
          115          120          125

Ala Leu Ile Phe Gln Pro Ala Glu Glu Asn Gly Gly Gly Ala Gly Val
          130          135          140

Met Val Asp Glu Gly Val Leu Asp Arg Phe Ala Ile Ala Glu Val Tyr
          145          150          155          160

Ala Leu His Asn Gln Pro Gly Leu Pro Leu Gly His Phe Met Thr Thr
          165          170          175

Ala Gly Pro Ile Met Ala Ala Val Asp Thr Phe Asp Ile Asn Ile Thr
          180          185          190

Gly Arg Gly Gly His Gly Ala Lys Pro His Gln Thr Arg Asp Pro Ile
          195          200          205

Val Ala Ala Val Gly Ile Val Gln Ala Phe Gln Thr Ile Val Ser Arg
          210          215          220

Asn His Asn Pro Val Glu Asp Leu Val Val Ser Val Thr Gln Ile His
          225          230          235          240

Thr Gly Ser Ala Asp Asn Ile Ile Pro Glu Thr Ala Tyr Ile Asn Gly
          245          250          255

Thr Val Arg Thr Phe Asn Lys Asp Val Gln Ala Met Val Ile Thr Arg
          260          265          270

Met Glu Glu Ile Val Ala Gly Gln Ala Ala Ala Tyr Gly Val Glu Ala
          275          280          285

Thr Leu Thr Tyr Asn Arg Asn Tyr Pro Ala Thr Ile Asn Asp Ala Ala
          290          295          300

Lys Ala Ala Ile Ala Ala Glu Val Ala Gly Glu Val Gly Leu Gly Val
          305          310          315          320

```

<400> 365																
gccatggaat	gctccgttga	acgcaacagc	cttaaataca	atccccctcct	ataagccaag	60										
agtttttagtg						tcgctgcgca	ggtactctac	tatctaatacc	atg	agc	cgc	att	tca	115		
									Met	Ser	Arg	Ile	Ser	5		
									1							
gaa ctt cta aac aat cat ggt gtt gat ctg tcg tgg caa gag gcc gca						163										
Glu	Leu	Leu	Asn	Asn	His	Gly	Val	Asp	Leu	Ser	Trp	Gln	Glu	Ala	Ala	
						10						15	20			
tat cag gat ttc cac gaa cat cct gag ctc tcc ggc ttc gaa tca gag						211										
Tyr	Gln	Asp	Phe	His	Glu	His	Pro	Glu	Leu	Ser	Gly	Phe	Glu	Ser	Glu	
						25						30	35			
acc gca gat cgc att cag aaa tac ctc gag cgt ttt gat tgt gag gtg						259										
Thr	Ala	Asp	Arg	Ile	Gln	Lys	Tyr	Leu	Glu	Arg	Phe	Asp	Cys	Glu	Val	
						40						45	50			
att cca aat gtt ggc ggt tac ggc att ctg gcc gtg ttc cga aat ggg						307										
Ile	Pro	Asn	Val	Gly	Gly	Tyr	Gly	Ile	Leu	Ala	Val	Phe	Arg	Asn	Gly	
						55						60	65			
tcg aca gat cct ggt gcc cct gtt gcg tta atg cgc gca gat ttc gat						355										
Ser	Thr	Asp	Pro	Gly	Ala	Pro	Val	Ala	Leu	Met	Arg	Ala	Asp	Phe	Asp	
						70						75	80			
ggc ctt ccc gtc aag gaa atc acc gga gtt ccg ttt gct tcc act cgt						403										
Gly	Leu	Pro	Val	Lys	Glu	Ile	Thr	Gly	Val	Pro	Phe	Ala	Ser	Thr	Arg	
						90						95	100			
atg cgt ccg cat gat ggg gca aat gtc cat gtc atg cac gca tgc ggc						451										
Met	Arg	Pro	His	Asp	Gly	Ala	Asn	Val	His	Val	Met	His	Ala	Cys	Gly	
						105						110	115			

cac gat gtc cac gtc acc gcg ctg ctt ggt gcg tgt gcc att tta gat 499
 His Asp Val His Val Thr Ala Leu Leu Gly Ala Cys Ala Ile Leu Asp
 120 125 130

gag cgt cgc gat gca tgg gaa ggc acg ttc atc gcg ttg ttc cag cca 547
 Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile Ala Leu Phe Gln Pro
 135 140 145

tcg gag gaa aac tcc caa ggc gct aac aag atg gtc gcc ggc ggt tta 595
 Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met Val Ala Gly Gly Leu
 150 155 160 165

gtt gat ctg atc cca cgc cct gat gtg tgc ttt ggc cag cat gta gtc 643
 Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe Gly Gln His Val Val
 170 175 180

ccc ggt gct gca gga acc gtg atg agc atg cct ggc ggt gct ctc gct 691
 Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro Gly Gly Ala Leu Ala
 185 190 195

gcc tgc gat tcc att gaa atc cgc att cag ggt cgc agc gcc cat ggt 739
 Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly Arg Ser Ala His Gly
 200 205 210

tcc atg cct cat aat tcc atc gat ccc act tat gtt gca gcg atg att 787
 Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr Val Ala Ala Met Ile
 215 220 225

gtc gtg cga ctc caa gga atc gtg ggc cgc gag gtt tct cca gag gat 835
 Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu Val Ser Pro Glu Asp
 230 235 240 245

ttc gcc gtt att tct gtg ggc acc ctc cag tcg ggc aac acc aac aac 883
 Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser Gly Asn Thr Asn Asn
 250 255 260

acc att cca gca agt gct cgt ttg gtg ttg aac tgc cgt ttc tac aac 931
 Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn Cys Arg Phe Tyr Asn
 265 270 275

gac aaa gtc aag cac aag gtc tac cga gcc atc gaa cgt gtt gtc cgt 979
 Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile Glu Arg Val Val Arg
 280 285 290

ggt gaa tgc ctt gct tcc ggt att gag gaa gaa cct gtc att gag tac
 1027
 Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu Pro Val Ile Glu Tyr
 295 300 305

ttc gcc cac ggt gat ctc acc aac aac acc cct gtt gtc ttc gat act
 1075
 Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro Val Val Phe Asp Thr
 310 315 320 325

gtg cgc cct gtc ttc gac gat gtt ttc ggc gag gat tct att gac gct
 1123
 Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu Asp Ser Ile Asp Ala
 330 335 340

tac cgg tgg act gcg tcg gag gat ttc ccc tcc att cct aag gca ttc
 1171

Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser Ile Pro Lys Ala Phe
345 350 355

aac agc cct tac ctg tac tgg acg att ggt gtc acg ccg cgc gat cag
1219

Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val Thr Pro Arg Asp Gln
360 365 370

tgg aca gaa gcc gta gaa aga gac cgc gtg gca tcg gat gtg cca gcc
1267

Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala Ser Asp Val Pro Ala
375 380 385

aat cac atg gga gat ttc ctc cct gat tat gcg ccg acg atg tcc gct
1315

Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala Pro Thr Met Ser Ala
390 395 400 405

gcc acc cgc gca gcc gca gcc gcg ctg ctg acc tac ttg gga act aac
1363

Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr Tyr Leu Gly Thr Asn
410 415 420

taatcatcta gttttctgcg acg
1386

<210> 366

<211> 421

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met Ser Arg Ile Ser Glu Leu Leu Asn Asn His Gly Val Asp Leu Ser
1 5 10 15

Trp Gln Glu Ala Ala Tyr Gln Asp Phe His Glu His Pro Glu Leu Ser
20 25 30

Gly Phe Glu Ser Glu Thr Ala Asp Arg Ile Gln Lys Tyr Leu Glu Arg
35 40 45

Phe Asp Cys Glu Val Ile Pro Asn Val Gly Gly Tyr Gly Ile Leu Ala
50 55 60

Val Phe Arg Asn Gly Ser Thr Asp Pro Gly Ala Pro Val Ala Leu Met
65 70 75 80

Arg Ala Asp Phe Asp Gly Leu Pro Val Lys Glu Ile Thr Gly Val Pro
85 90 95

Phe Ala Ser Thr Arg Met Arg Pro His Asp Gly Ala Asn Val His Val
100 105 110

Met His Ala Cys Gly His Asp Val His Val Thr Ala Leu Leu Gly Ala
115 120 125

Cys Ala Ile Leu Asp Glu Arg Arg Asp Ala Trp Glu Gly Thr Phe Ile
130 135 140

Ala Leu Phe Gln Pro Ser Glu Glu Asn Ser Gln Gly Ala Asn Lys Met

145	150	155	160
Val Ala Gly Gly Leu Val Asp Leu Ile Pro Arg Pro Asp Val Cys Phe	165	170	175
Gly Gln His Val Val Pro Gly Ala Ala Gly Thr Val Met Ser Met Pro	180	185	190
Gly Gly Ala Leu Ala Ala Cys Asp Ser Ile Glu Ile Arg Ile Gln Gly	195	200	205
Arg Ser Ala His Gly Ser Met Pro His Asn Ser Ile Asp Pro Thr Tyr	210	215	220
Val Ala Ala Met Ile Val Val Arg Leu Gln Gly Ile Val Gly Arg Glu	225	230	235
Val Ser Pro Glu Asp Phe Ala Val Ile Ser Val Gly Thr Leu Gln Ser	245	250	255
Gly Asn Thr Asn Asn Thr Ile Pro Ala Ser Ala Arg Leu Val Leu Asn	260	265	270
Cys Arg Phe Tyr Asn Asp Lys Val Lys His Lys Val Tyr Arg Ala Ile	275	280	285
Glu Arg Val Val Arg Gly Glu Cys Leu Ala Ser Gly Ile Glu Glu Glu	290	295	300
Pro Val Ile Glu Tyr Phe Ala His Gly Asp Leu Thr Asn Asn Thr Pro	305	310	315
Val Val Phe Asp Thr Val Arg Pro Val Phe Asp Asp Val Phe Gly Glu	325	330	335
Asp Ser Ile Asp Ala Tyr Arg Trp Thr Ala Ser Glu Asp Phe Pro Ser	340	345	350
Ile Pro Lys Ala Phe Asn Ser Pro Tyr Leu Tyr Trp Thr Ile Gly Val	355	360	365
Thr Pro Arg Asp Gln Trp Thr Glu Ala Val Glu Arg Asp Arg Val Ala	370	375	380
Ser Asp Val Pro Ala Asn His Met Gly Asp Phe Leu Pro Asp Tyr Ala	385	390	395
Pro Thr Met Ser Ala Ala Thr Arg Ala Ala Ala Ala Ala Leu Leu Thr	405	410	415
Tyr Leu Gly Thr Asn	420		

<210> 367

<211> 3462

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(3439)

<223> RXS02234

<400> 367

accagagggc cgctgccggc ccaaatgatg caagccccct gtttgaccag tttgttgagc 60

tgatggatgc	agacgctcag	aagaaaggcg	cataaataac	atg	cca	aag	cgt	tca	115
				Met	Pro	Lys	Arg	Ser	
				1				5	

gat	att	aac	cac	gtc	ctc	gtc	atc	ggg	tcc	ggc	ccc	atc	gtc	att	ggc	163
Asp	Ile	Asn	His	Val	Leu	Val	Ile	Gly	Ser	Gly	Pro	Ile	Val	Ile	Gly	
			10					15						20		

cag	gca	tgt	gaa	ttc	gac	tac	tcc	ggc	acc	cag	gct	tgc	cgc	gtg	ctg	211
Gln	Ala	Cys	Glu	Phe	Asp	Tyr	Ser	Gly	Thr	Gln	Ala	Cys	Arg	Val	Leu	
			25					30					35			

aag	gaa	gag	gga	ctg	cgc	gtc	acc	ctc	atc	aac	tcc	aac	cca	gca	acg	259
Lys	Glu	Glu	Gly	Leu	Arg	Val	Thr	Leu	Ile	Asn	Ser	Asn	Pro	Ala	Thr	
			40				45					50				

atc	atg	acc	gac	cca	gaa	atg	gct	gac	cac	acc	tac	gtg	gag	cca	atc	307
Ile	Met	Thr	Asp	Pro	Glu	Met	Ala	Asp	His	Thr	Tyr	Val	Glu	Pro	Ile	
	55					60					65					

gag	ccg	gaa	tac	atc	gac	aag	att	ttc	gct	aag	gaa	atc	gag	cag	ggc	355
Glu	Pro	Glu	Tyr	Ile	Asp	Lys	Ile	Phe	Ala	Lys	Glu	Ile	Glu	Gln	Gly	
	70				75					80					85	

cac	cca	atc	gac	gcc	gtc	ctg	gca	acc	ctt	ggg	ggc	cag	act	gca	ctt	403
His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly	Gly	Gln	Thr	Ala	Leu	
				90					95					100		

aac	gca	gct	atc	cag	ctg	gat	cgc	ctc	ggc	atc	ctg	gaa	aag	tac	ggc	451
Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile	Leu	Glu	Lys	Tyr	Gly	
			105				110						115			

gtt	gaa	ctc	atc	ggg	gca	gac	atc	gat	gcc	att	gag	cgc	ggc	gaa	gat	499
Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile	Glu	Arg	Gly	Glu	Asp	
		120					125					130				

cgc	cag	aag	ttc	aag	gat	att	gtc	acc	acc	atc	ggg	ggc	gaa	tcc	gcg	547
Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile	Gly	Gly	Glu	Ser	Ala	
	135				140					145						

cgt	tcc	cgc	gtc	tgc	cac	aac	atg	gaa	gaa	gtc	cac	gag	act	gtc	gca	595
Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val	His	Glu	Thr	Val	Ala	
	150				155					160					165	

gaa	ctc	ggc	ctt	cca	gta	gtc	gtg	cgt	cca	tcc	ttc	act	atg	ggg	ggc	643
Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser	Phe	Thr	Met	Gly	Gly	
				170				175						180		

ctg	ggc	tcc	ggg	ctt	gca	tac	aac	acc	gaa	gac	ctt	gag	cgc	atc	gct	691
Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp	Leu	Glu	Arg	Ile	Ala	
			185					190					195			

ggg	ggc	gga	ctt	gct	gca	tct	cct	gaa	gca	aac	gtc	ttg	atc	gaa	gaa	739
Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn	Val	Leu	Ile	Glu	Glu	
		200					205					210				

tcc atc ctt ggt tgg aag gaa ttc gag ctc gag ctc atg cgc gat acc	787
Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu Glu Leu Met Arg Asp Thr	
215 220 225	
gca gac aac gtt gtg gtt atc tgc tcc att gaa aac gtc gac gca ctg	835
Ala Asp Asn Val Val Val Ile Cys Ser Ile Glu Asn Val Asp Ala Leu	
230 235 240 245	
ggc gtg cac acc ggc gac tct gtc acc gtg gca cct gcc ctg acc ctg	883
Gly Val His Thr Gly Asp Ser Val Thr Val Ala Pro Ala Leu Thr Leu	
250 255 260	
act gac cgt gaa ttc cag aag atg cgc gat cag ggt atc gcc atc atc	931
Thr Asp Arg Glu Phe Gln Lys Met Arg Asp Gln Gly Ile Ala Ile Ile	
265 270 275	
cgc gag gtc ggc gtg gac acc ggt gga tgt aac atc cag ttc gcc atc	979
Arg Glu Val Gly Val Asp Thr Gly Gly Cys Asn Ile Gln Phe Ala Ile	
280 285 290	
aac cca gtt gat ggc cgc atc atc acc att gag atg aac cca cgt gtg	
1027	
Asn Pro Val Asp Gly Arg Ile Ile Thr Ile Glu Met Asn Pro Arg Val	
295 300 305	
tct cgt tcc tcc gct ctg gca tcc aag gca acg ggc ttc cca att gcc	
1075	
Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala Thr Gly Phe Pro Ile Ala	
310 315 320 325	
aag atg gct gcc aag ctg gct atc gga tac acc ctg gat gag atc acc	
1123	
Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr Thr Leu Asp Glu Ile Thr	
330 335 340	
aac gac atc act ggt gaa acc cca gct gcg ttt gag ccc acc atc gac	
1171	
Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala Phe Glu Pro Thr Ile Asp	
345 350 355	
tac gtc gtg gtc aag gcc cca cgc ttt gct ttc gag aag ttt gtc ggc	
1219	
Tyr Val Val Val Lys Ala Pro Arg Phe Ala Phe Glu Lys Phe Val Gly	
360 365 370	
gct gat gac act ttg acc acc acc atg aag tcc gtc ggt gag gtc atg	
1267	
Ala Asp Asp Thr Leu Thr Thr Thr Met Lys Ser Val Gly Glu Val Met	
375 380 385	
tcc ctg ggc cgc aac tac att gca gca ctg aac aag gca ctg cgt tcc	
1315	
Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu Asn Lys Ala Leu Arg Ser	
390 395 400 405	
ctg gaa acc aag cag cag ggt ttc tgg acc aag cct gat gag ttc ttc	
1363	
Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys Pro Asp Glu Phe Phe	
410 415 420	

gca ggg gag cgc gct acc gat aag gca gct gtt ctg gaa gat ctc aag
 1411
 Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val Leu Glu Asp Leu Lys
 425 430 435

cgc cca acc gaa ggc cgc ctc tac gac gtt gag ctg gca atg cgc ctt
 1459
 Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu Leu Ala Met Arg Leu
 440 445 450

ggc gca agc gtg gaa gaa ctc tac gaa gca tct tct att gat cct tgg
 1507
 Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser Ser Ile Asp Pro Trp
 455 460 465

ttc ctc gcc gag ctt gaa gct ctc gtg cag ttc cgc cag aag ctc gtt
 1555
 Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe Arg Gln Lys Leu Val
 470 475 480 485

gac gca cca ttc cta aac gaa gat ctc ctg cgc gaa gca aag ttc atg
 1603
 Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg Glu Ala Lys Phe Met
 490 495 500

ggt ctg tcc gac ctg cag atc gca gcc ctt cgc cca gag ttc gct ggc
 1651
 Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg Pro Glu Phe Ala Gly
 505 510 515

gaa gac ggc gta cgc acc ttg cgt ctg tcc cta ggc atc cgc cca gta
 1699
 Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu Gly Ile Arg Pro Val
 520 525 530

ttc aag act gtg gat acc tgt gca gca gag ttt gaa gct aag act ccg
 1747
 Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe Glu Ala Lys Thr Pro
 535 540 545

tac cac tac tcc gca tac gag ctg gat cca gca gct gag tct gag gtc
 1795
 Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala Ala Glu Ser Glu Val
 550 555 560 565

gca cca cag act gag cgt gaa aag gtc ctg atc ttg ggc tcc ggt cca
 1843
 Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile Leu Gly Ser Gly Pro
 570 575 580

aac cgc atc ggc cag ggc atc gag ttc gac tac tcc tgt gtt cac gca
 1891
 Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr Ser Cys Val His Ala
 585 590 595

gct ctt gag ctc tcc cgc gtc ggc tac gaa act gtc atg gtc aac tgc
 1939
 Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr Val Met Val Asn Cys
 600 605 610

aac cca gag acc gtg tcc acc gac tac gac acc gct gac cgc ctg tac
1987

Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr Ala Asp Arg Leu Tyr
615 620 625

ttc gag cca ctg acc ttc gaa gac gtc atg gag gtc tac cac gct gag
2035

Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu Val Tyr His Ala Glu
630 635 640 645

gcg cag tcc ggc acc gtc gca ggt gtt atc gtc cag ctt ggt ggc cag
2083

Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val Gln Leu Gly Gly Gln
650 655 660

act cct ctg ggc ttg gca gat cgt ttg aag aag gct ggc gtc cct gtc
2131

Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys Ala Gly Val Pro Val
665 670 675

att ggt acc tcc cca gag gca atc gac atg gct gag gac cgt ggc gag
2179

Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala Glu Asp Arg Gly Glu
680 685 690

ttc ggt gca ctg ctg aac cgc gag cag ctt cct gct cca gca ttc ggc
2227

Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro Ala Pro Ala Phe Gly
695 700 705

acc gca acc tct ttc gaa gag gct cgc aca gta gcc gat gag atc agc
2275

Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val Ala Asp Glu Ile Ser
710 715 720 725

tac cca gtg ctg gtt cgc cct tcc tac gtc ttg ggt ggc cgt ggc atg
2323

Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu Gly Gly Arg Gly Met
730 735 740

gag att gtc tac gat gag gct tcc ctc gag gat tac atc aac cgc gca
2371

Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu Asp Tyr Ile Asn Arg Ala
745 750 755

act gag ttg tct tct gac cac cca gtg ctg gtt gac cgc ttc cta gac
2419

Thr Glu Leu Ser Ser Asp His Pro Val Leu Val Asp Arg Phe Leu Asp
760 765 770

aac gct att gag atc gac gtc gac gca ctg tgc gac ggc gac gag gtc
2467

Asn Ala Ile Glu Ile Asp Val Asp Ala Leu Cys Asp Gly Asp Glu Val
775 780 785

tac ctg gca ggc gtc atg gag cac atc gag gaa gcc ggc att cac tcc
2515

Tyr Leu Ala Gly Val Met Glu His Ile Glu Glu Ala Gly Ile His Ser
790 795 800 805

ggt gac tcc gca tgt gca ctt cct cca atg act ttg ggc gca cag gac
2563

Gly Asp Ser Ala Cys Ala Leu Pro Pro Met Thr Leu Gly Ala Gln Asp
810 815 820

atc gag aag gtc cgc gaa gca acc aag aag ctg gct ctg ggc atc ggt
2611

Ile Glu Lys Val Arg Glu Ala Thr Lys Lys Leu Ala Leu Gly Ile Gly
825 830 835

gta cag ggc ctg atg aac gtc cag tac gca ctc aag gac gac atc ctc
2659

Val Gln Gly Leu Met Asn Val Gln Tyr Ala Leu Lys Asp Asp Ile Leu
840 845 850

tac gtc atc gag gca aac cca cgt gca tcc cgc acc gtg ccg ttc gtc
2707

Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser Arg Thr Val Pro Phe Val
855 860 865

tcc aag gca acg ggc gtc aac ctg gcc aag gca gca tcc cgt atc gca
2755

Ser Lys Ala Thr Gly Val Asn Leu Ala Lys Ala Ala Ser Arg Ile Ala
870 875 880 885

gtg ggc gcc acc atc aag gat ctc caa gat gag ggc atg att cct acc
2803

Val Gly Ala Thr Ile Lys Asp Leu Gln Asp Glu Gly Met Ile Pro Thr
890 895 900

gag tac gac ggc ggc tcc ttg cca ctg gac gct cca atc gct gtg aag
2851

Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp Ala Pro Ile Ala Val Lys
905 910 915

gaa gca gtg ttg ccg ttc aac cgc ttc cgt cgc cca gat gga aag acc
2899

Glu Ala Val Leu Pro Phe Asn Arg Phe Arg Arg Pro Asp Gly Lys Thr
920 925 930

ctg gac acc ctg ctt tcc cca gag atg aag tcc act ggc gag gtc atg
2947

Leu Asp Thr Leu Leu Ser Pro Glu Met Lys Ser Thr Gly Glu Val Met
935 940 945

ggc ttg gcc aac aac ttc ggc gct gca tat gca aag gct gaa gct ggc
2995

Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr Ala Lys Ala Glu Ala Gly
950 955 960 965

gcg ttt ggt gca ttg cca acc gaa ggc acc gtc ttc gtg acc gtg gct
3043

Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr Val Phe Val Thr Val Ala
970 975 980

aac cgc gac aag cgc acc ctg atc ctg cca atc cag cgc ctg gcg ttg
3091

Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro Ile Gln Arg Leu Ala Leu
985 990 995

atg ggc tac aag atc ctc gcc acc gaa ggc acc gca ggc atg ctg cgc
3139

Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly Thr Ala Gly Met Leu Arg
1000 1005 1010

cgc aac ggc att gag tgt gaa gtt gtg ctc aag gct tcc gac atc cgc
3187

Arg Asn Gly Ile Glu Cys Glu Val Val Leu Lys Ala Ser Asp Ile Arg
1015 1020 1025

gaa ggt gta gag ggc aag tcc atc gtg gat cgt atc cgc gaa ggc gaa
3235

Glu Gly Val Glu Gly Lys Ser Ile Val Asp Arg Ile Arg Glu Gly Glu
1030 1035 1040 1045

gtt gac ctc atc ctc aac acc cca gct ggt tct gct ggc gct cgc cac
3283

Val Asp Leu Ile Leu Asn Thr Pro Ala Gly Ser Ala Gly Ala Arg His
1050 1055 1060

gat ggc tac gat atc cgc gca gca gca gtg acc gtg ggt gtt ccg ctg
3331

Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr Val Gly Val Pro Leu
1065 1070 1075

atc acc act gtt cag ggt gtc acc gca gct gtc cag ggc ata gag gcc
3379

Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val Gln Gly Ile Glu Ala
1080 1085 1090

ctg cgt gag ggc gtt gtc agc gtc cgc gcg ctg cag gaa ctc gac cac
3427

Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu Gln Glu Leu Asp His
1095 1100 1105

gca gtc aag gct taagccctat gacattcggc gag
3462

Ala Val Lys Ala
1110

<210> 368

<211> 1113

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 368

Met Pro Lys Arg Ser Asp Ile Asn His Val Leu Val Ile Gly Ser Gly
1 5 10 15

Pro Ile Val Ile Gly Gln Ala Cys Glu Phe Asp Tyr Ser Gly Thr Gln
20 25 30

Ala Cys Arg Val Leu Lys Glu Glu Gly Leu Arg Val Thr Leu Ile Asn
35 40 45

Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His Thr
50 55 60

Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala Lys
65 70 75 80

Glu	Ile	Glu	Gln	Gly	His	Pro	Ile	Asp	Ala	Val	Leu	Ala	Thr	Leu	Gly		
				85						90						95	
Gly	Gln	Thr	Ala	Leu	Asn	Ala	Ala	Ile	Gln	Leu	Asp	Arg	Leu	Gly	Ile		
				100						105						110	
Leu	Glu	Lys	Tyr	Gly	Val	Glu	Leu	Ile	Gly	Ala	Asp	Ile	Asp	Ala	Ile		
				115						120						125	
Glu	Arg	Gly	Glu	Asp	Arg	Gln	Lys	Phe	Lys	Asp	Ile	Val	Thr	Thr	Ile		
				130						135						140	
Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu	Val		
				145						150						155	
His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro	Ser		
				165						170						175	
Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu	Asp		
				180						185						190	
Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala	Asn		
				195						200						205	
Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu	Glu		
				210						215						220	
Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile	Glu		
				225						230						235	
Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val	Ala		
				245						250						255	
Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp	Gln		
				260						265						270	
Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys	Asn		
				275						280						285	
Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile	Glu		
				290						295						300	
Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala	Thr		
				305						310						315	
Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr	Thr		
				325						330						335	
Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala	Phe		
				340						345						350	
Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala	Phe		
				355						360						365	
Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys	Ser		
				370						375						380	
Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu	Asn		
				385						390						395	
																400	

Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr Lys
 405 410 415
 Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala Val
 420 425 430
 Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val Glu
 435 440 445
 Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala Ser
 450 455 460
 Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln Phe
 465 470 475 480
 Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu Arg
 485 490 495
 Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu Arg
 500 505 510
 Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser Leu
 515 520 525
 Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu Phe
 530 535 540
 Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro Ala
 545 550 555 560
 Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu Ile
 565 570 575
 Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp Tyr
 580 585 590
 Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu Thr
 595 600 605
 Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp Thr
 610 615 620
 Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met Glu
 625 630 635 640
 Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile Val
 645 650 655
 Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys Lys
 660 665 670
 Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met Ala
 675 680 685
 Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu Pro
 690 695 700
 Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr Val
 705 710 715 720
 Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val Leu

725					730					735					
Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu	Asp
			740					745					750		
Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu	Val
		755					760					765			
Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu	Cys
	770					775					780				
Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu	Glu
	785					790					795				800
Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met	Thr
				805					810					815	
Leu	Gly	Ala	Gln	Asp	Ile	Glu	Lys	Val	Arg	Glu	Ala	Thr	Lys	Lys	Leu
			820					825					830		
Ala	Leu	Gly	Ile	Gly	Val	Gln	Gly	Leu	Met	Asn	Val	Gln	Tyr	Ala	Leu
		835					840					845			
Lys	Asp	Asp	Ile	Leu	Tyr	Val	Ile	Glu	Ala	Asn	Pro	Arg	Ala	Ser	Arg
	850					855					860				
Thr	Val	Pro	Phe	Val	Ser	Lys	Ala	Thr	Gly	Val	Asn	Leu	Ala	Lys	Ala
	865					870					875				880
Ala	Ser	Arg	Ile	Ala	Val	Gly	Ala	Thr	Ile	Lys	Asp	Leu	Gln	Asp	Glu
				885					890					895	
Gly	Met	Ile	Pro	Thr	Glu	Tyr	Asp	Gly	Gly	Ser	Leu	Pro	Leu	Asp	Ala
			900					905					910		
Pro	Ile	Ala	Val	Lys	Glu	Ala	Val	Leu	Pro	Phe	Asn	Arg	Phe	Arg	Arg
		915					920					925			
Pro	Asp	Gly	Lys	Thr	Leu	Asp	Thr	Leu	Leu	Ser	Pro	Glu	Met	Lys	Ser
	930					935					940				
Thr	Gly	Glu	Val	Met	Gly	Leu	Ala	Asn	Asn	Phe	Gly	Ala	Ala	Tyr	Ala
	945					950					955				960
Lys	Ala	Glu	Ala	Gly	Ala	Phe	Gly	Ala	Leu	Pro	Thr	Glu	Gly	Thr	Val
				965					970					975	
Phe	Val	Thr	Val	Ala	Asn	Arg	Asp	Lys	Arg	Thr	Leu	Ile	Leu	Pro	Ile
			980					985					990		
Gln	Arg	Leu	Ala	Leu	Met	Gly	Tyr	Lys	Ile	Leu	Ala	Thr	Glu	Gly	Thr
		995					1000					1005			
Ala	Gly	Met	Leu	Arg	Arg	Asn	Gly	Ile	Glu	Cys	Glu	Val	Val	Leu	Lys
	1010					1015					1020				
Ala	Ser	Asp	Ile	Arg	Glu	Gly	Val	Glu	Gly	Lys	Ser	Ile	Val	Asp	Arg
	1025					1030					1035				1040
Ile	Arg	Glu	Gly	Glu	Val	Asp	Leu	Ile	Leu	Asn	Thr	Pro	Ala	Gly	Ser
			1045						1050					1055	

Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Ala Val Thr
 1060 1065 1070

Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala Val
 1075 1080 1085

Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala Leu
 1090 1095 1100

Gln Glu Leu Asp His Ala Val Lys Ala
 1105 1110

<210> 369

<211> 3221

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(3198)

<223> FRXA02234

<400> 369

ggc tcc aac cca gca acg atc atg acc gac cca gaa atg gct gac cac 48
 Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His
 1 5 10 15

acc tac gtg gag cca atc gag ccg gaa tac atc gac aag att ttc gct 96
 Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
 20 25 30

aag gaa atc gag cag ggc cac cca atc gac gcc gtc ctg gca acc ctt 144
 Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
 35 40 45

ggc ggc cag act gca ctt aac gca gct atc cag ctg gat cgc ctc ggc 192
 Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
 50 55 60

atc ctg gaa aag tac ggc gtt gaa ctc atc ggt gca gac atc gat gcc 240
 Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
 65 70 75 80

att gag cgc ggc gaa gat cgc cag aag ttc aag gat att gtc acc acc 288
 Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr
 85 90 95

atc ggt ggc gaa tcc gcg cgt tcc cgc gtc tgc cac aac atg gaa gaa 336
 Ile Gly Gly Glu Ser Ala Arg Ser Arg Val Cys His Asn Met Glu Glu
 100 105 110

gtc cac gag act gtc gca gaa ctc ggc ctt cca gta gtc gtg cgt cca 384
 Val His Glu Thr Val Ala Glu Leu Gly Leu Pro Val Val Val Arg Pro
 115 120 125

tcc ttc act atg ggt ggc ctg ggc tcc ggt ctt gca tac aac acc gaa 432
 Ser Phe Thr Met Gly Gly Leu Gly Ser Gly Leu Ala Tyr Asn Thr Glu
 130 135 140

gac ctt gag cgc atc gct ggt ggc gga ctt gct gca tct cct gaa gca	480
Asp Leu Glu Arg Ile Ala Gly Gly Gly Leu Ala Ala Ser Pro Glu Ala	
145 150 155 160	
aac gtc ttg atc gaa gaa tcc atc ctt ggt tgg aag gaa ttc gag ctc	528
Asn Val Leu Ile Glu Glu Ser Ile Leu Gly Trp Lys Glu Phe Glu Leu	
165 170 175	
gag ctc atg cgc gat acc gca gac aac gtt gtg gtt atc tgc tcc att	576
Glu Leu Met Arg Asp Thr Ala Asp Asn Val Val Val Ile Cys Ser Ile	
180 185 190	
gaa aac gtc gac gca ctg ggc gtg cac acc ggc gac tct gtc acc gtg	624
Glu Asn Val Asp Ala Leu Gly Val His Thr Gly Asp Ser Val Thr Val	
195 200 205	
gca cct gcc ctg acc ctg act gac cgt gaa ttc cag aag atg cgc gat	672
Ala Pro Ala Leu Thr Leu Thr Asp Arg Glu Phe Gln Lys Met Arg Asp	
210 215 220	
cag ggt atc gcc atc atc cgc gag gtc ggc gtg gac acc ggt gga tgt	720
Gln Gly Ile Ala Ile Ile Arg Glu Val Gly Val Asp Thr Gly Gly Cys	
225 230 235 240	
aac atc cag ttc gcc atc aac cca gtt gat ggc cgc atc atc acc att	768
Asn Ile Gln Phe Ala Ile Asn Pro Val Asp Gly Arg Ile Ile Thr Ile	
245 250 255	
gag atg aac cca cgt gtg tct cgt tcc tcc gct ctg gca tcc aag gca	816
Glu Met Asn Pro Arg Val Ser Arg Ser Ser Ala Leu Ala Ser Lys Ala	
260 265 270	
acg ggc ttc cca att gcc aag atg gct gcc aag ctg gct atc gga tac	864
Thr Gly Phe Pro Ile Ala Lys Met Ala Ala Lys Leu Ala Ile Gly Tyr	
275 280 285	
acc ctg gat gag atc acc aac gac atc act ggt gaa acc cca gct gcg	912
Thr Leu Asp Glu Ile Thr Asn Asp Ile Thr Gly Glu Thr Pro Ala Ala	
290 295 300	
ttt gag ccc acc atc gac tac gtc gtg gtc aag gcc cca cgc ttt gct	960
Phe Glu Pro Thr Ile Asp Tyr Val Val Val Lys Ala Pro Arg Phe Ala	
305 310 315 320	
ttc gag aag ttt gtc ggc gct gat gac act ttg acc acc acc atg aag	
1008	
Phe Glu Lys Phe Val Gly Ala Asp Asp Thr Leu Thr Thr Thr Met Lys	
325 330 335	
tcc gtc ggt gag gtc atg tcc ctg ggc cgc aac tac att gca gca ctg	
1056	
Ser Val Gly Glu Val Met Ser Leu Gly Arg Asn Tyr Ile Ala Ala Leu	
340 345 350	
aac aag gca ctg cgt tcc ctg gaa acc aag cag cag ggt ttc tgg acc	
1104	
Asn Lys Ala Leu Arg Ser Leu Glu Thr Lys Gln Gln Gly Phe Trp Thr	
355 360 365	
aag cct gat gag ttc ttc gca ggg gag cgc gct acc gat aag gca gct	
1152	

Lys Pro Asp Glu Phe Phe Ala Gly Glu Arg Ala Thr Asp Lys Ala Ala
 370 375 380
 gtt ctg gaa gat ctc aag cgc cca acc gaa ggc cgc ctc tac gac gtt
 1200
 Val Leu Glu Asp Leu Lys Arg Pro Thr Glu Gly Arg Leu Tyr Asp Val
 385 390 395 400
 gag ctg gca atg cgc ctt ggc gca agc gtg gaa gaa ctc tac gaa gca
 1248
 Glu Leu Ala Met Arg Leu Gly Ala Ser Val Glu Glu Leu Tyr Glu Ala
 405 410 415
 tct tct att gat cct tgg ttc ctc gcc gag ctt gaa gct ctc gtg cag
 1296
 Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 ttc cgc cag aag ctc gtt gac gca cca ttc cta aac gaa gat ctc ctg
 1344
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445
 cgc gaa gca aag ttc atg ggt ctg tcc gac ctg cag atc gca gcc ctt
 1392
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 cgc cca gag ttc gct ggc gaa gac ggc gta cgc acc ttg cgt ctg tcc
 1440
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 cta ggc atc cgc cca gta ttc aag act gtg gat acc tgt gca gca gag
 1488
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
 ttt gaa gct aag act ccg tac cac tac tcc gca tac gag ctg gat cca
 1536
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 gca gct gag tct gag gtc gca cca cag act gag cgt gaa aag gtc ctg
 1584
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 atc ttg ggc tcc ggt cca aac cgc atc ggc cag ggc atc gag ttc gac
 1632
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 tac tcc tgt gtt cac gca gct ctt gag ctc tcc cgc gtc ggc tac gaa
 1680
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 act gtc atg gtc aac tgc aac cca gag acc gtg tcc acc gac tac gac
 1728
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp

565										570					575					
acc gct gac cgc ctg tac ttc gag cca ctg acc ttc gaa gac gtc atg																				
1776																				
Thr	Ala	Asp	Arg	Leu	Tyr	Phe	Glu	Pro	Leu	Thr	Phe	Glu	Asp	Val	Met					
			580					585					590							
gag gtc tac cac gct gag gcg cag tcc ggc acc gtc gca ggt gtt atc																				
1824																				
Glu	Val	Tyr	His	Ala	Glu	Ala	Gln	Ser	Gly	Thr	Val	Ala	Gly	Val	Ile					
		595					600					605								
gtc cag ctt ggt ggc cag act cct ctg ggc ttg gca gat cgt ttg aag																				
1872																				
Val	Gln	Leu	Gly	Gly	Gln	Thr	Pro	Leu	Gly	Leu	Ala	Asp	Arg	Leu	Lys					
	610					615					620									
aag gct ggc gtc cct gtc att ggt acc tcc cca gag gca atc gac atg																				
1920																				
Lys	Ala	Gly	Val	Pro	Val	Ile	Gly	Thr	Ser	Pro	Glu	Ala	Ile	Asp	Met					
	625				630						635				640					
gct gag gac cgt ggc gag ttc ggt gca ctg ctg aac cgc gag cag ctt																				
1968																				
Ala	Glu	Asp	Arg	Gly	Glu	Phe	Gly	Ala	Leu	Leu	Asn	Arg	Glu	Gln	Leu					
				645					650					655						
cct gct cca gca ttc ggc acc gca acc tct ttc gaa gag gct cgc aca																				
2016																				
Pro	Ala	Pro	Ala	Phe	Gly	Thr	Ala	Thr	Ser	Phe	Glu	Glu	Ala	Arg	Thr					
			660					665					670							
gta gcc gat gag atc agc tac cca gtg ctg gtt cgc cct tcc tac gtc																				
2064																				
Val	Ala	Asp	Glu	Ile	Ser	Tyr	Pro	Val	Leu	Val	Arg	Pro	Ser	Tyr	Val					
		675					680					685								
ttg ggt ggc cgt ggc atg gag att gtc tac gat gag gct tcc ctc gag																				
2112																				
Leu	Gly	Gly	Arg	Gly	Met	Glu	Ile	Val	Tyr	Asp	Glu	Ala	Ser	Leu	Glu					
	690					695					700									
gat tac atc aac cgc gca act gag ttg tct tct gac cac cca gtg ctg																				
2160																				
Asp	Tyr	Ile	Asn	Arg	Ala	Thr	Glu	Leu	Ser	Ser	Asp	His	Pro	Val	Leu					
	705				710						715				720					
gtt gac cgc ttc cta gac aac gct att gag atc gac gtc gac gca ctg																				
2208																				
Val	Asp	Arg	Phe	Leu	Asp	Asn	Ala	Ile	Glu	Ile	Asp	Val	Asp	Ala	Leu					
				725					730					735						
tgc gac ggc gac gag gtc tac ctg gca ggc gtc atg gag cac atc gag																				
2256																				
Cys	Asp	Gly	Asp	Glu	Val	Tyr	Leu	Ala	Gly	Val	Met	Glu	His	Ile	Glu					
			740					745					750							
gaa gcc ggc att cac tcc ggt gac tcc gca tgt gca ctt cct cca atg																				
2304																				
Glu	Ala	Gly	Ile	His	Ser	Gly	Asp	Ser	Ala	Cys	Ala	Leu	Pro	Pro	Met					
		755					760					765								

act ttg ggc gca cag gac atc gag aag gtc cgc gaa gca acc aag aag
2352

Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
770 775 780

ctg gct ctg ggc atc ggt gta cag ggc ctg atg aac gtc cag tac gca
2400

Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
785 790 795 800

ctc aag gac gac atc ctc tac gtc atc gag gca aac cca cgt gca tcc
2448

Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
805 810 815

cgc acc gtg ccg ttc gtc tcc aag gca acg ggc gtc aac ctg gcc aag
2496

Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
820 825 830

gca gca tcc cgt atc gca gtg ggc gcc acc atc aag gat ctc caa gat
2544

Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
835 840 845

gag ggc atg att cct acc gag tac gac ggc ggc tcc ttg cca ctg gac
2592

Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
850 855 860

gct cca atc gct gtg aag gaa gca gtg ttg ccg ttc aac cgc ttc cgt
2640

Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
865 870 875 880

cgc cca gat gga aag acc ctg gac acc ctg ctt tcc cca gag atg aag
2688

Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
885 890 895

tcc act ggc gag gtc atg ggc ttg gcc aac aac ttc ggc gct gca tat
2736

Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
900 905 910

gca aag gct gaa gct ggc gcg ttt ggt gca ttg cca acc gaa ggc acc
2784

Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
915 920 925

gtc ttc gtg acc gtg gct aac cgc gac aag cgc acc ctg atc ctg cca
2832

Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
930 935 940

atc cag cgc ctg gcg ttg atg ggc tac aag atc ctc gcc acc gaa ggc
2880

Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
945 950 955 960

acc gca ggc atg ctg cgc cgc aac ggc att gag tgt gaa gtt gtg ctc
2928

Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
965 970 975

aag gct tcc gac atc cgc gaa ggt gta gag ggc aag tcc atc gtg gat
2976

Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
980 985 990

cgt atc cgc gaa ggc gaa gtt gac ctc atc ctc aac acc cca gct ggt
3024

Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
995 1000 1005

tct gct ggc gct cgc cac gat ggc tac gat atc cgc gca gca gca gtg
3072

Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
1010 1015 1020

acc gtg ggt gtt ccg ctg atc acc act gtt cag ggt gtc acc gca gct
3120

Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
1025 1030 1035 1040

gtc cag ggc ata gag gcc ctg cgt gag ggc gtt gtc agc gtc cgc gcg
3168

Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
1045 1050 1055

ctg cag gaa ctc gac cac gca gtc aag gct taagccctat gacattcggc
3218

Leu Gln Glu Leu Asp His Ala Val Lys Ala
1060 1065

gag
3221

<210> 370

<211> 1066

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 370

Gly Ser Asn Pro Ala Thr Ile Met Thr Asp Pro Glu Met Ala Asp His
1 5 10 15

Thr Tyr Val Glu Pro Ile Glu Pro Glu Tyr Ile Asp Lys Ile Phe Ala
20 25 30

Lys Glu Ile Glu Gln Gly His Pro Ile Asp Ala Val Leu Ala Thr Leu
35 40 45

Gly Gly Gln Thr Ala Leu Asn Ala Ala Ile Gln Leu Asp Arg Leu Gly
50 55 60

Ile Leu Glu Lys Tyr Gly Val Glu Leu Ile Gly Ala Asp Ile Asp Ala
65 70 75 80

Ile Glu Arg Gly Glu Asp Arg Gln Lys Phe Lys Asp Ile Val Thr Thr

85					90					95					
Ile	Gly	Gly	Glu	Ser	Ala	Arg	Ser	Arg	Val	Cys	His	Asn	Met	Glu	Glu
			100					105					110		
Val	His	Glu	Thr	Val	Ala	Glu	Leu	Gly	Leu	Pro	Val	Val	Val	Arg	Pro
		115					120					125			
Ser	Phe	Thr	Met	Gly	Gly	Leu	Gly	Ser	Gly	Leu	Ala	Tyr	Asn	Thr	Glu
	130					135					140				
Asp	Leu	Glu	Arg	Ile	Ala	Gly	Gly	Gly	Leu	Ala	Ala	Ser	Pro	Glu	Ala
145					150					155					160
Asn	Val	Leu	Ile	Glu	Glu	Ser	Ile	Leu	Gly	Trp	Lys	Glu	Phe	Glu	Leu
				165					170					175	
Glu	Leu	Met	Arg	Asp	Thr	Ala	Asp	Asn	Val	Val	Val	Ile	Cys	Ser	Ile
			180					185					190		
Glu	Asn	Val	Asp	Ala	Leu	Gly	Val	His	Thr	Gly	Asp	Ser	Val	Thr	Val
		195					200					205			
Ala	Pro	Ala	Leu	Thr	Leu	Thr	Asp	Arg	Glu	Phe	Gln	Lys	Met	Arg	Asp
	210					215					220				
Gln	Gly	Ile	Ala	Ile	Ile	Arg	Glu	Val	Gly	Val	Asp	Thr	Gly	Gly	Cys
225					230					235					240
Asn	Ile	Gln	Phe	Ala	Ile	Asn	Pro	Val	Asp	Gly	Arg	Ile	Ile	Thr	Ile
				245					250					255	
Glu	Met	Asn	Pro	Arg	Val	Ser	Arg	Ser	Ser	Ala	Leu	Ala	Ser	Lys	Ala
			260					265					270		
Thr	Gly	Phe	Pro	Ile	Ala	Lys	Met	Ala	Ala	Lys	Leu	Ala	Ile	Gly	Tyr
		275					280					285			
Thr	Leu	Asp	Glu	Ile	Thr	Asn	Asp	Ile	Thr	Gly	Glu	Thr	Pro	Ala	Ala
	290					295					300				
Phe	Glu	Pro	Thr	Ile	Asp	Tyr	Val	Val	Val	Lys	Ala	Pro	Arg	Phe	Ala
305					310					315					320
Phe	Glu	Lys	Phe	Val	Gly	Ala	Asp	Asp	Thr	Leu	Thr	Thr	Thr	Met	Lys
				325					330					335	
Ser	Val	Gly	Glu	Val	Met	Ser	Leu	Gly	Arg	Asn	Tyr	Ile	Ala	Ala	Leu
			340					345					350		
Asn	Lys	Ala	Leu	Arg	Ser	Leu	Glu	Thr	Lys	Gln	Gln	Gly	Phe	Trp	Thr
		355					360					365			
Lys	Pro	Asp	Glu	Phe	Phe	Ala	Gly	Glu	Arg	Ala	Thr	Asp	Lys	Ala	Ala
	370					375					380				
Val	Leu	Glu	Asp	Leu	Lys	Arg	Pro	Thr	Glu	Gly	Arg	Leu	Tyr	Asp	Val
385					390					395					400
Glu	Leu	Ala	Met	Arg	Leu	Gly	Ala	Ser	Val	Glu	Glu	Leu	Tyr	Glu	Ala
				405					410					415	

Ser Ser Ile Asp Pro Trp Phe Leu Ala Glu Leu Glu Ala Leu Val Gln
 420 425 430
 Phe Arg Gln Lys Leu Val Asp Ala Pro Phe Leu Asn Glu Asp Leu Leu
 435 440 445
 Arg Glu Ala Lys Phe Met Gly Leu Ser Asp Leu Gln Ile Ala Ala Leu
 450 455 460
 Arg Pro Glu Phe Ala Gly Glu Asp Gly Val Arg Thr Leu Arg Leu Ser
 465 470 475 480
 Leu Gly Ile Arg Pro Val Phe Lys Thr Val Asp Thr Cys Ala Ala Glu
 485 490 495
 Phe Glu Ala Lys Thr Pro Tyr His Tyr Ser Ala Tyr Glu Leu Asp Pro
 500 505 510
 Ala Ala Glu Ser Glu Val Ala Pro Gln Thr Glu Arg Glu Lys Val Leu
 515 520 525
 Ile Leu Gly Ser Gly Pro Asn Arg Ile Gly Gln Gly Ile Glu Phe Asp
 530 535 540
 Tyr Ser Cys Val His Ala Ala Leu Glu Leu Ser Arg Val Gly Tyr Glu
 545 550 555 560
 Thr Val Met Val Asn Cys Asn Pro Glu Thr Val Ser Thr Asp Tyr Asp
 565 570 575
 Thr Ala Asp Arg Leu Tyr Phe Glu Pro Leu Thr Phe Glu Asp Val Met
 580 585 590
 Glu Val Tyr His Ala Glu Ala Gln Ser Gly Thr Val Ala Gly Val Ile
 595 600 605
 Val Gln Leu Gly Gly Gln Thr Pro Leu Gly Leu Ala Asp Arg Leu Lys
 610 615 620
 Lys Ala Gly Val Pro Val Ile Gly Thr Ser Pro Glu Ala Ile Asp Met
 625 630 635 640
 Ala Glu Asp Arg Gly Glu Phe Gly Ala Leu Leu Asn Arg Glu Gln Leu
 645 650 655
 Pro Ala Pro Ala Phe Gly Thr Ala Thr Ser Phe Glu Glu Ala Arg Thr
 660 665 670
 Val Ala Asp Glu Ile Ser Tyr Pro Val Leu Val Arg Pro Ser Tyr Val
 675 680 685
 Leu Gly Gly Arg Gly Met Glu Ile Val Tyr Asp Glu Ala Ser Leu Glu
 690 695 700
 Asp Tyr Ile Asn Arg Ala Thr Glu Leu Ser Ser Asp His Pro Val Leu
 705 710 715 720
 Val Asp Arg Phe Leu Asp Asn Ala Ile Glu Ile Asp Val Asp Ala Leu
 725 730 735

Cys Asp Gly Asp Glu Val Tyr Leu Ala Gly Val Met Glu His Ile Glu
 740 745 750
 Glu Ala Gly Ile His Ser Gly Asp Ser Ala Cys Ala Leu Pro Pro Met
 755 760 765
 Thr Leu Gly Ala Gln Asp Ile Glu Lys Val Arg Glu Ala Thr Lys Lys
 770 775 780
 Leu Ala Leu Gly Ile Gly Val Gln Gly Leu Met Asn Val Gln Tyr Ala
 785 790 795 800
 Leu Lys Asp Asp Ile Leu Tyr Val Ile Glu Ala Asn Pro Arg Ala Ser
 805 810 815
 Arg Thr Val Pro Phe Val Ser Lys Ala Thr Gly Val Asn Leu Ala Lys
 820 825 830
 Ala Ala Ser Arg Ile Ala Val Gly Ala Thr Ile Lys Asp Leu Gln Asp
 835 840 845
 Glu Gly Met Ile Pro Thr Glu Tyr Asp Gly Gly Ser Leu Pro Leu Asp
 850 855 860
 Ala Pro Ile Ala Val Lys Glu Ala Val Leu Pro Phe Asn Arg Phe Arg
 865 870 875 880
 Arg Pro Asp Gly Lys Thr Leu Asp Thr Leu Leu Ser Pro Glu Met Lys
 885 890 895
 Ser Thr Gly Glu Val Met Gly Leu Ala Asn Asn Phe Gly Ala Ala Tyr
 900 905 910
 Ala Lys Ala Glu Ala Gly Ala Phe Gly Ala Leu Pro Thr Glu Gly Thr
 915 920 925
 Val Phe Val Thr Val Ala Asn Arg Asp Lys Arg Thr Leu Ile Leu Pro
 930 935 940
 Ile Gln Arg Leu Ala Leu Met Gly Tyr Lys Ile Leu Ala Thr Glu Gly
 945 950 955 960
 Thr Ala Gly Met Leu Arg Arg Asn Gly Ile Glu Cys Glu Val Val Leu
 965 970 975
 Lys Ala Ser Asp Ile Arg Glu Gly Val Glu Gly Lys Ser Ile Val Asp
 980 985 990
 Arg Ile Arg Glu Gly Glu Val Asp Leu Ile Leu Asn Thr Pro Ala Gly
 995 1000 1005
 Ser Ala Gly Ala Arg His Asp Gly Tyr Asp Ile Arg Ala Ala Val
 1010 1015 1020
 Thr Val Gly Val Pro Leu Ile Thr Thr Val Gln Gly Val Thr Ala Ala
 1025 1030 1035 1040
 Val Gln Gly Ile Glu Ala Leu Arg Glu Gly Val Val Ser Val Arg Ala
 1045 1050 1055
 Leu Gln Glu Leu Asp His Ala Val Lys Ala

1060

1065

<210> 371
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXS02565

<400> 371
 ggaaattcga tacagtgcga tgacgcgata ttagaaagaa aaagatgcgc tttagcgacga 60

aaccctcacc ctccttcagg aacttatccg caacgcctgc gtg aat gat cta acc 115
 Val Asn Asp Leu Thr
 1 5

cca gat tca ggt cag gaa att aga aac gcg gaa agc cta gaa cgt ttc 163
 Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu Ser Leu Glu Arg Phe
 10 15 20

ttt gaa gga acc ccc aac gtt aaa atc acc aag ctg gaa ccg cat ccg 211
 Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys Leu Glu Pro His Pro
 25 30 35

ggc cgg acc tca att atc gtg act gtt cca ggc agc gat cca gat gct 259
 Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly Ser Asp Pro Asp Ala
 40 45 50

gag cct tta aca ctg ctt gga cat act gat gtt gtg cct gtt gat ctg 307
 Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val Val Pro Val Asp Leu
 55 60 65

cct aaa tgg act aaa gat cca ttc ggt gcg gag att tcg gat gga cag 355
 Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu Ile Ser Asp Gly Gln
 70 75 80 85

att tgg ggt aga ggg tcc gtc gat atg ctc ttt att acc gca acc caa 403
 Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe Ile Thr Ala Thr Gln
 90 95 100

gcg gcc gtc acc cgt caa gta gcc cgt gaa ggc ggc ctg cgt ggc acg 451
 Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly Gly Leu Arg Gly Thr
 105 110 115

ctg aca ttc gtt ggc gtt gct gat gag gaa gcc cgc ggc gga ctc gga 499
 Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala Arg Gly Gly Leu Gly
 120 125 130

gcg aag tgg ctt tcc gaa gaa cac caa aac ctc ttc agc tgg aaa aac 547
 Ala Lys Trp Leu Ser Glu His Gln Asn Leu Phe Ser Trp Lys Asn
 135 140 145

tgc ctc tcc gaa tcc ggt gga tcg cac ctt cca gtc cac gac ggc agc 595
 Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro Val His Asp Gly Ser
 150 155 160 165

gac gca gta gta att aac gtt gga gaa aaa ggt gca gct caa cgt cgt 643

Asp	Ala	Val	Val	Ile	Asn	Val	Gly	Glu	Lys	Gly	Ala	Ala	Gln	Arg	Arg		
				170					175					180			
att	cac	gtc	aat	ggc	gat	gct	ggg	cat	ggg	tcc	att	cct	ttc	gac	cgt	691	
Ile	His	Val	Asn	Gly	Asp	Ala	Gly	His	Gly	Ser	Ile	Pro	Phe	Asp	Arg		
			185					190					195				
gac	agc	gct	att	gtc	aag	atc	ggg	gaa	gtc	gcc	cgc	cga	atc	gct	gcc	739	
Asp	Ser	Ala	Ile	Val	Lys	Ile	Gly	Glu	Val	Ala	Arg	Arg	Ile	Ala	Ala		
		200					205					210					
gcc	gat	ctg	aag	gta	gcc	aag	gac	gat	atc	tgg	caa	ggc	ttc	gtc	caa	787	
Ala	Asp	Leu	Lys	Val	Ala	Lys	Asp	Asp	Ile	Trp	Gln	Gly	Phe	Val	Gln		
	215					220					225						
gcg	cac	cgt	ttc	gac	cca	gaa	acg	gag	cag	gcg	ctt	ctt	agc	ggg	acc	835	
Ala	His	Arg	Phe	Asp	Pro	Glu	Thr	Glu	Gln	Ala	Leu	Leu	Ser	Gly	Thr		
230					235					240					245		
tcc	cct	gag	gcc	tac	gca	gag	ttc	ggc	gga	ctc	tcc	cgc	ttc	gcc	cac	883	
Ser	Pro	Glu	Ala	Tyr	Ala	Glu	Phe	Gly	Gly	Leu	Ser	Arg	Phe	Ala	His		
				250				255						260			
gcg	gtg	tct	cat	ctc	acg	atc	gcc	caa	act	gtg	gtt	cgt	gca	ggg	caa	931	
Ala	Val	Ser	His	Leu	Thr	Ile	Ala	Gln	Thr	Val	Val	Arg	Ala	Gly	Gln		
			265				270						275				
gcc	atc	aat	gta	ttg	cca	tcg	cat	gcg	tac	ttg	gaa	ctg	gat	atc	cgt	979	
Ala	Ile	Asn	Val	Leu	Pro	Ser	His	Ala	Tyr	Leu	Glu	Leu	Asp	Ile	Arg		
		280					285					290					
acc	ctt	cca	ggc	caa	acc	aat	gac	tat	gtt	gat	gac	acc	ctg	cgt	gct		
1027																	
Thr	Leu	Pro	Gly	Gln	Thr	Asn	Asp	Tyr	Val	Asp	Asp	Thr	Leu	Arg	Ala		
	295					300					305						
gct	ctg	ggc	gat	ctt	gcc	gat	gaa	gta	gaa	atc	gaa	cac	ctc	atc	tct		
1075																	
Ala	Leu	Gly	Asp	Leu	Ala	Asp	Glu	Val	Glu	Ile	Glu	His	Leu	Ile	Ser		
310					315				320					325			
gaa	gaa	gca	acg	gtg	agc	cca	act	gat	tcc	agg	ttg	tat	aac	acc	ttg		
1123																	
Glu	Glu	Ala	Thr	Val	Ser	Pro	Thr	Asp	Ser	Arg	Leu	Tyr	Asn	Thr	Leu		
				330				335						340			
gaa	aaa	gtt	ctt	ggg	gat	ttc	ttc	ccc	gat	gcg	cct	gtg	gtc	cca	att		
1171																	
Glu	Lys	Val	Leu	Gly	Asp	Phe	Phe	Pro	Asp	Ala	Pro	Val	Val	Pro	Ile		
			345					350					355				
att	tcc	tct	ggg	ggc	tct	gac	ctg	cgc	ttt	ggg	cgt	cga	cta	ggc	ggg		
1219																	
Ile	Ser	Ser	Gly	Gly	Ser	Asp	Leu	Arg	Phe	Gly	Arg	Arg	Leu	Gly	Gly		
			360				365					370					
gtt	ggg	tat	ggg	ttt	gca	gtt	cat	gca	cgt	gaa	cga	act	ttg	gcg	gaa		
1267																	
Val	Gly	Tyr	Gly	Phe	Ala	Val	His	Ala	Arg	Glu	Arg	Thr	Leu	Ala	Glu		
	375					380					385						

gca atg ggg caa ctt cac tcc cat gac gag gcg ctg tac ctg gaa gat
1315

Ala Met Gly Gln Leu His Ser His Asp Glu Ala Leu Tyr Leu Glu Asp
390 395 400 405

ctt gaa ctg act gtt cgg ggt tat gac tcc gtc gtg cgt gaa ttc cta
1363

Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val Val Arg Glu Phe Leu
410 415 420

ggc taaaaacatg aagcaggagt ctt

1389

Gly

<210> 372

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 372

Val Asn Asp Leu Thr Pro Asp Ser Gly Gln Glu Ile Arg Asn Ala Glu
1 5 10 15

Ser Leu Glu Arg Phe Phe Glu Gly Thr Pro Asn Val Lys Ile Thr Lys
20 25 30

Leu Glu Pro His Pro Gly Arg Thr Ser Ile Ile Val Thr Val Pro Gly
35 40 45

Ser Asp Pro Asp Ala Glu Pro Leu Thr Leu Leu Gly His Thr Asp Val
50 55 60

Val Pro Val Asp Leu Pro Lys Trp Thr Lys Asp Pro Phe Gly Ala Glu
65 70 75 80

Ile Ser Asp Gly Gln Ile Trp Gly Arg Gly Ser Val Asp Met Leu Phe
85 90 95

Ile Thr Ala Thr Gln Ala Ala Val Thr Arg Gln Val Ala Arg Glu Gly
100 105 110

Gly Leu Arg Gly Thr Leu Thr Phe Val Gly Val Ala Asp Glu Glu Ala
115 120 125

Arg Gly Gly Leu Gly Ala Lys Trp Leu Ser Glu Glu His Gln Asn Leu
130 135 140

Phe Ser Trp Lys Asn Cys Leu Ser Glu Ser Gly Gly Ser His Leu Pro
145 150 155 160

Val His Asp Gly Ser Asp Ala Val Val Ile Asn Val Gly Glu Lys Gly
165 170 175

Ala Ala Gln Arg Arg Ile His Val Asn Gly Asp Ala Gly His Gly Ser
180 185 190

Ile Pro Phe Asp Arg Asp Ser Ala Ile Val Lys Ile Gly Glu Val Ala
195 200 205

Arg Arg Il Ala Ala Ala Asp Leu Lys Val Ala Lys Asp Asp Ile Trp
 210 215 220
 Gln Gly Phe Val Gln Ala His Arg Phe Asp Pro Glu Thr Glu Gln Ala
 225 230 235 240
 Leu Leu Ser Gly Thr Ser Pro Glu Ala Tyr Ala Glu Phe Gly Gly Leu
 245 250 255
 Ser Arg Phe Ala His Ala Val Ser His Leu Thr Ile Ala Gln Thr Val
 260 265 270
 Val Arg Ala Gly Gln Ala Ile Asn Val Leu Pro Ser His Ala Tyr Leu
 275 280 285
 Glu Leu Asp Ile Arg Thr Leu Pro Gly Gln Thr Asn Asp Tyr Val Asp
 290 295 300
 Asp Thr Leu Arg Ala Ala Leu Gly Asp Leu Ala Asp Glu Val Glu Ile
 305 310 315 320
 Glu His Leu Ile Ser Glu Glu Ala Thr Val Ser Pro Thr Asp Ser Arg
 325 330 335
 Leu Tyr Asn Thr Leu Glu Lys Val Leu Gly Asp Phe Phe Pro Asp Ala
 340 345 350
 Pro Val Val Pro Ile Ile Ser Ser Gly Gly Ser Asp Leu Arg Phe Gly
 355 360 365
 Arg Arg Leu Gly Gly Val Gly Tyr Gly Phe Ala Val His Ala Arg Glu
 370 375 380
 Arg Thr Leu Ala Glu Ala Met Gly Gln Leu His Ser His Asp Glu Ala
 385 390 395 400
 Leu Tyr Leu Glu Asp Leu Glu Leu Thr Val Arg Gly Tyr Asp Ser Val
 405 410 415
 Val Arg Glu Phe Leu Gly
 420

<210> 373

<211> 525

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(502)

<223> RXS02937

<400> 373

gctaccgcga agaactgtac tagttcttcc atcagcaccc gcagttgtct ttgcaagagt 60

tcgaaacatc caacgcattg gtgacaccgg tggtgtcgcg gtg atc agc aat ggg 115
 Val Ile Ser Asn Gly
 1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163

Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met
 10 15 20
 gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211
 Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val
 25 30 35
 gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259
 Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His
 40 45 50
 gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307
 Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser
 55 60 65
 cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355
 His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala
 70 75 80 85
 gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403
 Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala
 90 95 100
 ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451
 Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu
 105 110 115
 gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499
 Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val
 120 125 130
 aaa taattggcta atgaatcctt ttc 525
 Lys

<210> 374
 <211> 134
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 374
 Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile
 1 5 10 15
 Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
 20 25 30
 Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
 35 40 45
 His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
 50 55 60
 Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
 65 70 75 80
 Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
 85 90 95
 Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp

100	105	110	
Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala			
115	120	125	
Ser Ala Trp Leu Val Lys			
130			
<210> 375			
<211> 966			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(943)			
<223> RXA02194			
<400> 375			
gaaatctccc agctcattta ttggaccag gtcacatggtg ttgctcgcg cctgaagcca 60			
gaagatatct acaagaacct gtaggagttt taaagcaatc atg ttg aaa atc gct 115			
		Met Leu Lys Ile Ala	
		1 5	
gtc cca aac aaa ggc tcg ctg tcc gag cgc gcc atg gaa atc ctc gcc 163			
Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala Met Glu Ile Leu Ala			
	10	15	20
gaa gca ggc tac gca ggc cgt gga gat tcc aaa tcc ctc aac gtt ttt 211			
Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys Ser Leu Asn Val Phe			
	25	30	35
gat gaa gca aac aac gtt gaa ttc ttc ttc ctt cgc cct aaa gat atc 259			
Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu Arg Pro Lys Asp Ile			
	40	45	50
gcc atc tac gtt gct ggt ggc cag ctc gat ttg ggt atc acc ggc cgc 307			
Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu Gly Ile Thr Gly Arg			
	55	60	65
gac ctt gct cgc gat tcc cag gct gat gtc cac gaa gtt ctt tcc ctc 355			
Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His Glu Val Leu Ser Leu			
	70	75	80
ggc ttc ggt tcc tcc act ttc cgt tac gca gca cca gct gat gaa gag 403			
Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala Pro Ala Asp Glu Glu			
	90	95	100
tgg agc atc gaa aag ctc gac ggc aag cgc atc gct acc tct tac ccc 451			
Trp Ser Ile Glu Lys Leu Asp Gly Lys Arg Ile Ala Thr Ser Tyr Pro			
	105	110	115
aac ctt gtt cgc gat gac ctc gca gca cgt ggg ctt tcc gct gag gtg 499			
Asn Leu Val Arg Asp Asp Leu Ala Ala Arg Gly Leu Ser Ala Glu Val			
	120	125	130
ctc cgc ctc gac ggt gca gta gag gta tcc atc aag ctt ggt gtc gca 547			
Leu Arg Leu Asp Gly Ala Val Glu Val Ser Ile Lys Leu Gly Val Ala			
	135	140	145

gat gcc atc gcc gat gtt gta tcc acc ggc cgc acg ctg cgt cag caa 595
Asp Ala Ile Ala Asp Val Val Ser Thr Gly Arg Thr Leu Arg Gln Gln
150 155 160 165

ggt ctt gca cct ttc ggc gag gtt ctg tgc acc tct gag gct gtc att 643
Gly Leu Ala Pro Phe Gly Glu Val Leu Cys Thr Ser Glu Ala Val Ile
170 175 180

gtt ggc cgc aag gat gaa aag gtc acc cca gag cag cag atc ctg ctt 691
Val Gly Arg Lys Asp Glu Lys Val Thr Pro Glu Gln Gln Ile Leu Leu
185 190 195

cgc cgc atc cag gga att ttg cac gcg cag aac ttc ctc atg ctg gat 739
Arg Arg Ile Gln Gly Ile Leu His Ala Gln Asn Phe Leu Met Leu Asp
200 205 210

tac aac gtc gac cgc gac aac ctg gac gct gcc act gca gta acc cca 787
Tyr Asn Val Asp Arg Asp Asn Leu Asp Ala Ala Thr Ala Val Thr Pro
215 220 225

ggc tta tcc ggc cca acg gta tcc cca ctg gca cgc gac aac tgg gtt 835
Gly Leu Ser Gly Pro Thr Val Ser Pro Leu Ala Arg Asp Asn Trp Val
230 235 240 245

gct gta cgc gcc atg gtg cca cgc agg tca gct aac gcc atc atg gat 883
Ala Val Arg Ala Met Val Pro Arg Arg Ser Ala Asn Ala Ile Met Asp
250 255 260

aag ctt gct gga ctc ggc gct gaa gcc atc ctg gct tct gaa atc cgc 931
Lys Leu Ala Gly Leu Gly Ala Glu Ala Ile Leu Ala Ser Glu Ile Arg
265 270 275

atc gcc cgc atc tagttttaac taccgccgaa aat 966
Ile Ala Arg Ile
280

<210> 376

<211> 281

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 376

Met Leu Lys Ile Ala Val Pro Asn Lys Gly Ser Leu Ser Glu Arg Ala
1 5 10 15

Met Glu Ile Leu Ala Glu Ala Gly Tyr Ala Gly Arg Gly Asp Ser Lys
20 25 30

Ser Leu Asn Val Phe Asp Glu Ala Asn Asn Val Glu Phe Phe Phe Leu
35 40 45

Arg Pro Lys Asp Ile Ala Ile Tyr Val Ala Gly Gly Gln Leu Asp Leu
50 55 60

Gly Ile Thr Gly Arg Asp Leu Ala Arg Asp Ser Gln Ala Asp Val His
65 70 75 80

Glu Val Leu Ser Leu Gly Phe Gly Ser Ser Thr Phe Arg Tyr Ala Ala
85 90 95

Pro	Ala	Asp	Glu	Glu	Trp	Ser	Ile	Glu	Lys	Leu	Asp	Gly	Lys	Arg	Ile	
			100					105					110			
Ala	Thr	Ser	Tyr	Pro	Asn	Leu	Val	Arg	Asp	Asp	Leu	Ala	Ala	Arg	Gly	
			115				120					125				
Leu	Ser	Ala	Glu	Val	Leu	Arg	Leu	Asp	Gly	Ala	Val	Glu	Val	Ser	Ile	
			130				135					140				
Lys	Leu	Gly	Val	Ala	Asp	Ala	Ile	Ala	Asp	Val	Val	Ser	Thr	Gly	Arg	
			145				150					155				
Thr	Leu	Arg	Gln	Gln	Gly	Leu	Ala	Pro	Phe	Gly	Glu	Val	Leu	Cys	Thr	
							165				170				175	
Ser	Glu	Ala	Val	Ile	Val	Gly	Arg	Lys	Asp	Glu	Lys	Val	Thr	Pro	Glu	
			180					185					190			
Gln	Gln	Ile	Leu	Leu	Arg	Arg	Ile	Gln	Gly	Ile	Leu	His	Ala	Gln	Asn	
			195				200					205				
Phe	Leu	Met	Leu	Asp	Tyr	Asn	Val	Asp	Arg	Asp	Asn	Leu	Asp	Ala	Ala	
			210				215					220				
Thr	Ala	Val	Thr	Pro	Gly	Leu	Ser	Gly	Pro	Thr	Val	Ser	Pro	Leu	Ala	
			225				230					235				240
Arg	Asp	Asn	Trp	Val	Ala	Val	Arg	Ala	Met	Val	Pro	Arg	Arg	Ser	Ala	
							245					250				255
Asn	Ala	Ile	Met	Asp	Lys	Leu	Ala	Gly	Leu	Gly	Ala	Glu	Ala	Ile	Leu	
			260					265					270			
Ala	Ser	Glu	Ile	Arg	Ile	Ala	Arg	Ile								
			275				280									

```
<210> 377
<211> 393
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (370)  
<223> RXA02195
```

```

<400> 377
tcgagccggc aggtgtcgca aaataaaacc aggtggggga gtgaaattat tcgactaata 60

tcctccccca aacacacatt gataactgtt gtgtggaaga atg tac cga gtg aag      115
              Met Tyr Arg Val Lys
              1                      5

aca ttt gac tcg ctg tac gaa gaa ctt ctt aac cgt gct cag acc cgc      163
Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn Arg Ala Gln Thr Arg
              10                      15                      20

cct gaa ggg tct gga acc gtg gcc gcc ttg gat aaa ggc atc cat cat      211
Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp Lys Gly Ile His His

```

	25	30	35	
cta ggt aag aag gtc atc gaa gaa gcc gga gag gtc tgg att gca gcc				259
Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu Val Trp Ile Ala Ala				
	40	45	50	
gag tat gag acc gat gaa gag cta gcc gga gaa atc tcc cag ctc att				307
Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu Ile Ser Gln Leu Ile				
	55	60	65	
tat tgg acc cag gtc atc atg gtt gct cgc ggc ctg aag cca gaa gat				355
Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly Leu Lys Pro Glu Asp				
	70	75	80	85
atc tac aag aac ctg taggagtttt aaagcaatca tgt				393
Ile Tyr Lys Asn Leu				
	90			

<210> 378

<211> 90

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

Met Tyr Arg Val Lys Thr Phe Asp Ser Leu Tyr Glu Glu Leu Leu Asn				
1	5	10	15	
Arg Ala Gln Thr Arg Pro Glu Gly Ser Gly Thr Val Ala Ala Leu Asp				
	20	25	30	
Lys Gly Ile His His Leu Gly Lys Lys Val Ile Glu Glu Ala Gly Glu				
	35	40	45	
Val Trp Ile Ala Ala Glu Tyr Glu Thr Asp Glu Glu Leu Ala Gly Glu				
	50	55	60	
Ile Ser Gln Leu Ile Tyr Trp Thr Gln Val Ile Met Val Ala Arg Gly				
	65	70	75	80
Leu Lys Pro Glu Asp Ile Tyr Lys Asn Leu				
	85	90		

<210> 379

<211> 477

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(454)

<223> RXA01097

<400> 379

gcgccaacgc agtgcttgcc gcgaccattt tccacttccg cgaagtaacc atcgccgaag	60
taaagggagc cattaaagat gcaggatttg aggtgcgga	
atg agt gac aat cca	115
Met Ser Asp Asn Pro	
1	5

caa gag tat gag ctg gat tgg gac gtc gaa aag cga tta aag ctt aac 163
 Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys Arg Leu Lys Leu Asn
 10 15 20

 gac gcc ggc ctg gtg ccg gca atc gtc cag gcc gac ggg acc aac gag 211
 Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala Asp Gly Thr Asn Glu
 25 30 35

 gtc ctc atg atg gcc tgg atg gat acc cac gcg cta gcc tat act ttg 259
 Val Leu Met Met Ala Trp Met Asp Thr His Ala Leu Ala Tyr Thr Leu
 40 45 50

 gcg acc cgc cgt gga acc tat ttt tct agg tcc cgc aac gag tac tgg 307
 Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser Arg Asn Glu Tyr Trp
 55 60 65

 atc aag ggc ctg acc tct gga aac gtc caa gaa gtc acc gga ctt gcc 355
 Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu Val Thr Gly Leu Ala
 70 75 80 85

 ctc gac tgc gac ggc gac acc gtc ctt ctg acc gtg aaa caa acc ggc 403
 Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr Val Lys Gln Thr Gly
 90 95 100

 ggt gcg tgc cac act ggt gcc cac aca tgt ttc gac aat gac gtt ttg 451
 Gly Ala Cys His Thr Gly Ala His Thr Cys Phe Asp Asn Asp Val Leu
 105 110 115

 ctg taaaagcaac aacgattaag gaa 477
 Leu

<210> 380

<211> 118

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 380

Met Ser Asp Asn Pro Gln Glu Tyr Glu Leu Asp Trp Asp Val Glu Lys
 1 5 10 15

 Arg Leu Lys Leu Asn Asp Ala Gly Leu Val Pro Ala Ile Val Gln Ala
 20 25 30

 Asp Gly Thr Asn Glu Val Leu Met Met Ala Trp Met Asp Thr His Ala
 35 40 45

 Leu Ala Tyr Thr Leu Ala Thr Arg Arg Gly Thr Tyr Phe Ser Arg Ser
 50 55 60

 Arg Asn Glu Tyr Trp Ile Lys Gly Leu Thr Ser Gly Asn Val Gln Glu
 65 70 75 80

 Val Thr Gly Leu Ala Leu Asp Cys Asp Gly Asp Thr Val Leu Leu Thr
 85 90 95

 Val Lys Gln Thr Gly Gly Ala Cys His Thr Gly Ala His Thr Cys Phe
 100 105 110

 Asp Asn Asp Val Leu Leu

115

```
<210> 381
<211> 861
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(838)  
<223> RXA01100
```

<400> 381																
gctgtgtgggct actcaattcc acccagaaaa atcaggtgac gcaggcgcac agctactgcg 60																
aaactgggac aactacatct aacagatagg atcaatattc atg acc ttc act att 115																
Met Thr Phe Thr Ile 1 5																
ctt cct gca gtc gat gta gtt aac gga caa gca gtt cgc cta gat cag 163																
Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala Val Arg Leu Asp Gln 10 15 20																
ggc gag gcc ggc act gaa aag tct tat ggc acc cct ttg gaa tcc gca 211																
Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr Pro Leu Glu Ser Ala 25 30 35																
ctg aag tgg cag gag cag ggt gca aag tgg ttg cac ttt gtg gac ctg 259																
Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu His Phe Val Asp Leu 40 45 50																
gac gca gcg ttc aac cgt ggt tcc aac cat gag atg atg gcg gaa att 307																
Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu Met Met Ala Glu Ile 55 60 65																
gtc ggc aag ctc gat gtt gat gtg gag ctc act ggc ggt atc cgt gat 355																
Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr Gly Gly Ile Arg Asp 70 75 80 85																
gat gag tct ctg gag cgc gcg ctg gca acc ggt gca cgt cgt gta aac 403																
Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly Ala Arg Arg Val Asn 90 95 100																
att ggt acc gct gct ctg gag aag cca gag tgg att gct tct gcg att 451																
Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp Ile Ala Ser Ala Ile 105 110 115																
caa cgc tat ggc gag aag att gct gtc gat atc gct gtg cgt ttg gaa 499																
Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile Ala Val Arg Leu Glu 120 125 130																
gat ggt gaa tgg cgc acc cgt gga aac ggt tgg gtc tcc gat ggt ggc 547																
Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp Val Ser Asp Gly Gly 135 140 145																
gat ctg tgg gaa gtt ctc gag cgt ttg gat tcc caa ggt tgt gca cgt 595																
Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser Gln Gly Cys Ala Arg 150 155 160 165																
ttc gtg gtt acc gat gtg tcc aag gac ggc acc ttg agt ggt cca aat 643																

Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr Leu Ser Gly Pro Asn
 170 175 180
 gtt gag ctg ctg cgt gag gtt gct gca gct aca gac gca cct atc gtg 691
 Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr Asp Ala Pro Ile Val
 185 190 195
 gca tct ggt gga att tct gtt ttg gaa gat gtt ttg gaa cta gcc aag 739
 Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val Leu Glu Leu Ala Lys
 200 205 210
 tac cag gat gag ggc att gat tcc gtc atc att ggc aag gca ctt tat 787
 Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile Gly Lys Ala Leu Tyr
 215 220 225
 gag cac aag ttc acc ctc gaa gag gct ttg gct gca gta gaa aag ctc 835
 Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala Ala Val Glu Lys Leu
 230 235 240 245
 ggt taatacatgg atgctcgtgg gat 861
 Gly

<210> 382

<211> 246

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 382

Met Thr Phe Thr Ile Leu Pro Ala Val Asp Val Val Asn Gly Gln Ala
 1 5 10 15
 Val Arg Leu Asp Gln Gly Glu Ala Gly Thr Glu Lys Ser Tyr Gly Thr
 20 25 30
 Pro Leu Glu Ser Ala Leu Lys Trp Gln Glu Gln Gly Ala Lys Trp Leu
 35 40 45
 His Phe Val Asp Leu Asp Ala Ala Phe Asn Arg Gly Ser Asn His Glu
 50 55 60
 Met Met Ala Glu Ile Val Gly Lys Leu Asp Val Asp Val Glu Leu Thr
 65 70 75 80
 Gly Gly Ile Arg Asp Asp Glu Ser Leu Glu Arg Ala Leu Ala Thr Gly
 85 90 95
 Ala Arg Arg Val Asn Ile Gly Thr Ala Ala Leu Glu Lys Pro Glu Trp
 100 105 110
 Ile Ala Ser Ala Ile Gln Arg Tyr Gly Glu Lys Ile Ala Val Asp Ile
 115 120 125
 Ala Val Arg Leu Glu Asp Gly Glu Trp Arg Thr Arg Gly Asn Gly Trp
 130 135 140
 Val Ser Asp Gly Gly Asp Leu Trp Glu Val Leu Glu Arg Leu Asp Ser
 145 150 155 160
 Gln Gly Cys Ala Arg Phe Val Val Thr Asp Val Ser Lys Asp Gly Thr

	165		170		175
Leu Ser Gly Pro Asn Val Glu Leu Leu Arg Glu Val Ala Ala Ala Thr	180		185		190
Asp Ala Pro Ile Val Ala Ser Gly Gly Ile Ser Val Leu Glu Asp Val	195		200		205
Leu Glu Leu Ala Lys Tyr Gln Asp Glu Gly Ile Asp Ser Val Ile Ile	210		215		220
Gly Lys Ala Leu Tyr Glu His Lys Phe Thr Leu Glu Glu Ala Leu Ala	225		230		235
Ala Val Glu Lys Leu Gly	245				

<210> 383

<211> 756

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(733)

<223> RXA01101

<400> 383

```

atcgcagcta ggccagtgtg gtggatataa aacccttttg gggagaaaga aactcgactg 60
cgggttcttga tcctgaaagc acgtgacata aactatcggc atg acc aaa act gtc 115
                                     Met Thr Lys Thr Val 5
                                     1
gcc ctt ctc gac tac gga tct gga aac ctt cgt tct gct caa cgc gca 163
Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg Ser Ala Gln Arg Ala 20
                                     10
cta gag cgt gcc ggt gca gaa gtt atc gtg agc tcc gat cca gaa gtt 211
Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser Ser Asp Pro Glu Val 35
                                     25
tgc acc aac gct gat ggc ctc cta gtt cct gga gtg ggc gca ttt gat 259
Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly Val Gly Ala Phe Asp 50
                                     40
gcc tgc atg aag ggt ttg aaa aac gtc ttc gga cat cgc att atc gga 307
Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly His Arg Ile Ile Gly 65
                                     55
cag cgt ctt gct ggt gga cgt cca gtg atg ggt att tgt gtg ggc atg 355
Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly Ile Cys Val Gly Met 85
                                     70
cag atc ctg ttc gat gaa ggc gat gag cac ggc att aag tca gct ggt 403
Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly Ile Lys Ser Ala Gly 100
                                     90
tgc ggc gag tgg cct ggc aaa gtg gaa cgc ctc caa gcg gag atc ctg 451
Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu Gln Ala Glu Ile Leu

```

105	110	115	
cct cac atg ggg tgg aac aca ctt gaa atg cct acc aac tca cca atg			499
Pro His Met Gly Trp Asn Thr Leu Glu Met Pro Thr Asn Ser Pro Met			
120	125	130	
ttt gag gga att tca cct gat gag cgt ttc tac ttc gtg cac tcc tat			547
Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr Phe Val His Ser Tyr			
135	140	145	
ggg gtg cgc aag tgg acg ttg gaa acc gac gat ctg acc acg cct cca			595
Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp Leu Thr Thr Pro Pro			
150	155	160	165
gag gtt gtg tgg gcg aag cac gaa aat gat cgt ttt gtg gca gct gtg			643
Glu Val Val Trp Ala Lys His Glu Asn Asp Arg Phe Val Ala Ala Val			
170	175	180	
gaa aac ggc acg ctg tgg gct act caa ttc cac cca gaa aaa tca ggt			691
Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His Pro Glu Lys Ser Gly			
185	190	195	
gac gca ggc gca cag cta ctg cga aac tgg atc aac tac atc			733
Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile Asn Tyr Ile			
200	205	210	
taacagatag gatcaatatt cat			756

<210> 384

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 384

Met Thr Lys Thr Val Ala Leu Leu Asp Tyr Gly Ser Gly Asn Leu Arg	
1 5 10 15	
Ser Ala Gln Arg Ala Leu Glu Arg Ala Gly Ala Glu Val Ile Val Ser	
20 25 30	
Ser Asp Pro Glu Val Cys Thr Asn Ala Asp Gly Leu Leu Val Pro Gly	
35 40 45	
Val Gly Ala Phe Asp Ala Cys Met Lys Gly Leu Lys Asn Val Phe Gly	
50 55 60	
His Arg Ile Ile Gly Gln Arg Leu Ala Gly Gly Arg Pro Val Met Gly	
65 70 75 80	
Ile Cys Val Gly Met Gln Ile Leu Phe Asp Glu Gly Asp Glu His Gly	
85 90 95	
Ile Lys Ser Ala Gly Cys Gly Glu Trp Pro Gly Lys Val Glu Arg Leu	
100 105 110	
Gln Ala Glu Ile Leu Pro His Met Gly Trp Asn Thr Leu Glu Met Pro	
115 120 125	
Thr Asn Ser Pro Met Phe Glu Gly Ile Ser Pro Asp Glu Arg Phe Tyr	
130 135 140	

Phe Val His Ser Tyr Gly Val Arg Lys Trp Thr Leu Glu Thr Asp Asp
 145 150 155 160
 Leu Thr Thr Pro Pro Glu Val Val Trp Ala Lys His Glu Asn Asp Arg
 165 170 175
 Phe Val Ala Ala Val Glu Asn Gly Thr Leu Trp Ala Thr Gln Phe His
 180 185 190
 Pro Glu Lys Ser Gly Asp Ala Gly Ala Gln Leu Leu Arg Asn Trp Ile
 195 200 205
 Asn Tyr Ile
 210

<210> 385

<211> 723

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(700)

<223> RXN01657

<400> 385

cctccgtcat tgccgacgta tcccgcggcc tgggtgaagc catggtgggc atcaacgtat 60

ccgacgttcc agcaccacac cgactcgccg agcgcggctg gtg atc gtt gga gtt 115
 Val Ile Val Gly Val
 1 5

tta gct ctc cag ggc ggg gtg gaa gaa cac ctc acc gcc ttg gaa gct 163
 Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu Thr Ala Leu Glu Ala
 10 15 20

ctc gga gcg acg acc cga aaa gta cgt gtg cca aag gac ctt gat ggt 211
 Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro Lys Asp Leu Asp Gly
 25 30 35

ctc gaa ggc atc gtc atc ccc ggc ggg gaa tcc acc gtg ttg gac aaa 259
 Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser Thr Val Leu Asp Lys
 40 45 50

ctg gct cgg aca ttc gac gtg gta gaa cct cta gcg aat ctc att cgc 307
 Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu Ala Asn Leu Ile Arg
 55 60 65

gac ggc cta ccc gtt ttc gct acc tgc gct ggc ctg atc tat ctg gcg 355
 Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly Leu Ile Tyr Leu Ala
 70 75 80 85

aaa cac ctc gac aac cca gca agg gga caa caa acc ttg gcg gta gtg 403
 Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln Thr Leu Ala Val Val
 90 95 100

gac gtg gtg gtg cgt cga aac gca ttt ggc gcc caa cgc gaa tcc ttc 451
 Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala Gln Arg Glu Ser Phe
 105 110 115

gac acc acc gtg gat gtt tcc ttc gac ggt gca aca ttc ccc gga gtg 499
 Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala Thr Phe Pro Gly Val
 120 125 130
 cag gcc tcg ttt atc cga gct ccc atc gtc act gct ttt ggt cct acg 547
 Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165
 caa ggc aac atc atc gcg ctg tct ttc cat ccc gaa gaa acc ggc gat 643
 Gln Gly Asn Ile Ile Ala Leu Ser Phe His Pro Glu Glu Thr Gly Asp
 170 175 180
 tac cgc atc cac caa gcc tgg ctg gac ctg gtg aga aaa cac gct gaa 691
 Tyr Arg Ile His Gln Ala Trp Leu Asp Leu Val Arg Lys His Ala Glu
 185 190 195
 ctg gcg att tgatgttttc ggtagcgctc tgt 723
 Leu Ala Ile
 200

<210> 386

<211> 200

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 386

Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
 1 5 10 15
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160

Val	Val	Gly	Val	Arg	Gln	Gly	Asn	Ile	Ile	Ala	Leu	Ser	Phe	His	Pro
				165					170					175	
Glu	Glu	Thr	Gly	Asp	Tyr	Arg	Ile	His	Gln	Ala	Trp	Leu	Asp	Leu	Val
			180					185					190		
Arg	Lys	His	Ala	Glu	Leu	Ala	Ile								
		195					200								

```
<210> 387
<211> 601
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101)..(601)  
<223> FRXA01657
```

<400> 387																	
cctccg	tc	at	tg	ccg	acg	ta	tccc	gcg	gcc	tg	gg	tga	agc	cat	gg	tggg	10
ccg	acg	ttc	agc	acc	acac	cg	act	cg	ccg	agc	gcg	gctg	gtg	atc	gtt	gga	115
													Val	Ile	Val	Gly	5
													1				
tta	gct	ctc	cag	ggc	ggg	gtg	gaa	gaa	cac	ctc	acc	gcc	ttg	gaa	gct		163
Leu	Ala	Leu	Gln	Gly	Gly	Val	Glu	Glu	His	Leu	Thr	Ala	Leu	Glu	Ala		
				10					15					20			
ctc	gga	gcg	acg	acc	cga	aaa	gta	cgt	gtg	cca	aag	gac	ctt	gat	gg		211
Leu	Gly	Ala	Thr	Thr	Arg	Lys	Val	Arg	Val	Pro	Lys	Asp	Leu	Asp	Gly		
			25					30					35				
ctc	gaa	ggc	atc	gtc	atc	ccc	ggc	ggg	gaa	tcc	acc	gtg	ttg	gac	aaa		259
Leu	Glu	Gly	Ile	Val	Ile	Pro	Gly	Gly	Glu	Ser	Thr	Val	Leu	Asp	Lys		
		40					45					50					
ctg	gct	cg	aca	ttc	gac	gtg	gta	gaa	cct	cta	gcg	aat	ctc	att	cgc		307
Leu	Ala	Arg	Thr	Phe	Asp	Val	Val	Glu	Pro	Leu	Ala	Asn	Leu	Ile	Arg		
	55					60					65						
gac	ggc	cta	ccc	gtt	ttc	gct	acc	tgc	gct	ggc	ctg	atc	tat	ctg	gcg		355
Asp	Gly	Leu	Pro	Val	Phe	Ala	Thr	Cys	Ala	Gly	Leu	Ile	Tyr	Leu	Ala		
70					75					80					85		
aaa	cac	ctc	gac	aac	cca	gca	agg	gga	caa	caa	acc	ttg	gcg	gta	gtg		403
Lys	His	Leu	Asp	Asn	Pro	Ala	Arg	Gly	Gln	Gln	Thr	Leu	Ala	Val	Val		
				90					95					100			
gac	gtg	gtg	gtg	cgt	cga	aac	gca	ttt	ggc	gcc	caa	cgc	gaa	tcc	ttc		451
Asp	Val	Val	Val	Arg	Arg	Asn	Ala	Phe	Gly	Ala	Gln	Arg	Glu	Ser	Phe		
			105					110					115				
gac	acc	acc	gtg	gat	gtt	tcc	ttc	gac	gg	gca	aca	ttc	ccc	gga	gtg		499
Asp	Thr	Thr	Val	Asp	Val	Ser	Phe	Asp	Gly	Ala	Thr	Phe	Pro	Gly	Val		
		120					125					130					
ca	gc	tc	ttt	atc	cga	gct	ccc	atc	gtc	act	gct	ttt	ggt	cct	aca		547

Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr Ala Phe Gly Pro Thr
 135 140 145
 gta gaa gcg atc gct gct ctc aac ggt ggg gag gtg gtt ggt gta cgc 595
 Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu Val Val Gly Val Arg
 150 155 160 165
 caa ggc 601
 Gln Gly

<210> 388
 <211> 167
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 388
 Val Ile Val Gly Val Leu Ala Leu Gln Gly Gly Val Glu Glu His Leu
 1 5 10 15
 Thr Ala Leu Glu Ala Leu Gly Ala Thr Thr Arg Lys Val Arg Val Pro
 20 25 30
 Lys Asp Leu Asp Gly Leu Glu Gly Ile Val Ile Pro Gly Gly Glu Ser
 35 40 45
 Thr Val Leu Asp Lys Leu Ala Arg Thr Phe Asp Val Val Glu Pro Leu
 50 55 60
 Ala Asn Leu Ile Arg Asp Gly Leu Pro Val Phe Ala Thr Cys Ala Gly
 65 70 75 80
 Leu Ile Tyr Leu Ala Lys His Leu Asp Asn Pro Ala Arg Gly Gln Gln
 85 90 95
 Thr Leu Ala Val Val Asp Val Val Val Arg Arg Asn Ala Phe Gly Ala
 100 105 110
 Gln Arg Glu Ser Phe Asp Thr Thr Val Asp Val Ser Phe Asp Gly Ala
 115 120 125
 Thr Phe Pro Gly Val Gln Ala Ser Phe Ile Arg Ala Pro Ile Val Thr
 130 135 140
 Ala Phe Gly Pro Thr Val Glu Ala Ile Ala Ala Leu Asn Gly Gly Glu
 145 150 155 160
 Val Val Gly Val Arg Gln Gly
 165

<210> 389
 <211> 897
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(874)
 <223> RXA01098

<400> 389

```

aaaagggctc acgatgtgct gttaagtaag attgaaaaag ttcggttgat gcatgcagat 60
gcaggtaatg accagtcggt aaatgaggag tacaagtaaa atg ggc gtg gca att 115
                                         Met Gly Val Ala Ile
                                         1 5

cga gtt att cct tgc ctg gac gtg gac aac ggc cgg gtt gtt aaa ggc 163
Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly Arg Val Val Lys Gly
                        10 15 20

gtg aac ttt gaa aac ctc cgc gat gct ggc gat cct gtg gag ttg gca 211
Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp Pro Val Glu Leu Ala
                        25 30 35

aag cgc tat gac gag gaa ggg gca gat gag ctg acc ttc ctg gat gtc 259
Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu Thr Phe Leu Asp Val
                        40 45 50

acc gcc tcg aag cat ggt cgc ggc acc atg ctg gat gtt gtt cga cgc 307
Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu Asp Val Val Arg Arg
                        55 60 65

acc gct gat cag gtg ttc atc cct ctg act gtc ggt ggc ggc gtg cgc 355
Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val Gly Gly Gly Val Arg
                        70 75 80 85

agc gaa gaa gat gtt gat caa ttg ctg cgc gct ggc gcc gac aag gtt 403
Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala Gly Ala Asp Lys Val
                        90 95 100

tcg gtg aac acg tct gcg att gcc cgt cca gaa ctg ctg tca gag ctg 451
Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu Leu Leu Ser Glu Leu
                        105 110 115

tcc aag cgt ttt ggt gct cag tgc atc gtg ttg tct gtg gat gcc agg 499
Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu Ser Val Asp Ala Arg
                        120 125 130

cgc gtt cct gaa ggt gga act cct cag cca tct ggt ttt gaa gtc acc 547
Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser Gly Phe Glu Val Thr
                        135 140 145

acc cac ggc ggt tcc aag tcc gca gaa ctt gat gca atc gag tgg gca 595
Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp Ala Ile Glu Trp Ala
                        150 155 160 165

aag cgc ggc gaa gag ctg ggc gtt ggc gaa att ctg ctc aac tcc atg 643
Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile Leu Leu Asn Ser Met
                        170 175 180

gac ggc gac ggc acc aaa aac ggc ttt gac cta gag ctg ctg gaa aaa 691
Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu Glu Leu Leu Glu Lys
                        185 190 195

gtt cgc gca gcc gta tcc att cct gta atc gcc tcc ggc ggc gct ggc 739
Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala Ser Gly Gly Ala Gly
                        200 205 210

aag gcg gag cat ttc cca cca gct gtt gca gct ggc gcc aac gca gtg 787

```

Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala Gly Ala Asn Ala Val
 215 220 225
 ctt gcc gcg acc att ttc cac ttc cgc gaa gta acc atc gcc gaa gta 835
 Leu Ala Ala Thr Ile Phe His Ph Arg Glu Val Thr Ile Ala Glu Val
 230 235 240 245
 aag gga gcc att aaa gat gca gga ttt gag gtg cgg aaa tgagtgacaa 884
 Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val Arg Lys
 250 255
 tccacaagag tat 897

<210> 390
 <211> 258
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 390
 Met Gly Val Ala Ile Arg Val Ile Pro Cys Leu Asp Val Asp Asn Gly
 1 5 10 15
 Arg Val Val Lys Gly Val Asn Phe Glu Asn Leu Arg Asp Ala Gly Asp
 20 25 30
 Pro Val Glu Leu Ala Lys Arg Tyr Asp Glu Glu Gly Ala Asp Glu Leu
 35 40 45
 Thr Phe Leu Asp Val Thr Ala Ser Lys His Gly Arg Gly Thr Met Leu
 50 55 60
 Asp Val Val Arg Arg Thr Ala Asp Gln Val Phe Ile Pro Leu Thr Val
 65 70 75 80
 Gly Gly Gly Val Arg Ser Glu Glu Asp Val Asp Gln Leu Leu Arg Ala
 85 90 95
 Gly Ala Asp Lys Val Ser Val Asn Thr Ser Ala Ile Ala Arg Pro Glu
 100 105 110
 Leu Leu Ser Glu Leu Ser Lys Arg Phe Gly Ala Gln Cys Ile Val Leu
 115 120 125
 Ser Val Asp Ala Arg Arg Val Pro Glu Gly Gly Thr Pro Gln Pro Ser
 130 135 140
 Gly Phe Glu Val Thr Thr His Gly Gly Ser Lys Ser Ala Glu Leu Asp
 145 150 155 160
 Ala Ile Glu Trp Ala Lys Arg Gly Glu Glu Leu Gly Val Gly Glu Ile
 165 170 175
 Leu Leu Asn Ser Met Asp Gly Asp Gly Thr Lys Asn Gly Phe Asp Leu
 180 185 190
 Glu Leu Leu Glu Lys Val Arg Ala Ala Val Ser Ile Pro Val Ile Ala
 195 200 205
 Ser Gly Gly Ala Gly Lys Ala Glu His Phe Pro Pro Ala Val Ala Ala
 210 215 220

Gly Ala Asn Ala Val Leu Ala Ala Thr Ile Phe His Phe Arg Glu Val
225 230 235 240

Thr Ile Ala Glu Val Lys Gly Ala Ile Lys Asp Ala Gly Phe Glu Val
245 250 255

Arg Lys

<210> 391

<211> 729

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(706)

<223> RXN01104

<400> 391

cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttgga cgcagctgca 60

gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
Met Thr Val Ala Pro
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547

Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
 135 140 145
 gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
 Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
 150 155 160 165
 gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180
 ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195
 act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
 200

<210> 392

<211> 202

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 392

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15
 Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30
 Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45
 Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60
 Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80
 Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95
 Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110
 Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125
 Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140
 Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160
 Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175
 Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
195 200

<210> 393

<211> 729

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(706)

<223> FRXA01104

<400> 393

cacttgcgca ctaccattgg tgtgcctgag gaaaatgatg cgtttttgga cgcagctgca 60

gagatcatca agctgaacct gtaagagaga agaatttttc atg act gtc gca cca 115
Met Thr Val Ala Pro
1 5

aga att ggt acc gca acc cgc acc acc agc gaa tcc gac atc acc gtc 163
Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu Ser Asp Ile Thr Val
10 15 20

gag atc aac ctg gac ggc acc ggc aaa gta gat atc gat acc ggc ctg 211
Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp Ile Asp Thr Gly Leu
25 30 35

cca ttt ttc gac cac atg ctc act gca ttc ggc gtg cac ggc agt ttt 259
Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly Val His Gly Ser Phe
40 45 50

gat ctg aaa gtc cat gcc aag ggc gac atc gag atc gac gca cac cac 307
Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu Ile Asp Ala His His
55 60 65

acc gtg gaa gat acc gcc atc gtg ctc ggc caa gca ctc ctt gac gct 355
Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln Ala Leu Leu Asp Ala
70 75 80 85

att ggc gac aag aaa ggc atc cgc cgt ttc gca tcc tgc cag ctg ccc 403
Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala Ser Cys Gln Leu Pro
90 95 100

atg gat gag gca tta gtg gag tcc gtg gtg gat atc tcc ggt cgc cca 451
Met Asp Glu Ala Leu Val Glu Ser Val Val Asp Ile Ser Gly Arg Pro
105 110 115

tac ttc gtg atc tcc ggc gaa cca gac cac atg atc acc tcc gtg atc 499
Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met Ile Thr Ser Val Ile
120 125 130

ggt gga cac tac gca acc gtg atc aac gag cac ttc ttt gaa acc ctc 547
Gly Gly His Tyr Ala Thr Val Ile Asn Glu His Phe Phe Glu Thr Leu
135 140 145

gcg ctc aac tcc cga atc acc ctc cac gtg atc tgc cac tac ggc cgc 595
Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile Cys His Tyr Gly Arg
150 155 160 165

gac cct cac cac atc acc gaa gca gag tac aag gct gtt gcc cgt gcg 643
 Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys Ala Val Ala Arg Ala
 170 175 180

ctg cgc ggt gcc gta gag atg gat cct cgt caa aca gga atc cca tcc 691
 Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln Thr Gly Ile Pro Ser
 185 190 195

act aag gga gcg ctc tagacatgaa ctcttctccc atc 729
 Thr Lys Gly Ala Leu
 200

<210> 394

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 394

Met Thr Val Ala Pro Arg Ile Gly Thr Ala Thr Arg Thr Thr Ser Glu
 1 5 10 15

Ser Asp Ile Thr Val Glu Ile Asn Leu Asp Gly Thr Gly Lys Val Asp
 20 25 30

Ile Asp Thr Gly Leu Pro Phe Phe Asp His Met Leu Thr Ala Phe Gly
 35 40 45

Val His Gly Ser Phe Asp Leu Lys Val His Ala Lys Gly Asp Ile Glu
 50 55 60

Ile Asp Ala His His Thr Val Glu Asp Thr Ala Ile Val Leu Gly Gln
 65 70 75 80

Ala Leu Leu Asp Ala Ile Gly Asp Lys Lys Gly Ile Arg Arg Phe Ala
 85 90 95

Ser Cys Gln Leu Pro Met Asp Glu Ala Leu Val Glu Ser Val Val Asp
 100 105 110

Ile Ser Gly Arg Pro Tyr Phe Val Ile Ser Gly Glu Pro Asp His Met
 115 120 125

Ile Thr Ser Val Ile Gly Gly His Tyr Ala Thr Val Ile Asn Glu His
 130 135 140

Phe Phe Glu Thr Leu Ala Leu Asn Ser Arg Ile Thr Leu His Val Ile
 145 150 155 160

Cys His Tyr Gly Arg Asp Pro His His Ile Thr Glu Ala Glu Tyr Lys
 165 170 175

Ala Val Ala Arg Ala Leu Arg Gly Ala Val Glu Met Asp Pro Arg Gln
 180 185 190

Thr Gly Ile Pro Ser Thr Lys Gly Ala Leu
 195 200

<210> 395

```
<211> 987
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(964)
<223> RXN00446
```

<400> 395																
tgctacgaag ttatctagta atgaagttag tttttcccct ctcccggcag cagttgatgc																60
ggtgacggag gctacttggg gggctaatacg gtacccggat atg ggt gcg gtt gag																115
Met Gly Ala Val Glu																5
1																
ctc cgt gag gct ctt gca gag cat tta gag gtt gag ttt gac cag gtc																163
Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val Glu Phe Asp Gln Val																20
10 15																
acg gta ggt tgc ggc tcg tct gcg ctg tgt caa cag ctg gtt cag gca																211
Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln Gln Leu Val Gln Ala																35
25 30																
acg tgc gct cag ggc gat gag gtc att ttt cca tgg cgc agc ttt gag																259
Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro Trp Arg Ser Phe Glu																50
40 45																
gct tat cca att ttc gcg cag gtc gcg ggc gcc act cct gtt gcc att																307
Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala Thr Pro Val Ala Ile																65
55 60																
ccg ctg act gct gat cag aat cat gat ctt gat gcg atg gca gcc gcg																355
Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp Ala Met Ala Ala Ala																85
70 75 80																
atc act gat aag acc cgc ctc att ttc atc tgc aac ccc aac aat cct																403
Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys Asn Pro Asn Asn Pro																100
90 95																
tcg ggc acc acc atc acc cag gcg cag ttt gat aat ttc atg gaa aag																451
Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp Asn Phe Met Glu Lys																115
105 110																
gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat ttt gag ttc																499
Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr Phe Glu Phe																130
120 125																
aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc cac cgc cac																547
Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile His Arg His																145
135 140																
gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat ggc ctg gcg																595
Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr Gly Leu Ala																165
150 155 160																
ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc atc gca gcg																643
Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile Ile Ala Ala																180
170 175																
atg aat aag gtg gct att cct ttc gcg gtg aat tca gca gct cag gcg																691

Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala Ala Gln Ala
 185 190 195

gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg gaa cgg gtg 739
 Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met Glu Arg Val
 200 205 210

gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg ctt ggt gct 787
 Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala Leu Gly Ala
 215 220 225

gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag ggc gcc gct 835
 Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu Gly Ala Ala
 230 235 240 245

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtcctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 396

<211> 288

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 396

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu

130	135	140
Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys 145 150 155 160		
Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala 165 170 175		
Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn 180 185 190		
Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu 195 200 205		
Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val 210 215 220		
Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro 225 230 235 240		
Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile 245 250 255		
Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala 260 265 270		
Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly 275 280 285		

<210> 397

<211> 545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(522)

<223> FRXA00446

<400> 397

atg gaa aag gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat	48
Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr	
1 5 10 15	

ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc	96
Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile	
20 25 30	

cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat	144
His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr	
35 40 45	

ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc	192
Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile	
50 55 60	

atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca	240
---	-----

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
65 70 75 80

gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn S r Ala Asp Glu Leu Met
85 90 95

gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
100 105 110

ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
165 170

tagtcctttgg cgttttgcgg tgc 545

<210> 398

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 398

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
1 5 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile

130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
165 170

<210> 399
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA01105

<400> 399
ttgtcatcaa ctttgccaac gccgaagatc ttccagcgca cggcgaagca atccgtgcac 60
gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
Met Thr Lys Ile Thr
1 5

ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
10 15 20

ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
25 30 35

cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
40 45 50

gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
55 60 65

gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
70 75 80 85

gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
90 95 100

ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
105 110 115

gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
120 125 130

cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
135 140 145

atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt	595
Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val	
150 155 160 165	
ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac	643
Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp	
170 175 180	
gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat	691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp	
185 190 195	
gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg	739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu	
200 205 210	
gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct	787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala	
215 220 225	
ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg	835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala	
230 235 240 245	
ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg	883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala	
250 255 260	
ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg	931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr	
265 270 275	
ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca	979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala	
280 285 290	
cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt	
1027	
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe	
295 300 305	
gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt	
1075	
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe	
310 315 320 325	
ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg	
1123	
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu	
330 335 340	
cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca	
1171	
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala	
345 350 355	
gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca	
1218	
Ala Ala Glu Ile Ile Lys Leu Asn Leu	
360 365	

tga
1221

<210> 400

<211> 366

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 400

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
1 5 10 15

Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
20 25 30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
35 40 45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
50 55 60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
65 70 75 80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
85 90 95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
100 105 110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
115 120 125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
130 135 140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
145 150 155 160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
165 170 175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
180 185 190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
195 200 205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
210 215 220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
225 230 235 240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
245 250 255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
260 265 270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
 275 280 285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
 290 295 300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
 305 310 315 320

Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
 325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
 340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
 355 360 365

<210> 401

<211> 1449

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1426)

<223> RXA01106

<400> 401

ggtaaacaatg cgggcttaag aacttggtgtt gagggccgctt ggattcgggc accgagctcg 60

aagaatttcg attcaacctt ttaagggaga acttttcgcc atg ttg aat gtc act 115
 Met Leu Asn Val Thr
 1 5

gac ctg cga ggt caa aca cca tcc aag agc gac atc cga cgt gct ttg 163
 Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp Ile Arg Arg Ala Leu
 10 15 20

cca cgt ggt ggc act gac gtg tgg tct gtg ctt ccc ata gtg cag cct 211
 Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu Pro Ile Val Gln Pro
 25 30 35

gtt gta gaa gat gtc caa aac cgc ggc gct gaa gct gct ttg gat tac 259
 Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu Ala Ala Leu Asp Tyr
 40 45 50

ggc gag aag ttc gac cat att cgc ccc gcc tcg gtg cgg gtg cca gct 307
 Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser Val Arg Val Pro Ala
 55 60 65

gag gtt att gct gca gca gaa aac acc tta gat ccg ttg gtg cgt gaa 355
 Glu Val Ile Ala Ala Glu Asn Thr Leu Asp Pro Leu Val Arg Glu
 70 75 80 85

tcg att gaa gag tcg att cgt cgc gtc cgc aag gtt cac gct gag caa 403
 Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys Val His Ala Glu Gln
 90 95 100

aag cca tcc gag cac acc act gaa ctt tca cca ggt ggc acc gtc act	451
Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro Gly Gly Thr Val Thr	
105 110 115	
gag cgt ttc atg ccg att gat cgc gtg gga ctg tac gtt cca ggc ggc	499
Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu Tyr Val Pro Gly Gly	
120 125 130	
aat gcg gtg tac cca tca agc gtg att atg aat act gtc cca gct caa	547
Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn Thr Val Pro Ala Gln	
135 140 145	
gag gct ggt gtg aac tcc ctt gtg gtt gcg tcg cct cct cag gct gag	595
Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser Pro Pro Gln Ala Glu	
150 155 160 165	
cac ggt ggc tgg cct cac ccc acc att ttg gcg gcg tgt tcc atc ttg	643
His Gly Gly Trp Pro His Pro Thr Ile Leu Ala Ala Cys Ser Ile Leu	
170 175 180	
ggt gtt gat gag gtg tgg gct gtc ggc ggc ggt cag gcc gtg gcg ttg	691
Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly Gln Ala Val Ala Leu	
185 190 195	
ctg gct tat ggt gat gac gct gca ggt ctc gag cct gtg gat atg atc	739
Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu Pro Val Asp Met Ile	
200 205 210	
act gga cct ggc aat atc ttt gtc acc gct gcg aag cgc ctg gtc agg	787
Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala Lys Arg Leu Val Arg	
215 220 225	
gga gtg gta ggt act gat tct gag gct ggc cct aca gaa atc gct gtg	835
Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro Thr Glu Ile Ala Val	
230 235 240 245	
ctt gct gat gcc tct gcc aac gcc gtc aac gtt gcc tac gat ctg atc	883
Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val Ala Tyr Asp Leu Ile	
250 255 260	
agc caa gca gaa cac gat gtc atg gct gcg tcc gtg ctc atc act gac	931
Ser Gln Ala Glu His Asp Val Met Ala Ala Ser Val Leu Ile Thr Asp	
265 270 275	
tcc gag cag ctt gcc aag gac gta aac agg gaa atc gag gcg cgt tac	979
Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu Ile Glu Ala Arg Tyr	
280 285 290	
tca atc acg cgc aac gcc gag cgc gtc gca gaa gct ttg cgc ggg gcc	
1027	
Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu Ala Leu Arg Gly Ala	
295 300 305	
cag agt ggc atc gtg ctt gtc gac gac att tcc gtg ggt atc caa gta	
1075	
Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser Val Gly Ile Gln Val	
310 315 320 325	
gcc gat caa tac gca gcg gaa cac ctg gaa atc cac act gag aac gcg	
1123	
Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile His Thr Glu Asn Ala	

330 335 340
 cgc gcc gta gca gag cag atc acc aac gcg ggt gcg atc ttc gtg ggc
 1171
 Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly Ala Ile Phe Val Gly
 345 350 355
 gat ttc tca cca gta cca ctg ggt gat tac tcc gca gga tcc aac cac
 1219
 Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser Ala Gly Ser Asn His
 360 365 370
 gtg ctg cca acc tct gga tcc gct cgt ttc tcc gca ggt cta tcc acg
 1267
 Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser Ala Gly Leu Ser Thr
 375 380 385
 cac acg ttc ctt cgc cca gtc aac ctc att gaa tac gat gag gct gct
 1315
 His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu Tyr Asp Glu Ala Ala
 390 395 400 405
 ctg aag gac gtc tcg cag gtt gtc atc aac ttt gcc aac gcc gaa gat
 1363
 Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe Ala Asn Ala Glu Asp
 410 415 420
 ctt cca gcg cac ggc gaa gca atc cgt gca cgc ttt gaa aac ctc ccc
 1411
 Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg Phe Glu Asn Leu Pro
 425 430 435
 acc acc gac gag gcc taagaaaaat gaccaaatt act
 1449
 Thr Thr Asp Glu Ala
 440

<210> 402
 <211> 442
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 402
 Met Leu Asn Val Thr Asp Leu Arg Gly Gln Thr Pro Ser Lys Ser Asp
 1 5 10 15
 Ile Arg Arg Ala Leu Pro Arg Gly Gly Thr Asp Val Trp Ser Val Leu
 20 25 30
 Pro Ile Val Gln Pro Val Val Glu Asp Val Gln Asn Arg Gly Ala Glu
 35 40 45
 Ala Ala Leu Asp Tyr Gly Glu Lys Phe Asp His Ile Arg Pro Ala Ser
 50 55 60
 Val Arg Val Pro Ala Glu Val Ile Ala Ala Ala Glu Asn Thr Leu Asp
 65 70 75 80
 Pro Leu Val Arg Glu Ser Ile Glu Glu Ser Ile Arg Arg Val Arg Lys
 85 90 95

Val His Ala Glu Gln Lys Pro Ser Glu His Thr Thr Glu Leu Ser Pro
 100 105 110
 Gly Gly Thr Val Thr Glu Arg Phe Met Pro Ile Asp Arg Val Gly Leu
 115 120 125
 Tyr Val Pro Gly Gly Asn Ala Val Tyr Pro Ser Ser Val Ile Met Asn
 130 135 140
 Thr Val Pro Ala Gln Glu Ala Gly Val Asn Ser Leu Val Val Ala Ser
 145 150 155 160
 Pro Pro Gln Ala Glu His Gly Gly Trp Pro His Pro Thr Ile Leu Ala
 165 170 175
 Ala Cys Ser Ile Leu Gly Val Asp Glu Val Trp Ala Val Gly Gly Gly
 180 185 190
 Gln Ala Val Ala Leu Leu Ala Tyr Gly Asp Asp Ala Ala Gly Leu Glu
 195 200 205
 Pro Val Asp Met Ile Thr Gly Pro Gly Asn Ile Phe Val Thr Ala Ala
 210 215 220
 Lys Arg Leu Val Arg Gly Val Val Gly Thr Asp Ser Glu Ala Gly Pro
 225 230 235 240
 Thr Glu Ile Ala Val Leu Ala Asp Ala Ser Ala Asn Ala Val Asn Val
 245 250 255
 Ala Tyr Asp Leu Ile Ser Gln Ala Glu His Asp Val Met Ala Ala Ser
 260 265 270
 Val Leu Ile Thr Asp Ser Glu Gln Leu Ala Lys Asp Val Asn Arg Glu
 275 280 285
 Ile Glu Ala Arg Tyr Ser Ile Thr Arg Asn Ala Glu Arg Val Ala Glu
 290 295 300
 Ala Leu Arg Gly Ala Gln Ser Gly Ile Val Leu Val Asp Asp Ile Ser
 305 310 315 320
 Val Gly Ile Gln Val Ala Asp Gln Tyr Ala Ala Glu His Leu Glu Ile
 325 330 335
 His Thr Glu Asn Ala Arg Ala Val Ala Glu Gln Ile Thr Asn Ala Gly
 340 345 350
 Ala Ile Phe Val Gly Asp Phe Ser Pro Val Pro Leu Gly Asp Tyr Ser
 355 360 365
 Ala Gly Ser Asn His Val Leu Pro Thr Ser Gly Ser Ala Arg Phe Ser
 370 375 380
 Ala Gly Leu Ser Thr His Thr Phe Leu Arg Pro Val Asn Leu Ile Glu
 385 390 395 400
 Tyr Asp Glu Ala Ala Leu Lys Asp Val Ser Gln Val Val Ile Asn Phe
 405 410 415

Ala Asn Ala Glu Asp Leu Pro Ala His Gly Glu Ala Ile Arg Ala Arg
 420 425 430

Phe Glu Asn Leu Pro Thr Thr Asp Glu Ala
 435 440

<210> 403

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXC00930

<400> 403

acggcgcacc acacatttgg tgggtgtattg agctatctct gggctgcgtg agaaaccatt 60

ttccggtgga tgatggaagc tagacgacga aagggagcat atg tct ggc cac tca 115
 Met Ser Gly His Ser
 1 5

aaa tgg gcg act acc aag cac aag aag gct gct aac gac gcc aag cga 163
 Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala Asn Asp Ala Lys Arg
 10 15 20

ggc aag gaa ttt gcc aag ctg atc aag aac atc gaa gtt gcg gca cgt 211
 Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile Glu Val Ala Ala Arg
 25 30 35

aca ggc ggt gga gat ccg tct gcg aac cca acg ctt gat gac atg atc 259
 Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr Leu Asp Asp Met Ile
 40 45 50

aag aaa gcc aag aag gct tct gtg ccg aac gat aac atc gaa cgt gca 307
 Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp Asn Ile Glu Arg Ala
 55 60 65

cgc aag cgt ggc tcc ggc gaa gaa gct ggt ggc gct gac tgg atg aac 355
 Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly Ala Asp Trp Met Asn
 70 75 80 85

atc atg tac gag gga tac ggc ccc aac ggc gtt gcc atg ctt atc gag 403
 Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val Ala Met Leu Ile Glu
 90 95 100

tgt ctg acc gac aac cgt aac cgc gca gct acc gaa gtt cgc acc gca 451
 Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr Glu Val Arg Thr Ala
 105 110 115

atg acc aaa aac ggt ggc aac ttg ggc gag tcc ggt tcc gtg tcc tac 499
 Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser Gly Ser Val Ser Tyr
 120 125 130

atg ttc acc cgc acc ggt gtc gtc acc gta caa aag ggc gat ctt agt 547
 Met Phe Thr Arg Thr Gly Val Val Thr Val Gln Lys Gly Asp Leu Ser
 135 140 145

gaa gat gac gtg ctc atg gct gtt ctt gaa gct ggt gct gaa gaa gtc 595

Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala Gly Ala Glu Glu Val
 150 155 160 165
 aac gac aac ggc gat ctg ttc gag gtt acc tgc gca cca act gac att 643
 Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys Ala Pro Thr Asp Ile
 170 175 180
 cag gct gtt cgc gac gca ctc gtg gaa gct ggc att gaa gta gaa gat 691
 Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly Ile Glu Val Glu Asp
 185 190 195
 tct gaa tca gac ttc cgg gca tct gtt cag gtc ccc ctg gac gct gac 739
 Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val Pro Leu Asp Ala Asp
 200 205 210
 ggt gca cgc aag atc ttc aag ctt gtg gac gcg ttg gaa gat tcc gac 787
 Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala Leu Glu Asp Ser Asp
 215 220 225
 gat gtg caa aac gtc tac acc aac atc gac ttg agc gat gag gtt ttg 835
 Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu Ser Asp Glu Val Leu
 230 235 240 245
 aca gag ctg gaa aac gac tagttcgtat tttccgcact ccg 876
 Thr Glu Leu Glu Asn Asp
 250

<210> 404

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 404

Met Ser Gly His Ser Lys Trp Ala Thr Thr Lys His Lys Lys Ala Ala
 1 5 10 15
 Asn Asp Ala Lys Arg Gly Lys Glu Phe Ala Lys Leu Ile Lys Asn Ile
 20 25 30
 Glu Val Ala Ala Arg Thr Gly Gly Gly Asp Pro Ser Ala Asn Pro Thr
 35 40 45
 Leu Asp Asp Met Ile Lys Lys Ala Lys Lys Ala Ser Val Pro Asn Asp
 50 55 60
 Asn Ile Glu Arg Ala Arg Lys Arg Gly Ser Gly Glu Glu Ala Gly Gly
 65 70 75 80
 Ala Asp Trp Met Asn Ile Met Tyr Glu Gly Tyr Gly Pro Asn Gly Val
 85 90 95
 Ala Met Leu Ile Glu Cys Leu Thr Asp Asn Arg Asn Arg Ala Ala Thr
 100 105 110
 Glu Val Arg Thr Ala Met Thr Lys Asn Gly Gly Asn Leu Gly Glu Ser
 115 120 125
 Gly Ser Val Ser Tyr Met Phe Thr Arg Thr Gly Val Val Thr Val Gln
 130 135 140

Lys Gly Asp Leu Ser Glu Asp Asp Val Leu Met Ala Val Leu Glu Ala
 145 150 155 160
 Gly Ala Glu Glu Val Asn Asp Asn Gly Asp Leu Phe Glu Val Thr Cys
 165 170 175
 Ala Pro Thr Asp Ile Gln Ala Val Arg Asp Ala Leu Val Glu Ala Gly
 180 185 190
 Ile Glu Val Glu Asp Ser Glu Ser Asp Phe Arg Ala Ser Val Gln Val
 195 200 205
 Pro Leu Asp Ala Asp Gly Ala Arg Lys Ile Phe Lys Leu Val Asp Ala
 210 215 220
 Leu Glu Asp Ser Asp Asp Val Gln Asn Val Tyr Thr Asn Ile Asp Leu
 225 230 235 240
 Ser Asp Glu Val Leu Thr Glu Leu Glu Asn Asp
 245 250

<210> 405

<211> 547

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(547)

<223> RXC01096

<400> 405

accgtgaaac aaaccggcgg tgcgtgccac actggtgccc acacatgttt cgacaatgac 60

gttttgctgt aaaagcaaca acgattaagg aagaaatctt atg aag cca cgc gtg 115
 Met Lys Pro Arg Val
 1 5

ctg tca gca tta ggc att gga gct ggc gcc ctg gtt gtc tgg atc agc 163
 Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu Val Val Trp Ile Ser
 10 15 20

tca cgc atg aac tgg gta acc atc gag gct ttc gac gat aaa tca ggt 211
 Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe Asp Asp Lys Ser Gly
 25 30 35

agt gtc acc caa tct att gtg ggt gca acc tgg tct aca gaa atc atg 259
 Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp Ser Thr Glu Ile Met
 40 45 50

gcg ctt gca ctt gct ttg ctc gct gcc ttc gcc gcc gcg ttg gtg ctc 307
 Ala Leu Ala Leu Ala Leu Leu Ala Ala Phe Ala Ala Ala Leu Val Leu
 55 60 65

aag cgc atg ggt cgg cgc atc att ggt ggt att tcg gcg ctg atc gcg 355
 Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile Ser Ala Leu Ile Ala
 70 75 80 85

gtg ggt gcc agc ctg tct cca ctc gcg ctt ctc acc caa gac cca gac 403
 Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu Thr Gln Asp Pro Asp

	90	95	100	
gca gaa cgg gcc cga acc ctg ctg acc tcc ggt gtg gcc tca cag aag				451
Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly Val Ala Ser Gln Lys				
	105	110	115	
gct aat tcc gga acc ctg ctg tct gat tgg gcg gag atc atc aat acc				499
Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala Glu Ile Ile Asn Thr				
	120	125	130	
acc acc cat cca ctg gcg gca gtg gta gcc atg att ggc tgc gcg cta				547
Thr Thr His Pro Leu Ala Ala Val Val Ala Met Ile Gly Cys Ala Leu				
	135	140	145	

<210> 406

<211> 149

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 406

Met Lys Pro Arg Val Leu Ser Ala Leu Gly Ile Gly Ala Gly Ala Leu				
1	5	10	15	
Val Val Trp Ile Ser Ser Arg Met Asn Trp Val Thr Ile Glu Ala Phe				
20	25	30		
Asp Asp Lys Ser Gly Ser Val Thr Gln Ser Ile Val Gly Ala Thr Trp				
35	40	45		
Ser Thr Glu Ile Met Ala Leu Ala Leu Ala Leu Ala Ala Phe Ala				
50	55	60		
Ala Ala Leu Val Leu Lys Arg Met Gly Arg Arg Ile Ile Gly Gly Ile				
65	70	75	80	
Ser Ala Leu Ile Ala Val Gly Ala Ser Leu Ser Pro Leu Ala Leu Leu				
85	90	95		
Thr Gln Asp Pro Asp Ala Glu Arg Ala Arg Thr Leu Leu Thr Ser Gly				
100	105	110		
Val Ala Ser Gln Lys Ala Asn Ser Gly Thr Leu Leu Ser Asp Trp Ala				
115	120	125		
Glu Ile Ile Asn Thr Thr Thr His Pro Leu Ala Ala Val Val Ala Met				
130	135	140		
Ile Gly Cys Ala Leu				
145				

<210> 407

<211> 1020

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(997)

<223> RXC01656

<400> 407

tcggcaagca tggcttcacg gtcctcaaaa aagtgggtcta atgcaagtga ctgaaagtgg 60

atctaccgct agtccacttt gtggcggttg atcatctgtc atg acc gaa act caa 115
Met Thr Glu Thr Gln
1 5

gaa act tac caa gca acc act cgt gtg aag cgc ggc ctt gcc gac atg 163
Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg Gly Leu Ala Asp Met
10 15 20

ctc aag ggt ggt gtg atc atg gat gtg gtc acc cct gaa caa gcg cgc 211
Leu Lys Gly Gly Val Ile Met Asp Val Val Thr Pro Glu Gln Ala Arg
25 30 35

atc gcc gaa gat gca ggt gcc agc gca gtt atg gca ctc gag cgc gtt 259
Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met Ala Leu Glu Arg Val
40 45 50

ccc gcc gat atc cgt tct cag ggc ggc gtt gct cgc atg agt gat cct 307
Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala Arg Met Ser Asp Pro
55 60 65

gac ctg atc gaa gga atc gtc aat gcg gtc tcc atc ccg gtc atg gcg 355
Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser Ile Pro Val Met Ala
70 75 80 85

aaa gct cgc atc ggt cac ttc gtg gaa gct cag gtt ctg gaa gct ctc 403
Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln Val Leu Glu Ala Leu
90 95 100

ggt gtt gat ttc atc gac gag tcc gaa gtt ctc agc cct gcc gac tac 451
Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu Ser Pro Ala Asp Tyr
105 110 115

acg cac cac atc aac aag tgg aag ttc gac gtt cct ttc gtc tgt ggc 499
Thr His His Ile Asn Lys Trp Lys Phe Asp Val Pro Phe Val Cys Gly
120 125 130

gcg acc aac ctc ggc gaa gct ttg cga cgc atc acc gaa ggc gct gca 547
Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile Thr Glu Gly Ala Ala
135 140 145

atg atc cgt tcc aag ggc gaa gcc ggc acc ggc gat gtc tct gaa gct 595
Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly Asp Val Ser Glu Ala
150 155 160 165

gtc cgt cac ctg cgc acc atc cgc ggc gac atc aat cgc ctg cgc tcc 643
Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile Asn Arg Leu Arg Ser
170 175 180

ctg gat gag gat gaa ctc ttc gtc gcc gcc aag gaa ttc cag gca cca 691
Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys Glu Phe Gln Ala Pro
185 190 195

tac gac ctg gtc cgc gaa gtc gcc tcc acc ggc aag ctc cct gtg gtc 739
Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly Lys Leu Pro Val Val
200 205 210

acc ttc gtt gca ggt ggc gtc gca acc cca gcc gac gct gca ctc gtg 787

Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala Asp Ala Ala Leu Val
 215 220 225
 cgc caa atg ggc gcc gaa ggc gtc ttt gtc ggc tcc ggc atc ttc aaa 835
 Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly Ser Gly Ile Phe Lys
 230 235 240 245
 tcc ggc aat cca gcc gcc cgc gcc gca gcg atc gtc aag gct gca acg 883
 Ser Gly Asn Pro Ala Ala Arg Ala Ala Ile Val Lys Ala Ala Thr
 250 255 260
 ctt ttc gac gac ccc tcc gtc att gcc gac gta tcc cgc ggc ctg ggt 931
 Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val Ser Arg Gly Leu Gly
 265 270 275
 gaa gcc atg gtg ggc atc aac gta tcc gac gtt cca gca cca cac cga 979
 Glu Ala Met Val Gly Ile Asn Val Ser Asp Val Pro Ala Pro His Arg
 280 285 290
 ctc gcc gag cgc ggc tgg tgatcgttgg agtttttagct ctc
 1020
 Leu Ala Glu Arg Gly Trp
 295
 <210> 408
 <211> 299
 <212> PRT
 <213> *Corynebacterium glutamicum*
 <400> 408
 Met Thr Glu Thr Gln Glu Thr Tyr Gln Ala Thr Thr Arg Val Lys Arg
 1 5 10 15
 Gly Leu Ala Asp Met Leu Lys Gly Gly Val Ile Met Asp Val Val Thr
 20 25 30
 Pro Glu Gln Ala Arg Ile Ala Glu Asp Ala Gly Ala Ser Ala Val Met
 35 40 45
 Ala Leu Glu Arg Val Pro Ala Asp Ile Arg Ser Gln Gly Gly Val Ala
 50 55 60
 Arg Met Ser Asp Pro Asp Leu Ile Glu Gly Ile Val Asn Ala Val Ser
 65 70 75 80
 Ile Pro Val Met Ala Lys Ala Arg Ile Gly His Phe Val Glu Ala Gln
 85 90 95
 Val Leu Glu Ala Leu Gly Val Asp Phe Ile Asp Glu Ser Glu Val Leu
 100 105 110
 Ser Pro Ala Asp Tyr Thr His His Ile Asn Lys Trp Lys Phe Asp Val
 115 120 125
 Pro Phe Val Cys Gly Ala Thr Asn Leu Gly Glu Ala Leu Arg Arg Ile
 130 135 140
 Thr Glu Gly Ala Ala Met Ile Arg Ser Lys Gly Glu Ala Gly Thr Gly
 145 150 155 160

Asp Val Ser Glu Ala Val Arg His Leu Arg Thr Ile Arg Gly Asp Ile
 165 170 175
 Asn Arg Leu Arg Ser Leu Asp Glu Asp Glu Leu Phe Val Ala Ala Lys
 180 185 190
 Glu Phe Gln Ala Pro Tyr Asp Leu Val Arg Glu Val Ala Ser Thr Gly
 195 200 205
 Lys Leu Pro Val Val Thr Phe Val Ala Gly Gly Val Ala Thr Pro Ala
 210 215 220
 Asp Ala Ala Leu Val Arg Gln Met Gly Ala Glu Gly Val Phe Val Gly
 225 230 235 240
 Ser Gly Ile Phe Lys Ser Gly Asn Pro Ala Ala Arg Ala Ala Ala Ile
 245 250 255
 Val Lys Ala Ala Thr Leu Phe Asp Asp Pro Ser Val Ile Ala Asp Val
 260 265 270
 Ser Arg Gly Leu Gly Glu Ala Met Val Gly Ile Asn Val Ser Asp Val
 275 280 285
 Pro Ala Pro His Arg Leu Ala Glu Arg Gly Trp
 290 295

<210> 409

<211> 1065

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1042)

<223> RXC01158

<400> 409

taggacgttc aaggaattgg ctgaatcaac aagcgccaag gtgggtaagc gccctcggcg 60
 agttatctca aaaaagaaga agaagtctcc tacgggagag atg tcc att gtt gag 115
 Met Ser Ile Val Glu
 1 5
 cac atc aaa gag ttt cga cgc cga ctt ctt atc gct ctg gcg ggc atc 163
 His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile Ala Leu Ala Gly Ile
 10 15 20
 ctc gtg ggc acc att atc ggc ttt att tgg tac gat ttc tca ttt tgg 211
 Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr Asp Phe Ser Phe Trp
 25 30 35
 cag atc ccc act ttg ggc gag ctg ctg agg gat ccg tac tgt tct ctg 259
 Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp Pro Tyr Cys Ser Leu
 40 45 50
 cct gct gaa tcc cgc tgg gcc atg agc gac tca gag gaa tgt cga ctg 307
 Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser Glu Glu Cys Arg Leu
 55 60 65

ctc gca acc ggc ccg ttt gat cca ttc atg ctt cgc ctt aaa gta gcg	355
Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu Arg Leu Lys Val Ala	
70 75 80 85	
gcg ttg gtg ggt atg gtt ctt ggc tca ccc gtg tgg ctg agc cag ctg	403
Ala Leu Val Gly Met Val Leu Gly Ser Pro Val Trp Leu Ser Gln Leu	
90 95 100	
tgg ggc ttt atc acc cca ggt ttg atg aag aat gag cgc cgt tac acc	451
Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn Glu Arg Arg Tyr Thr	
105 110 115	
gca atc ttc gtc acg att gct gtt gtg ctg ttt gtc ggc ggt gct gtt	499
Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe Val Gly Gly Ala Val	
120 125 130	
ctt gcg tac ttc gtc gtt gca tat ggt ttg gag ttc ctc ctt acc att	547
Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu Phe Leu Leu Thr Ile	
135 140 145	
ggg gga gac acc cag gca gcg gcc ctg act ggt gat aag tac ttc gga	595
Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly Asp Lys Tyr Phe Gly	
150 155 160 165	
ttc ttg ctc gcg ttg ttg gcg att ttc ggc gtg agc ttc gaa gtt cca	643
Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val Ser Phe Glu Val Pro	
170 175 180	
ctg gtg atc ggc atg ctc aac att gtg ggt atc ttg cct tac gat gcc	691
Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile Leu Pro Tyr Asp Ala	
185 190 195	
att aaa gat aag cga cgc atg atc atc atg att ttg ttc gtg ttc gct	739
Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile Leu Phe Val Phe Ala	
200 205 210	
gct ttc atg aca ccc ggc cag gat cct ttc acc atg ttg gtg ttg gcg	787
Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr Met Leu Val Leu Ala	
215 220 225	
ctt tca ctc acc gtt ctg gta gag ctt gcc ctg cag ttc tgt cgc ttc	835
Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu Gln Phe Cys Arg Phe	
230 235 240 245	
aac gac aaa cgc cgg gac aag aag cgc cca gaa tgg ctt gat ggc gat	883
Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu Trp Leu Asp Gly Asp	
250 255 260	
gac ctc tct gca tca cca ctg gat act tct gct ggt gga gaa gat gct	931
Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala Gly Gly Glu Asp Ala	
265 270 275	
cca agc cca gtc gaa acc cca gag gcg gtg gag cct tcg cgg atg ctg	979
Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu Pro Ser Arg Met Leu	
280 285 290	
aac cca agt ggg gag gcg tcg ata agc tat aaa ccc ggg cgc gcc gac	1027
Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys Pro Gly Arg Ala Asp	
295 300 305	

ttc ggt gac gtg ctc tagggcctag ccaggtaccc tta
 1065
 Phe Gly Asp Val Leu
 310

<210> 410
 <211> 314
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 410
 Met Ser Ile Val Glu His Ile Lys Glu Phe Arg Arg Arg Leu Leu Ile
 1 5 10 15
 Ala Leu Ala Gly Ile Leu Val Gly Thr Ile Ile Gly Phe Ile Trp Tyr
 20 25 30
 Asp Phe Ser Phe Trp Gln Ile Pro Thr Leu Gly Glu Leu Leu Arg Asp
 35 40 45
 Pro Tyr Cys Ser Leu Pro Ala Glu Ser Arg Trp Ala Met Ser Asp Ser
 50 55 60
 Glu Glu Cys Arg Leu Leu Ala Thr Gly Pro Phe Asp Pro Phe Met Leu
 65 70 75 80
 Arg Leu Lys Val Ala Ala Leu Val Gly Met Val Leu Gly Ser Pro Val
 85 90 95
 Trp Leu Ser Gln Leu Trp Gly Phe Ile Thr Pro Gly Leu Met Lys Asn
 100 105 110
 Glu Arg Arg Tyr Thr Ala Ile Phe Val Thr Ile Ala Val Val Leu Phe
 115 120 125
 Val Gly Gly Ala Val Leu Ala Tyr Phe Val Val Ala Tyr Gly Leu Glu
 130 135 140
 Phe Leu Leu Thr Ile Gly Gly Asp Thr Gln Ala Ala Ala Leu Thr Gly
 145 150 155 160
 Asp Lys Tyr Phe Gly Phe Leu Leu Ala Leu Leu Ala Ile Phe Gly Val
 165 170 175
 Ser Phe Glu Val Pro Leu Val Ile Gly Met Leu Asn Ile Val Gly Ile
 180 185 190
 Leu Pro Tyr Asp Ala Ile Lys Asp Lys Arg Arg Met Ile Ile Met Ile
 195 200 205
 Leu Phe Val Phe Ala Ala Phe Met Thr Pro Gly Gln Asp Pro Phe Thr
 210 215 220
 Met Leu Val Leu Ala Leu Ser Leu Thr Val Leu Val Glu Leu Ala Leu
 225 230 235 240
 Gln Phe Cys Arg Phe Asn Asp Lys Arg Arg Asp Lys Lys Arg Pro Glu
 245 250 255
 Trp Leu Asp Gly Asp Asp Leu Ser Ala Ser Pro Leu Asp Thr Ser Ala

260	265	270	
Gly Gly Glu Asp Ala Pro Ser Pro Val Glu Thr Pro Glu Ala Val Glu			
275	280	285	
Pro Ser Arg Met Leu Asn Pro Ser Gly Glu Ala Ser Ile Ser Tyr Lys			
290	295	300	
Pro Gly Arg Ala Asp Phe Gly Asp Val Leu			
305	310		
<210> 411			
<211> 1413			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1390)			
<223> RXA02458			
<400> 411			
ttgcggagcc acgactgac ggtcaagtgc tatctcgggtt gcatcaataa gcgaatcacc	60		
ggtggtgaac aaaacaaatc ttccacacat aacatctatt atg gtc ttt gtg tct	115		
	Met Val Phe Val Ser		
	1	5	
gat tcg tct atc tct ttg ccc att tgg gat gct ccg cgc gct cgc ggc	163		
Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala Pro Arg Ala Arg Gly			
10	15	20	
ccc ata gtc tcg gac ctg gct atc cct ggt tcc aag tcg atc acc aac	211		
Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser Lys Ser Ile Thr Asn			
25	30	35	
cgc gcc ctc atc ttg gct gcg ctc gca tca act cca tcc acc atc att	259		
Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr Pro Ser Thr Ile Ile			
40	45	50	
gat gtc ctt cgt agt cgt gat acc gat ctc atg act gat ggt cta cgc	307		
Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met Thr Asp Gly Leu Arg			
55	60	65	
agc ctc gga atc acc att act gaa gag gca gtc gat cgc tac cgc gtt	355		
Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val Asp Arg Tyr Arg Val			
70	75	80	85
gag ccc gga cag ttg tct gct ggc tcc gtt gag tgt ggt ctt gct ggt	403		
Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu Cys Gly Leu Ala Gly			
90	95	100	
acg gtc atg cgc ttt ttg cct cct gtt gct gct ttc gct gat ggt cct	451		
Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala Phe Ala Asp Gly Pro			
105	110	115	
gtt cat ttt gat ggc gat cct caa gct cgt gtt cgt ccg atg acc agc	499		
Val His Phe Asp Gly Asp Pro Gln Ala Arg Val Arg Pro Met Thr Ser			
120	125	130	

att ttg gat gcg ctg cgt tcg ctt ggt gtg gag gta gac aac aac aat 547
 Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu Val Asp Asn Asn Asn
 135 140 145

ctg cct ttc act gtt aat gct ggt gag gtc cct gag ggt ggc gtg gtt 595
 Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro Glu Gly Gly Val Val
 150 155 160 165

gag att gat gct tcc ggc tca tct cag ttt gtt tct ggt ctt ttg ctt 643
 Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val Ser Gly Leu Leu Leu
 170 175 180

tca gcg cct cgt ttt aaa aat ggc gtc acc gtt aag cac gtc ggt ggt 691
 Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val Lys His Val Gly Gly
 185 190 195

cgt ctg ccg agc atg ccg cat att gag atg acc gtc gat atg ctt cgt 739
 Arg Leu Pro Ser Met Pro His Ile Glu Met Thr Val Asp Met Leu Arg
 200 205 210

tcc gca ggc att gag atc gaa gag tca gaa aat cag tgg gtt gtt cat 787
 Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn Gln Trp Val Val His
 215 220 225

cct ggt gag atc ttg ggt cgg acc tgg cgc att gag ccg gat ctt tct 835
 Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile Glu Pro Asp Leu Ser
 230 235 240 245

aat gcg act ccg ttc cta gct gcc gct gcg gtc act ggt gga acc atc 883
 Asn Ala Thr Pro Phe Leu Ala Ala Ala Val Thr Gly Gly Thr Ile
 250 255 260

aag att aac cac tgg cca atc aaa act act cag cct ggc gat gct att 931
 Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln Pro Gly Asp Ala Ile
 265 270 275

cgt tcg att ctt gag cgc atg ggc tgc gaa gtt gag ctg gtt gct cag 979
 Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val Glu Leu Val Ala Gln
 280 285 290

ggt gaa ggt tac gat ctg tcg gtg act ggt ccg gtt gct ctc aag ggc
 1027
 Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro Val Ala Leu Lys Gly
 295 300 305

att gag atc gat atg tcc gat atc ggt gag ttg acc cct acc gtg gcg
 1075
 Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu Thr Pro Thr Val Ala
 310 315 320 325

gcg ttg gct gcg ttg gcg tcg aca gag tct cgt ttg acc ggt att gct
 1123
 Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg Leu Thr Gly Ile Ala
 330 335 340

cat ctt cgt ggc cat gag acg gat cgt ttg gct gcg ttg act gcg gag
 1171
 His Leu Arg Gly His Glu Thr Asp Arg Leu Ala Ala Leu Thr Ala Glu
 345 350 355

atc aac aaa ctt ggt gga aag tgc act gag ctt aag gat ggt ctg ttg
1219

Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu Lys Asp Gly Leu Leu
360 365 370

att gag cct gcg tcg ctg cac ggt ggt gtg tgg cat tca tat gct gat
1267

Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp His Ser Tyr Ala Asp
375 380 385

cac cgt atg gct act gct ggt gcg atc att ggc ctc gcg gtt gat ggc
1315

His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly Leu Ala Val Asp Gly
390 395 400 405

gtt cag gtt gaa gac att aag acc act tcc aaa act ttc cct ggt ttt
1363

Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys Thr Phe Pro Gly Phe
410 415 420

gaa aat gtt tgg gag gag atg gtt ggc tagacgcagc tatgacgaat
1410

Glu Asn Val Trp Glu Glu Met Val Gly
425 430

ccg
1413

<210> 412

<211> 430

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 412

Met Val Phe Val Ser Asp Ser Ser Ile Ser Leu Pro Ile Trp Asp Ala
1 5 10 15

Pro Arg Ala Arg Gly Pro Ile Val Ser Asp Leu Ala Ile Pro Gly Ser
20 25 30

Lys Ser Ile Thr Asn Arg Ala Leu Ile Leu Ala Ala Leu Ala Ser Thr
35 40 45

Pro Ser Thr Ile Ile Asp Val Leu Arg Ser Arg Asp Thr Asp Leu Met
50 55 60

Thr Asp Gly Leu Arg Ser Leu Gly Ile Thr Ile Thr Glu Glu Ala Val
65 70 75 80

Asp Arg Tyr Arg Val Glu Pro Gly Gln Leu Ser Ala Gly Ser Val Glu
85 90 95

Cys Gly Leu Ala Gly Thr Val Met Arg Phe Leu Pro Pro Val Ala Ala
100 105 110

Phe Ala Asp Gly Pro Val His Phe Asp Gly Asp Pro Gln Ala Arg Val
115 120 125

Arg Pro Met Thr Ser Ile Leu Asp Ala Leu Arg Ser Leu Gly Val Glu
130 135 140

Val Asp Asn Asn Asn Leu Pro Phe Thr Val Asn Ala Gly Glu Val Pro
 145 150 155 160
 Glu Gly Gly Val Val Glu Ile Asp Ala Ser Gly Ser Ser Gln Phe Val
 165 170 175
 Ser Gly Leu Leu Leu Ser Ala Pro Arg Phe Lys Asn Gly Val Thr Val
 180 185 190
 Lys His Val Gly Gly Arg Leu Pro Ser Met Pro His Ile Glu Met Thr
 195 200 205
 Val Asp Met Leu Arg Ser Ala Gly Ile Glu Ile Glu Glu Ser Glu Asn
 210 215 220
 Gln Trp Val Val His Pro Gly Glu Ile Leu Gly Arg Thr Trp Arg Ile
 225 230 235 240
 Glu Pro Asp Leu Ser Asn Ala Thr Pro Phe Leu Ala Ala Ala Ala Val
 245 250 255
 Thr Gly Gly Thr Ile Lys Ile Asn His Trp Pro Ile Lys Thr Thr Gln
 260 265 270
 Pro Gly Asp Ala Ile Arg Ser Ile Leu Glu Arg Met Gly Cys Glu Val
 275 280 285
 Glu Leu Val Ala Gln Gly Glu Gly Tyr Asp Leu Ser Val Thr Gly Pro
 290 295 300
 Val Ala Leu Lys Gly Ile Glu Ile Asp Met Ser Asp Ile Gly Glu Leu
 305 310 315 320
 Thr Pro Thr Val Ala Ala Leu Ala Ala Leu Ala Ser Thr Glu Ser Arg
 325 330 335
 Leu Thr Gly Ile Ala His Leu Arg Gly His Glu Thr Asp Arg Leu Ala
 340 345 350
 Ala Leu Thr Ala Glu Ile Asn Lys Leu Gly Gly Lys Cys Thr Glu Leu
 355 360 365
 Lys Asp Gly Leu Leu Ile Glu Pro Ala Ser Leu His Gly Gly Val Trp
 370 375 380
 His Ser Tyr Ala Asp His Arg Met Ala Thr Ala Gly Ala Ile Ile Gly
 385 390 395 400
 Leu Ala Val Asp Gly Val Gln Val Glu Asp Ile Lys Thr Thr Ser Lys
 405 410 415
 Thr Phe Pro Gly Phe Glu Asn Val Trp Glu Glu Met Val Gly
 420 425 430

<210> 413

<211> 1266

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1243)

<223> RXA02790

<400> 413

```

tggatgctcg caccgagcc cttgaaccac aatccacaga cacccaagat ttcgacgaga 60

agggaaattt cccaggatga accaaatccg aaaccgccgg atg gag ccc gtc tac 115
                                         Met Glu Pro Val Tyr
                                         1           5

gta aag cgc cgc caa cgg ttt att gcc gtg acg atc gct tca ctc atc 163
Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr Ile Ala Ser Leu Ile
                        10                        15                        20

ctc att atc ggt gcc atc atc tat atc ggt gta gcc acc tca aac cgg 211
Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val Ala Thr Ser Asn Arg
                        25                        30                        35

acg cca cat gac tat gaa ggc tcc gga aac ggt gtg gtt cag ctg gtc 259
Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly Val Val Gln Leu Val
                        40                        45                        50

gaa atc cct gaa ggt tcc tcc ata tca gag ctc ggc cca gag ttg gaa 307
Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu Gly Pro Glu Leu Glu
                        55                        60                        65

gaa cga gat atc gtg gcc acc aac tca gcg ttc caa aca gcg gcc agc 355
Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe Gln Thr Ala Ala Ser
70                        75                        80                        85

aac aac ccc aac gcg ggt agt gta cag cca ggt ttc tac cgt ctg cag 403
Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly Phe Tyr Arg Leu Gln
                        90                        95                        100

gaa caa atg aac gca gca gct gca gtg tcg gct ctg ctt gat cca gac 451
Glu Gln Met Asn Ala Ala Ala Val Ser Ala Leu Leu Asp Pro Asp
105                        110                        115

aac cag gtt gat ctc ctc gac att cac ggc ggc gcc acc ttg atg gac 499
Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly Ala Thr Leu Met Asp
120                        125                        130

gtc act gtt gtc ggc gga aac acc cgc gcg gga atc tac tcc cag atc 547
Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly Ile Tyr Ser Gln Ile
135                        140                        145

gca gcc gtg acc tgc acc gaa ggc tcc gcc aac tgc atc acc gct gag 595
Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn Cys Ile Thr Ala Glu
150                        155                        160                        165

gat ttg cag cag gtt gcc tcc acc gtg tcg cct gca gaa ttg ggt gtc 643
Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro Ala Glu Leu Gly Val
170                        175                        180

cca gat tgg gca atc gct gct gtg gaa gct cgc gga act gat cca aag 691
Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg Gly Thr Asp Pro Lys
185                        190                        195

cgc ctc gaa ggc ctg atc atg cct ggc caa tac gtg gtg gat cca tcc 739

```

Arg	Leu	Glu	Gly	Leu	Ile	Met	Pro	Gly	Gln	Tyr	Val	Val	Asp	Pro	Ser		
	200						205					210					
aac	gac	gcc	cag	gga	atc	ctc	acc	gat	ctg	atc	acg	cga	tca	gca	aac	787	
Asn	Asp	Ala	Gln	Gly	Ile	Leu	Thr	Asp	Leu	Ile	Thr	Arg	Ser	Ala	Asn		
	215					220					225						
cat	ttc	caa	gaa	acc	gac	atc	acg	ggc	cgt	gca	gat	gcc	atc	gga	ctt	835	
His	Phe	Gln	Glu	Thr	Asp	Ile	Thr	Gly	Arg	Ala	Asp	Ala	Ile	Gly	Leu		
	230				235				240					245			
act	cca	tat	gag	ctg	gtc	acc	gca	gca	tct	tta	atc	gag	cgc	gaa	gca	883	
Thr	Pro	Tyr	Glu	Leu	Val	Thr	Ala	Ala	Ser	Leu	Ile	Glu	Arg	Glu	Ala		
				250					255					260			
cca	gca	gga	gat	ttt	gat	aag	gtc	gcc	cgc	gtc	atc	ttg	aac	cgt	ctc	931	
Pro	Ala	Gly	Asp	Phe	Asp	Lys	Val	Ala	Arg	Val	Ile	Leu	Asn	Arg	Leu		
			265				270						275				
gcc	gag	cca	atg	cag	ctg	caa	ttc	gac	tcc	acc	gtc	aac	tac	ggg	ctg	979	
Ala	Glu	Pro	Met	Gln	Leu	Gln	Phe	Asp	Ser	Thr	Val	Asn	Tyr	Gly	Leu		
		280				285						290					
tct	gaa	caa	gaa	gta	gca	acc	acc	gac	gaa	gac	cgt	cag	acc	gtc	acc		
1027																	
Ser	Glu	Gln	Glu	Val	Ala	Thr	Thr	Asp	Glu	Asp	Arg	Gln	Thr	Val	Thr		
	295					300					305						
cca	tgg	aac	act	tac	gcc	atg	gac	ggc	ctg	cca	caa	acc	ccc	atc	gcc		
1075																	
Pro	Trp	Asn	Thr	Tyr	Ala	Met	Asp	Gly	Leu	Pro	Gln	Thr	Pro	Ile	Ala		
310					315					320					325		
gca	gta	tcc	acc	gaa	gca	ctc	caa	gcc	atg	gaa	aac	cct	gca	gaa	gga		
1123																	
Ala	Val	Ser	Thr	Glu	Ala	Leu	Gln	Ala	Met	Glu	Asn	Pro	Ala	Glu	Gly		
				330				335						340			
aac	tgg	ctg	tac	ttt	gtc	acc	atc	gac	acc	gat	gga	acc	acc	gtg	ttc		
1171																	
Asn	Trp	Leu	Tyr	Phe	Val	Thr	Ile	Asp	Thr	Asp	Gly	Thr	Thr	Val	Phe		
			345					350					355				
aac	gac	acc	ttc	gaa	gag	cac	gaa	gcc	gac	att	gag	caa	gct	ttg	aac		
1219																	
Asn	Asp	Thr	Phe	Glu	Glu	His	Glu	Ala	Asp	Ile	Glu	Gln	Ala	Leu	Asn		
		360					365					370					
agt	ggc	gtt	cta	gac	agc	aac	cga	taaggatcag	cgaataaaaat	tgg							
1266																	
Ser	Gly	Val	Leu	Asp	Ser	Asn	Arg										
		375				380											

<210> 414
 <211> 381
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 414
 Met Glu Pro Val Tyr Val Lys Arg Arg Gln Arg Phe Ile Ala Val Thr

1	5	10	15
Ile Ala Ser Leu Ile Leu Ile Ile Gly Ala Ile Ile Tyr Ile Gly Val	20	25	30
Ala Thr Ser Asn Arg Thr Pro His Asp Tyr Glu Gly Ser Gly Asn Gly	35	40	45
Val Val Gln Leu Val Glu Ile Pro Glu Gly Ser Ser Ile Ser Glu Leu	50	55	60
Gly Pro Glu Leu Glu Glu Arg Asp Ile Val Ala Thr Asn Ser Ala Phe	65	70	75
Gln Thr Ala Ala Ser Asn Asn Pro Asn Ala Gly Ser Val Gln Pro Gly	85	90	95
Phe Tyr Arg Leu Gln Glu Gln Met Asn Ala Ala Ala Val Ser Ala	100	105	110
Leu Leu Asp Pro Asp Asn Gln Val Asp Leu Leu Asp Ile His Gly Gly	115	120	125
Ala Thr Leu Met Asp Val Thr Val Val Gly Gly Asn Thr Arg Ala Gly	130	135	140
Ile Tyr Ser Gln Ile Ala Ala Val Thr Cys Thr Glu Gly Ser Ala Asn	145	150	155
Cys Ile Thr Ala Glu Asp Leu Gln Gln Val Ala Ser Thr Val Ser Pro	165	170	175
Ala Glu Leu Gly Val Pro Asp Trp Ala Ile Ala Ala Val Glu Ala Arg	180	185	190
Gly Thr Asp Pro Lys Arg Leu Glu Gly Leu Ile Met Pro Gly Gln Tyr	195	200	205
Val Val Asp Pro Ser Asn Asp Ala Gln Gly Ile Leu Thr Asp Leu Ile	210	215	220
Thr Arg Ser Ala Asn His Phe Gln Glu Thr Asp Ile Thr Gly Arg Ala	225	230	235
Asp Ala Ile Gly Leu Thr Pro Tyr Glu Leu Val Thr Ala Ala Ser Leu	245	250	255
Ile Glu Arg Glu Ala Pro Ala Gly Asp Phe Asp Lys Val Ala Arg Val	260	265	270
Ile Leu Asn Arg Leu Ala Glu Pro Met Gln Leu Gln Phe Asp Ser Thr	275	280	285
Val Asn Tyr Gly Leu Ser Glu Gln Glu Val Ala Thr Thr Asp Glu Asp	290	295	300
Arg Gln Thr Val Thr Pro Trp Asn Thr Tyr Ala Met Asp Gly Leu Pro	305	310	315
Gln Thr Pro Ile Ala Ala Val Ser Thr Glu Ala Leu Gln Ala Met Glu	325	330	335

Asn Pro Ala Glu Gly Asn Trp Leu Tyr Phe Val Thr Ile Asp Thr Asp
 340 345 350

Gly Thr Thr Val Phe Asn Asp Thr Phe Glu Glu His Glu Ala Asp Ile
 355 360 365

Glu Gln Ala Leu Asn Ser Gly Val Leu Asp Ser Asn Arg
 370 375 380

<210> 415

<211> 644

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(621)

<223> RXN00954

<400> 415

gct	gtg	aag	tgg	ttc	gaa	gcg	tcc	aac	ttc	acc	ttc	ctg	ttc	gca	cct	48
Ala	Val	Lys	Trp	Phe	Glu	Ala	Ser	Asn	Phe	Thr	Phe	Leu	Phe	Ala	Pro	
1				5				10						15		
gcg	tac	aac	cct	gcg	att	gcg	cat	gtg	cag	ccg	gtt	cg	cag	gcg	ctg	96
Ala	Tyr	Asn	Pro	Ala	Ile	Ala	His	Val	Gln	Pro	Val	Arg	Gln	Ala	Leu	
			20					25					30			
aaa	ttc	ccc	acc	atc	ttc	aac	acg	ctt	gga	cca	ttg	ctg	tcc	ccg	gcg	144
Lys	Phe	Pro	Thr	Ile	Phe	Asn	Thr	Leu	Gly	Pro	Leu	Leu	Ser	Pro	Ala	
		35					40					45				
cg	ccg	gag	cgt	cag	atc	atg	ggc	gtg	gcc	aat	gcc	aat	cat	gga	cag	192
Arg	Pro	Glu	Arg	Gln	Ile	Met	Gly	Val	Ala	Asn	Ala	Asn	His	Gly	Gln	
	50					55				60						
ctc	atc	gcc	gag	gtc	ttc	cg	gag	ttg	ggc	cgt	aca	cg	gcg	ctt	gtt	240
Leu	Ile	Ala	Glu	Val	Phe	Arg	Glu	Leu	Gly	Arg	Thr	Arg	Ala	Leu	Val	
65				70				75						80		
gtg	cat	ggc	gca	ggc	acc	gat	gag	atc	gca	gtc	cac	ggc	acc	acc	ttg	288
Val	His	Gly	Ala	Gly	Thr	Asp	Glu	Ile	Ala	Val	His	Gly	Thr	Thr	Leu	
				85				90					95			
gtg	tgg	gag	ctt	aaa	gaa	gac	ggc	acc	atc	gag	cat	tac	acc	atc	gag	336
Val	Trp	Glu	Leu	Lys	Glu	Asp	Gly	Thr	Ile	Glu	His	Tyr	Thr	Ile	Glu	
		100					105					110				
cct	gag	gac	ctt	ggc	ctt	ggc	cg	tac	acc	ctt	gag	gat	ctc	gta	ggt	384
Pro	Glu	Asp	Leu	Gly	Leu	Gly	Arg	Tyr	Thr	Leu	Glu	Asp	Leu	Val	Gly	
		115				120						125				
ggc	ctc	ggc	act	gag	aac	gcc	gaa	gct	atg	cg	gct	act	ttc	gcg	ggc	432
Gly	Leu	Gly	Thr	Glu	Asn	Ala	Glu	Ala	Met	Arg	Ala	Thr	Phe	Ala	Gly	
	130					135					140					
acc	ggc	cct	gat	gca	cac	cgt	gat	gcg	ttg	gct	gcg	tcc	gca	ggt	gcg	480
Thr	Gly	Pro	Asp	Ala	His	Arg	Asp	Ala	Leu	Ala	Ala	Ser	Ala	Gly	Ala	
145					150			155							160	

atg ttc tac ctc aac ggc gat gtc gac tcc ttg aaa gat ggt gca caa 528
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175
 aag gcg ctt tcc ttg ctt gcc gac ggc acc acc cag gca tgg ttg gcc 576
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190
 aag cac gaa gag atc gat tac tca gaa aag gag tct tcc aat gac 621
 Lys His Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205
 tagtaataat ctgcccacag tgt 644

<210> 416
 <211> 207
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 416
 Ala Val Lys Trp Phe Glu Ala Ser Asn Phe Thr Phe Leu Phe Ala Pro
 1 5 10 15
 Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro Val Arg Gln Ala Leu
 20 25 30
 Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro Leu Leu Ser Pro Ala
 35 40 45
 Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn Ala Asn His Gly Gln
 50 55 60
 Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg Thr Arg Ala Leu Val
 65 70 75 80
 Val His Gly Ala Gly Thr Asp Glu Ile Ala Val His Gly Thr Thr Leu
 85 90 95
 Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu His Tyr Thr Ile Glu
 100 105 110
 Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu Glu Asp Leu Val Gly
 115 120 125
 Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg Ala Thr Phe Ala Gly
 130 135 140
 Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala Ala Ser Ala Gly Ala
 145 150 155 160
 Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu Lys Asp Gly Ala Gln
 165 170 175
 Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr Gln Ala Trp Leu Ala
 180 185 190
 Lys His Glu Ile Asp Tyr Ser Glu Lys Glu Ser Ser Asn Asp
 195 200 205

<210> 417

<211> 611

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(588)

<223> FRXA00954

<400> 417

ttc ctg ttc gca cct gcg tac aac cct gcg att gcg cat gtg cag ccg	48
Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro	
1 5 10 15	
ggt cgc cag gcg ctg aaa ttc ccc acc atc ttc aac acg ctt gga cca	96
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro	
20 25 30	
ttg ctg tcc ccg gcg cgc ccg gag cgt cag atc atg ggc gtg gcc aat	144
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn	
35 40 45	
gcc aat cat gga cag ctc atc gcc gag gtc ttc cgc gag ttg ggc cgt	192
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg	
50 55 60	
aca cgc gcg ctt gtt gtg cat ggc gca ggc acc gat gag atc gca gtc	240
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val	
65 70 75 80	
cac ggc acc acc ttg gtg tgg gag ctt aaa gaa gac ggc acc atc gag	288
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu	
85 90 95	
cat tac acc atc gag cct gag gac ctt ggc ctt ggc cgc tac acc ctt	336
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu	
100 105 110	
gag gat ctc gta ggt ggc ctc ggc act gag aac gcc gaa gct atg cgc	384
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg	
115 120 125	
gct act ttc gcg ggc acc ggc cct gat gca cac cgt gat gcg ttg gct	432
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala	
130 135 140	
gcg tcc gca ggt gcg atg ttc tac ctc aac ggc gat gtc gac tcc ttg	480
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu	
145 150 155 160	
aaa gat ggt gca caa aag gcg ctt tcc ttg ctt gcc gac ggc acc acc	528
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr	
165 170 175	
cag gca tgg ttg gcc aag cac gaa gag atc gat tac tca gaa aag gag	576
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu	
180 185 190	
tct tcc aat gac tagtaataat ctgcccacag tgt	611

Ser Ser Asn Asp
195

<210> 418
<211> 196
<212> PRT
<213> Corynebacterium glutamicum

<400> 418
Phe Leu Phe Ala Pro Ala Tyr Asn Pro Ala Ile Ala His Val Gln Pro
1 5 10 15
Val Arg Gln Ala Leu Lys Phe Pro Thr Ile Phe Asn Thr Leu Gly Pro
20 25 30
Leu Leu Ser Pro Ala Arg Pro Glu Arg Gln Ile Met Gly Val Ala Asn
35 40 45
Ala Asn His Gly Gln Leu Ile Ala Glu Val Phe Arg Glu Leu Gly Arg
50 55 60
Thr Arg Ala Leu Val Val His Gly Ala Gly Thr Asp Glu Ile Ala Val
65 70 75 80
His Gly Thr Thr Leu Val Trp Glu Leu Lys Glu Asp Gly Thr Ile Glu
85 90 95
His Tyr Thr Ile Glu Pro Glu Asp Leu Gly Leu Gly Arg Tyr Thr Leu
100 105 110
Glu Asp Leu Val Gly Gly Leu Gly Thr Glu Asn Ala Glu Ala Met Arg
115 120 125
Ala Thr Phe Ala Gly Thr Gly Pro Asp Ala His Arg Asp Ala Leu Ala
130 135 140
Ala Ser Ala Gly Ala Met Phe Tyr Leu Asn Gly Asp Val Asp Ser Leu
145 150 155 160
Lys Asp Gly Ala Gln Lys Ala Leu Ser Leu Leu Ala Asp Gly Thr Thr
165 170 175
Gln Ala Trp Leu Ala Lys His Glu Glu Ile Asp Tyr Ser Glu Lys Glu
180 185 190
Ser Ser Asn Asp
195

<210> 419
<211> 1677
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101) .. (1654)
<223> RXN00957

<400> 419

aaccggcaag ccctggatcg aatgaagctc gcagcgagta attatttgat gtttcccaga 60
aaggcttcag ccccaaatg atttcctcgg taggtgcccc atg agc acg aat ccc 115
Met Ser Thr Asn Pro
1 5
cat gtt ttc tcc cta gat gtc cgc tat cac gag gat gct tct gca ttg 163
His Val Phe Ser Leu Asp Val Arg Tyr His Glu Asp Ala Ser Ala Leu
10 15 20
ttt gcc cac ttg ggt ggc aca acc gca gat gat gca gcc ctg ttg gaa 211
Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp Ala Ala Leu Leu Glu
25 30 35
agc gct gat atc acc acc aag aat ggt att tct tcc ctc gcg gtg ttg 259
Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser Ser Leu Ala Val Leu
40 45 50
aag agt tcg gtg cgc att acg tgc acg ggc aac acg gtg gta acg cag 307
Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn Thr Val Val Thr Gln
55 60 65
ccg ctg acg gac tcg ggt agg gca gtg gtt gcg cgc cta acg cag cag 355
Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala Arg Leu Thr Gln Gln
70 75 80 85
ctt ggc cag tac aac acc gca gag aac acc ttt agc ttc ccc gcc tca 403
Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe Ser Phe Pro Ala Ser
90 95 100
gat gcg gtt gat gag cgc gag cgc ctc acc gca cca agc acc atc gaa 451
Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala Pro Ser Thr Ile Glu
105 110 115
gtg ctg cgc aag ttg cag ttc gag tcc ggt tac agc gac gcg tcc ctg 499
Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr Ser Asp Ala Ser Leu
120 125 130
cca ctg ctc atg ggc ggt ttc gcg ttt gat ttc tta gaa acc ttt gaa 547
Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe Leu Glu Thr Phe Glu
135 140 145
acg ctc ccc gct gtc gag gag agc gtc aac act tac ccc gat tac cag 595
Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr Tyr Pro Asp Tyr Gln
150 155 160 165
ttc gtc ctc gcg gaa atc gtc ctg gac atc aat cac cag gac cag acc 643
Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn His Gln Asp Gln Thr
170 175 180
gcc aaa ctc gcc ggc gtc tcc aac gcc cca ggc gag ctc gag gcc gag 691
Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly Glu Leu Glu Ala Glu
185 190 195
ctc aac aag ctt tca ttg ctt atc gac gcc gcc ctc ccc gca acc gaa 739
Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala Leu Pro Ala Thr Glu
200 205 210
cac gcc tac caa acc acc cct cac gac ggc gac act ctt cgc gtt gtg 787
His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp Thr Leu Arg Val Val
215 220 225

gct gat att ccc gat gct cag ttc cgc acc cag atc aat gag ctg aaa 835
 Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln Ile Asn Glu Leu Lys
 230 235 240 245

gaa aac att tac aac ggt gac atc tac caa gtt gtc ccg gcg cgc act 883
 Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val Val Pro Ala Arg Thr
 250 255 260

ttc acc gca cca tgt cct gat gca ttc gct gct tat ctg cag ctg cgt 931
 Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala Tyr Leu Gln Leu Arg
 265 270 275

gcc acc aac ccg tcg ccg tac atg ttc tat atc cgt ggc ctc aac gaa 979
 Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile Arg Gly Leu Asn Glu
 280 285 290

ggc cgc tcc tat gaa ctt ttt ggc gca tcc cct gag tcc aac ctc aag
 1027
 Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro Glu Ser Asn Leu Lys
 295 300 305

ttc acc gct gct aac cgt gag ctg cag ctg tac cca atc gca ggt acc
 1075
 Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr Pro Ile Ala Gly Thr
 310 315 320 325

cgc ccc cgt gga ctc aac cca gat ggc tcc atc aac gat gag cta gat
 1123
 Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile Asn Asp Glu Leu Asp
 330 335 340

atc cgc aat gag ttg gat atg cgc act gat gcc aaa gag atc gcg gag
 1171
 Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala Lys Glu Ile Ala Glu
 345 350 355

cac acc atg ctt gtc gat ctc gcc cgc aac gac ctg gcc cgc gtc tcg
 1219
 His Thr Met Leu Val Asp Leu Ala Arg Asn Asp Leu Ala Arg Val Ser
 360 365 370

gtc cca gcg tcg cgc cgg gtt gcg gat ctt ttg cag gtg gat cgc tat
 1267
 Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu Gln Val Asp Arg Tyr
 375 380 385

tcc cgc gtg atg cac ttg gtg tcc cgt gtg acg gcg acg ttg gac cca
 1315
 Ser Arg Val Met His Leu Val Ser Arg Val Thr Ala Thr Leu Asp Pro
 390 395 400 405

gag ctt gat gct ttg gac gcc tat cgg gcg tgc atg aat atg ggc acg
 1363
 Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys Met Asn Met Gly Thr
 410 415 420

ttg acc ggc gct ccg aag ttg cgc gct atg gag ctg ttg cgc ggc gtc
 1411
 Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu Leu Leu Arg Gly Val
 425 430 435

gaa aag cgc agg cgt ggt tct tat ggt ggg gca gtg ggg tac ctg cgc
1459

Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala Val Gly Tyr Leu Arg
440 445 450

ggc aat ggc gat atg gat aat tgc att gtt att cgt tcg gcg ttt gtc
1507

Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile Arg Ser Ala Phe Val
455 460 465

cag gat ggt gtg gct gct gtg cag gct ggt gct ggt gtg gtc cgc gat
1555

Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala Gly Val Val Arg Asp
470 475 480 485

tct aat cct caa tct gaa gcc gat gag acg ttg cac aag gcg tat gcc
1603

Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu His Lys Ala Tyr Ala
490 495 500

gtg ttg aat gcc att gcg ctt gct gct ggt tcc act ttg gag gtc atc
1651

Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser Thr Leu Glu Val Ile
505 510 515

cga tgacacacgt tgttctcatt gat
1677

Arg

<210> 420

<211> 518

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Ser Thr Asn Pro His Val Phe Ser Leu Asp Val Arg Tyr His Glu
1 5 10 15

Asp Ala Ser Ala Leu Phe Ala His Leu Gly Gly Thr Thr Ala Asp Asp
20 25 30

Ala Ala Leu Leu Glu Ser Ala Asp Ile Thr Thr Lys Asn Gly Ile Ser
35 40 45

Ser Leu Ala Val Leu Lys Ser Ser Val Arg Ile Thr Cys Thr Gly Asn
50 55 60

Thr Val Val Thr Gln Pro Leu Thr Asp Ser Gly Arg Ala Val Val Ala
65 70 75 80

Arg Leu Thr Gln Gln Leu Gly Gln Tyr Asn Thr Ala Glu Asn Thr Phe
85 90 95

Ser Phe Pro Ala Ser Asp Ala Val Asp Glu Arg Glu Arg Leu Thr Ala
100 105 110

Pro Ser Thr Ile Glu Val Leu Arg Lys Leu Gln Phe Glu Ser Gly Tyr
115 120 125

Ser Asp Ala Ser Leu Pro Leu Leu Met Gly Gly Phe Ala Phe Asp Phe
 130 135 140
 Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val Asn Thr
 145 150 155 160
 Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp Ile Asn
 165 170 175
 His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala Pro Gly
 180 185 190
 Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp Ala Ala
 195 200 205
 Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp Gly Asp
 210 215 220
 Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg Thr Gln
 225 230 235 240
 Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr Gln Val
 245 250 255
 Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe Ala Ala
 260 265 270
 Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe Tyr Ile
 275 280 285
 Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala Ser Pro
 290 295 300
 Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln Leu Tyr
 305 310 315 320
 Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly Ser Ile
 325 330 335
 Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr Asp Ala
 340 345 350
 Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg Asn Asp
 355 360 365
 Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp Leu Leu
 370 375 380
 Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg Val Thr
 385 390 395 400
 Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg Ala Cys
 405 410 415
 Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala Met Glu
 420 425 430
 Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly Gly Ala
 435 440 445

Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile Val Ile
 450 455 460

Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala Gly Ala
 465 470 475 480

Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu Thr Leu
 485 490 495

His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala Gly Ser
 500 505 510

Thr Leu Glu Val Ile Arg
 515

<210> 421
 <211> 1151
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1128)
 <223> FRXA00957

<400> 421
 gat ttc tta gaa acc ttt gaa acg ctc ccc gct gtc gag gag agc gtc 48
 Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
 1 5 10 15

aac act tac ccc gat tac cag ttc gtc ctc gcg gaa atc gtc ctg gac 96
 Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
 20 25 30

atc aat cac cag gac cag acc gcc aaa ctc gcc ggc gtc tcc aac gcc 144
 Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
 35 40 45

cca ggc gag ctc gag gcc gag ctc aac aag ctt tca ttg ctt atc gac 192
 Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
 50 55 60

gcc gcc ctc ccc gca acc gaa cac gcc tac caa acc acc cct cac gac 240
 Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
 65 70 75 80

ggc gac act ctt cgc gtt gtg gct gat att ccc gat gct cag ttc cgc 288
 Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
 85 90 95

acc cag atc aat gag ctg aaa gaa aac att tac aac ggt gac atc tac 336
 Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
 100 105 110

caa gtt gtc ccg gcg cgc act ttc acc gca cca tgt cct gat gca ttc 384
 Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
 115 120 125

gct gct tat ctg cag ctg cgt gcc acc aac ccg tcg ccg tac atg ttc 432
 Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe

130	135	140	
tat atc cgt ggc ctc aac gaa ggc cgc tcc tat gaa ctt ttt ggc gca Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala 145 150 155 160			480
tcc cct gag tcc aac ctc aag ttc acc gct gct aac cgt gag ctg cag Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln 165 170 175			528
ctg tac cca atc gca ggt acc cgc ccc cgt gga ctc aac cca gat ggc Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly 180 185 190			576
tcc atc aac gat gag cta gat atc cgc aat gag ttg gat atg cgc act Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr 195 200 205			624
gat gcc aaa gag atc gcg gag cac acc atg ctt gtc gat ctc gcc cgc Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg 210 215 220			672
aac gac ctg gcc cgc gtc tcg gtc cca gcg tcg cgc cgg gtt gcg gat Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp 225 230 235 240			720
ctt ttg cag gtg gat cgc tat tcc cgc gtg atg cac ttg gtg tcc cgt Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg 245 250 255			768
gtg acg gcg acg ttg gac cca gag ctt gat gct ttg gac gcc tat cgg Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg 260 265 270			816
gcg tgc atg aat atg ggc acg ttg acc ggc gct ccg aag ttg cgc gct Ala Cys Met Asn Met Gly Thr Leu Thr Gly Ala Pro Lys Leu Arg Ala 275 280 285			864
atg gag ctg ttg cgc ggc gtc gaa aag cgc agg cgt ggt tct tat ggt Met Glu Leu Leu Arg Gly Val Glu Lys Arg Arg Arg Gly Ser Tyr Gly 290 295 300			912
ggg gca gtg ggg tac ctg cgc ggc aat ggc gat atg gat aat tgc att Gly Ala Val Gly Tyr Leu Arg Gly Asn Gly Asp Met Asp Asn Cys Ile 305 310 315 320			960
gtt att cgt tcg gcg ttt gtc cag gat ggt gtg gct gct gtg cag gct 1008 Val Ile Arg Ser Ala Phe Val Gln Asp Gly Val Ala Ala Val Gln Ala 325 330 335			
ggt gct ggt gtg gtc cgc gat tct aat cct caa tct gaa gcc gat gag 1056 Gly Ala Gly Val Val Arg Asp Ser Asn Pro Gln Ser Glu Ala Asp Glu 340 345 350			
acg ttg cac aag gcg tat gcc gtg ttg aat gcc att gcg ctt gct gct 1104 Thr Leu His Lys Ala Tyr Ala Val Leu Asn Ala Ile Ala Leu Ala Ala 355 360 365			

ggt tcc act ttg gag gtc atc cga tgacacacgt tgttctcatt gat
1151

Gly Ser Thr Leu Glu Val Ile Arg
370 375

<210> 422

<211> 376

<212> PRT

<213> Corynebacterium glutamicum

<400> 422

Asp Phe Leu Glu Thr Phe Glu Thr Leu Pro Ala Val Glu Glu Ser Val
1 5 10 15

Asn Thr Tyr Pro Asp Tyr Gln Phe Val Leu Ala Glu Ile Val Leu Asp
20 25 30

Ile Asn His Gln Asp Gln Thr Ala Lys Leu Ala Gly Val Ser Asn Ala
35 40 45

Pro Gly Glu Leu Glu Ala Glu Leu Asn Lys Leu Ser Leu Leu Ile Asp
50 55 60

Ala Ala Leu Pro Ala Thr Glu His Ala Tyr Gln Thr Thr Pro His Asp
65 70 75 80

Gly Asp Thr Leu Arg Val Val Ala Asp Ile Pro Asp Ala Gln Phe Arg
85 90 95

Thr Gln Ile Asn Glu Leu Lys Glu Asn Ile Tyr Asn Gly Asp Ile Tyr
100 105 110

Gln Val Val Pro Ala Arg Thr Phe Thr Ala Pro Cys Pro Asp Ala Phe
115 120 125

Ala Ala Tyr Leu Gln Leu Arg Ala Thr Asn Pro Ser Pro Tyr Met Phe
130 135 140

Tyr Ile Arg Gly Leu Asn Glu Gly Arg Ser Tyr Glu Leu Phe Gly Ala
145 150 155 160

Ser Pro Glu Ser Asn Leu Lys Phe Thr Ala Ala Asn Arg Glu Leu Gln
165 170 175

Leu Tyr Pro Ile Ala Gly Thr Arg Pro Arg Gly Leu Asn Pro Asp Gly
180 185 190

Ser Ile Asn Asp Glu Leu Asp Ile Arg Asn Glu Leu Asp Met Arg Thr
195 200 205

Asp Ala Lys Glu Ile Ala Glu His Thr Met Leu Val Asp Leu Ala Arg
210 215 220

Asn Asp Leu Ala Arg Val Ser Val Pro Ala Ser Arg Arg Val Ala Asp
225 230 235 240

Leu Leu Gln Val Asp Arg Tyr Ser Arg Val Met His Leu Val Ser Arg
245 250 255

Val Thr Ala Thr Leu Asp Pro Glu Leu Asp Ala Leu Asp Ala Tyr Arg

260										265										270									
Ala	Cys	Met	Asn	Met	Gly	Thr	Leu	Thr	Gly	Ala	Pro	Lys	Leu	Arg	Ala														
		275						280					285																
Met	Glu	Leu	Leu	Arg	Gly	Val	Glu	Lys	Arg	Arg	Arg	Gly	Ser	Tyr	Gly														
		290					295					300																	
Gly	Ala	Val	Gly	Tyr	Leu	Arg	Gly	Asn	Gly	Asp	Met	Asp	Asn	Cys	Ile														
305					310					315					320														
Val	Ile	Arg	Ser	Ala	Phe	Val	Gln	Asp	Gly	Val	Ala	Ala	Val	Gln	Ala														
				325					330					335															
Gly	Ala	Gly	Val	Val	Arg	Asp	Ser	Asn	Pro	Gln	Ser	Glu	Ala	Asp	Glu														
			340					345					350																
Thr	Leu	His	Lys	Ala	Tyr	Ala	Val	Leu	Asn	Ala	Ile	Ala	Leu	Ala	Ala														
		355					360					365																	
Gly	Ser	Thr	Leu	Glu	Val	Ile	Arg																						
		370				375																							

<210> 423
 <211> 1068
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1045)
 <223> RXA02687

<400> 423
 caaaaccatg ctcggcgggg gagagttggg ccaagcgggt cgctaattga gcaacagaca 60
 tggacaccca ccttagttcg gcgggttaag ctgtgtaacc atg agc gac gca cca 115
 Met Ser Asp Ala Pro 5
 1
 act gtt gtg gcc tat ttg ggg cct gcc gga acc ttc acc gaa gaa gcc 163
 Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr Phe Thr Glu Glu Ala 20
 10 15
 ctc tac aaa ttt gcc gac gcc ggc gta ttc ggc gac ggt gag atc gag 211
 Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly Asp Gly Glu Ile Glu 35
 25 30
 cag cta cca gcc aaa tcg cca caa gaa gct gtc gac gcc gtc cgc cac 259
 Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val Asp Ala Val Arg His 50
 40 45
 ggc acc gcc cag ttc gcg gtg gtc gcc atc gaa aac ttc gtc gac ggc 307
 Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu Asn Phe Val Asp Gly 65
 55 60
 ccc gtc acc ccc acc ttc gac gcc ctt gac cag ggc tcc aac gtg caa 355
 Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln Gly Ser Asn Val Gln 85
 70 75 80

atc atc gcc gaa gaa gaa ctc gac atc gcc ttt tcc atc atg gtc cgg 403
 Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe Ser Ile Met Val Arg
 90 95 100

cca ggg act tcg ctt gcc gac gtc aaa acc ctc gcc acc cac ccg gtt 451
 Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu Ala Thr His Pro Val
 105 110 115

ggg tac caa caa gtg aaa aac tgg atg gca acc acc att ccg gac gcc 499
 Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr Thr Ile Pro Asp Ala
 120 125 130

atg tat ctt tca gca agc tcc aac ggc gcc ggc gca caa atg gtt gcc 547
 Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly Ala Gln Met Val Ala
 135 140 145

gaa gga acc gcc gac gca gcc gca gcg ccc tcc cgc gca gcc gaa ctc 595
 Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser Arg Ala Ala Glu Leu
 150 155 160 165

ttc gga ctg gaa cgc ctt gtt gat gat gtc gcc gac gtc cgt ggc gcc 643
 Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala Asp Val Arg Gly Ala
 170 175 180

cgc acc cgc ttc gtt gct gtc caa gcc caa gca gcc gtt tcc gaa ccg 691
 Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala Ala Val Ser Glu Pro
 185 190 195

acc ggc cac gac cgc acc tcc gtc att ttc tcc cta ccg aat gtg cca 739
 Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser Leu Pro Asn Val Pro
 200 205 210

ggc agc ctc gtg cgc gcc ctc aac gaa ttc gcc atc cgc ggc gtt gac 787
 Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala Ile Arg Gly Val Asp
 215 220 225

ctc acc cgc atc gaa tcc cgc ccc acc cgc aaa gtc ttc gga acc tac 835
 Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys Val Phe Gly Thr Tyr
 230 235 240 245

cgc ttc cac ctg gac ata tcc gga cat atc cgc gat atc ccc gtc gcc 883
 Arg Phe His Leu Asp Ile Ser Gly His Ile Arg Asp Ile Pro Val Ala
 250 255 260

gaa gcc ctc cgc gca ctc cac ctc caa gcc gaa gaa ctc gtc ttc gtc 931
 Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu Glu Leu Val Phe Val
 265 270 275

ggc tcc tgg ccc tcc aac cgt gcg gaa gac agc acg ccc caa acc gac 979
 Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser Thr Pro Gln Thr Asp
 280 285 290

caa cta gct aag cta cac aag gcg gac gaa tgg gtt cgc gca gca agc
 1027
 Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp Val Arg Ala Ala Ser
 295 300 305

gaa gga agg aaa ctt aac tagccatggc cggccggatt att
 1068
 Glu Gly Arg Lys Leu Asn
 310 315

<210> 424

<211> 315

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Ser Asp Ala Pro Thr Val Val Ala Tyr Leu Gly Pro Ala Gly Thr
 1 5 10 15

Phe Thr Glu Glu Ala Leu Tyr Lys Phe Ala Asp Ala Gly Val Phe Gly
 20 25 30

Asp Gly Glu Ile Glu Gln Leu Pro Ala Lys Ser Pro Gln Glu Ala Val
 35 40 45

Asp Ala Val Arg His Gly Thr Ala Gln Phe Ala Val Val Ala Ile Glu
 50 55 60

Asn Phe Val Asp Gly Pro Val Thr Pro Thr Phe Asp Ala Leu Asp Gln
 65 70 75 80

Gly Ser Asn Val Gln Ile Ile Ala Glu Glu Glu Leu Asp Ile Ala Phe
 85 90 95

Ser Ile Met Val Arg Pro Gly Thr Ser Leu Ala Asp Val Lys Thr Leu
 100 105 110

Ala Thr His Pro Val Gly Tyr Gln Gln Val Lys Asn Trp Met Ala Thr
 115 120 125

Thr Ile Pro Asp Ala Met Tyr Leu Ser Ala Ser Ser Asn Gly Ala Gly
 130 135 140

Ala Gln Met Val Ala Glu Gly Thr Ala Asp Ala Ala Ala Pro Ser
 145 150 155 160

Arg Ala Ala Glu Leu Phe Gly Leu Glu Arg Leu Val Asp Asp Val Ala
 165 170 175

Asp Val Arg Gly Ala Arg Thr Arg Phe Val Ala Val Gln Ala Gln Ala
 180 185 190

Ala Val Ser Glu Pro Thr Gly His Asp Arg Thr Ser Val Ile Phe Ser
 195 200 205

Leu Pro Asn Val Pro Gly Ser Leu Val Arg Ala Leu Asn Glu Phe Ala
 210 215 220

Ile Arg Gly Val Asp Leu Thr Arg Ile Glu Ser Arg Pro Thr Arg Lys
 225 230 235 240

Val Phe Gly Thr Tyr Arg Phe His Leu Asp Ile Ser Gly His Ile Arg
 245 250 255

Asp Ile Pro Val Ala Glu Ala Leu Arg Ala Leu His Leu Gln Ala Glu
 260 265 270

Glu Leu Val Phe Val Gly Ser Trp Pro Ser Asn Arg Ala Glu Asp Ser
 275 280 285

Thr Pro Gln Thr Asp Gln Leu Ala Lys Leu His Lys Ala Asp Glu Trp
 290 295 300

Val Arg Ala Ala Ser Glu Gly Arg Lys Leu Asn
 305 310 315

<210> 425

<211> 1353

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1330)

<223> RXN01698

<400> 425

cgctagtgcc tgcagttatg tcgctttttg acgtcgaaaa gcaatttttaa aaagcccttg 60

gggtgggctg gatacgtctt ctgcggcctt tcgtgcgata atg cta ggc atg ctt 115
 Met Leu Gly Met Leu
 1 5

cga tgg act aca gca ggt gaa tcc cac ggc cag gcg ctt atc gcc acg 163
 Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln Ala Leu Ile Ala Thr
 10 15 20

gtt gaa cac atg cca gca ggc gtg ccc gtg act aaa gat gag gtc tcg 211
 Val Glu His Met Pro Ala Gly Val Pro Val Thr Lys Asp Glu Val Ser
 25 30 35

tat caa ttg gcg cgc cga cgc ctt gga tat ggt cgc ggc gct cgc atg 259
 Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly Arg Gly Ala Arg Met
 40 45 50

aag ttt gag caa gac gcg ttg acc ttc ctc acc ggc atc cgc cac ggc 307
 Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr Gly Ile Arg His Gly
 55 60 65

ctc act ttg ggt agc ccc atc tca atc atg atc ggc aac act gag tgg 355
 Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile Gly Asn Thr Glu Trp
 70 75 80 85

gat aag tgg acc acc atc atg tcc tct gac gct ttg gac atg gaa gac 403
 Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala Leu Asp Met Glu Asp
 90 95 100

cca gat aac gtt gcg gcg atg tct tcg ggt cgg ggc gca aaa ctg act 451
 Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg Gly Ala Lys Leu Thr
 105 110 115

cgt ccg cgt cca ggc cac gct gat tac gca ggc atg ctc aag tac gga 499
 Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly Met Leu Lys Tyr Gly
 120 125 130

ttc gat gat gcc cgc aac gtg ctg gag cgt tct tca gcc cgt gag acg 547
 Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser Ser Ala Arg Glu Thr
 135 140 145

gca gca cgc gtg gca gca gca acc gtt gcg cgt tcc ttc ctg cgt gaa 595
 Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg Ser Phe Leu Arg Glu
 150 155 160 165

acc ttg ggc gtg gaa gtg ctt tcc cac gta att tcc att ggt gcg tcc 643
 Thr Leu Gly Val Glu Val Leu Ser His Val Ile Ser Ile Gly Ala Ser
 170 175 180

gag cct tac act ggc gcg gag cca acc ttt gca gat att caa gca atc 691
 Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala Asp Ile Gln Ala Ile
 185 190 195

gat gat tcc cca gtt cgt gca ttc ggt aaa gac gct gaa gaa tcc atg 739
 Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp Ala Glu Glu Ser Met
 200 205 210

atc gcg gaa atc gag gcc gca aag aaa gcc ggc gat acc ctc ggt ggc 787
 Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly Asp Thr Leu Gly Gly
 215 220 225

atc gtg gaa gtg att gtt gaa ggc ctg ccc atc ggt ttg ggc tca cac 835
 Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile Gly Leu Gly Ser His
 230 235 240 245

att tct ggc gaa gat cgc ctc gat gcg cag atc gca gct gca ctc atg 883
 Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile Ala Ala Ala Leu Met
 250 255 260

ggc att cag gcc atc aag ggc gtg gaa atc ggt gac ggt ttc gaa gaa 931
 Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly Asp Gly Phe Glu Glu
 265 270 275

gct cgt cga cgt ggc tcc gaa gcc cac gat gaa gtg ttc ctg gat gac 979
 Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu Val Phe Leu Asp Asp
 280 285 290

aac ggc gta tac cgc aac acc aac cgt gca ggt ggc ctc gaa ggc ggc
 1027
 Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly Gly Leu Glu Gly Gly
 295 300 305

atg acc aac ggt gaa acc ctg cgc gtt cgt gct ggc atg aag cca att
 1075
 Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala Gly Met Lys Pro Ile
 310 315 320 325

tct act gtg cct cgc gcc ctg aaa acc att gat atg gaa aac ggc aag
 1123
 Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp Met Glu Asn Gly Lys
 330 335 340

gca gca acc gga atc cac cag cgt tcc gac gtg tgc gct gtt cca gcc
 1171
 Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val Cys Ala Val Pro Ala
 345 350 355

gcc ggt gtc gtt gca gaa gca atg gtc acc ctg gtt ctc gcc cgc gca
 1219
 Ala Gly Val Val Ala Glu Ala Met Val Thr Leu Val Leu Ala Arg Ala
 360 365 370

gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc gaa acc aag agc aac
1267

Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser Glu Thr Lys Ser Asn
375 380 385

att gac acc tac ctc aaa aac att gag gaa cga atg aaa ttc gaa ggt
1315

Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg Met Lys Phe Glu Gly
390 395 400 405

tta gag gat gga gcg taatgaagtg aatgatcaaaa ttc
1353

Leu Glu Asp Gly Ala
410

<210> 426

<211> 410

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 426

Met Leu Gly Met Leu Arg Trp Thr Thr Ala Gly Glu Ser His Gly Gln
1 5 10 15

Ala Leu Ile Ala Thr Val Glu His Met Pro Ala Gly Val Pro Val Thr
20 25 30

Lys Asp Glu Val Ser Tyr Gln Leu Ala Arg Arg Arg Leu Gly Tyr Gly
35 40 45

Arg Gly Ala Arg Met Lys Phe Glu Gln Asp Ala Leu Thr Phe Leu Thr
50 55 60

Gly Ile Arg His Gly Leu Thr Leu Gly Ser Pro Ile Ser Ile Met Ile
65 70 75 80

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
85 90 95

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
100 105 110

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
115 120 125

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
130 135 140

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
145 150 155 160

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
165 170 175

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
180 185 190

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
195 200 205

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 210 215 220

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 225 230 235 240

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 245 250 255

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 260 265 270

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu
 275 280 285

Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly
 290 295 300

Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala
 305 310 315 320

Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp
 325 330 335

Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val
 340 345 350

Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu
 355 360 365

Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 370 375 380

Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 385 390 395 400

Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 405 410

<210> 427

<211> 1013

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(990)

<223> FRXA01698

<400> 427

ggc aac act gag tgg gat aag tgg acc acc atc atg tcc tct gac gct 48
 Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 1 5 10 15

ttg gac atg gaa gac cca gat aac gtt gcg gcg atg tct tcg ggt cgg 96
 Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

ggc gca aaa ctg act cgt ccg cgt cca ggc cac gct gat tac gca ggc 144
 Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly

35	40	45	
atg ctc aag tac gga ttc gat gat gcc cgc aac gtg ctg gag cgt tct Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser 50 55 60			192
tca gcc cgt gag acg gca gca cgc gtg gca gca gca acc gtt gcg cgt Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg 65 70 75 80			240
tcc ttc ctg cgt gaa acc ttg ggc gtg gaa gtg ctt tcc cac gta att Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile 85 90 95			288
tcc att ggt gcg tcc gag cct tac act ggc gcg gag cca acc ttt gca Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala 100 105 110			336
gat att caa gca atc gat gat tcc cca gtt cgt gca ttc ggt aaa gac Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp 115 120 125			384
gct gaa gaa tcc atg atc gcg gaa atc gag gcc gca aag aaa gcc ggc Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly 130 135 140			432
gat acc ctc ggt ggc atc gtg gaa gtg att gtt gaa ggc ctg ccc atc Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile 145 150 155 160			480
ggt ttg ggc tca cac att tct ggc gaa gat cgc ctc gat gcg cag atc Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile 165 170 175			528
gca gct gca ctc atg ggc att cag gcc atc aag ggc gtg gaa atc ggt Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly 180 185 190			576
gac ggt ttc gaa gaa gct cgt cga cgt ggc tcc gaa gcc cac gat gaa Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu 195 200 205			624
gtg ttc ctg gat gac aac ggc gta tac cgc aac acc aac cgt gca ggt Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220			672
ggc ctc gaa ggc ggc atg acc aac ggt gaa acc ctg cgc gtt cgt gct Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240			720
ggc atg aag cca att tct act gtg cct cgc gcc ctg aaa acc att gat Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255			768
atg gaa aac ggc aag gca gca acc gga atc cac cag cgt tcc gac gtg Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270			816
tgc gct gtt cca gcc gcc ggt gtc gtt gca gaa gca atg gtc acc ctg Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285			864

gtt ctc gcc cgc gca gtc ctg cag aaa ttc ggc ggt gac tcc ctg agc 912
 Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser
 290 295 300

gaa acc aag agc aac att gac acc tac ctc aaa aac att gag gaa cga 960
 Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg
 305 310 315 320

atg aaa ttc gaa ggt tta gag gat gga gcg taatgaagtg aatgatcaaa
 1010
 Met Lys Phe Glu Gly Leu Glu Asp Gly Ala
 325 330

ttc
 1013

<210> 428

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 428

Gly Asn Thr Glu Trp Asp Lys Trp Thr Thr Ile Met Ser Ser Asp Ala
 1 5 10 15

Leu Asp Met Glu Asp Pro Asp Asn Val Ala Ala Met Ser Ser Gly Arg
 20 25 30

Gly Ala Lys Leu Thr Arg Pro Arg Pro Gly His Ala Asp Tyr Ala Gly
 35 40 45

Met Leu Lys Tyr Gly Phe Asp Asp Ala Arg Asn Val Leu Glu Arg Ser
 50 55 60

Ser Ala Arg Glu Thr Ala Ala Arg Val Ala Ala Ala Thr Val Ala Arg
 65 70 75 80

Ser Phe Leu Arg Glu Thr Leu Gly Val Glu Val Leu Ser His Val Ile
 85 90 95

Ser Ile Gly Ala Ser Glu Pro Tyr Thr Gly Ala Glu Pro Thr Phe Ala
 100 105 110

Asp Ile Gln Ala Ile Asp Asp Ser Pro Val Arg Ala Phe Gly Lys Asp
 115 120 125

Ala Glu Glu Ser Met Ile Ala Glu Ile Glu Ala Ala Lys Lys Ala Gly
 130 135 140

Asp Thr Leu Gly Gly Ile Val Glu Val Ile Val Glu Gly Leu Pro Ile
 145 150 155 160

Gly Leu Gly Ser His Ile Ser Gly Glu Asp Arg Leu Asp Ala Gln Ile
 165 170 175

Ala Ala Ala Leu Met Gly Ile Gln Ala Ile Lys Gly Val Glu Ile Gly
 180 185 190

Asp Gly Phe Glu Glu Ala Arg Arg Arg Gly Ser Glu Ala His Asp Glu

195	200	205
Val Phe Leu Asp Asp Asn Gly Val Tyr Arg Asn Thr Asn Arg Ala Gly 210 215 220		
Gly Leu Glu Gly Gly Met Thr Asn Gly Glu Thr Leu Arg Val Arg Ala 225 230 235 240		
Gly Met Lys Pro Ile Ser Thr Val Pro Arg Ala Leu Lys Thr Ile Asp 245 250 255		
Met Glu Asn Gly Lys Ala Ala Thr Gly Ile His Gln Arg Ser Asp Val 260 265 270		
Cys Ala Val Pro Ala Ala Gly Val Val Ala Glu Ala Met Val Thr Leu 275 280 285		
Val Leu Ala Arg Ala Val Leu Gln Lys Phe Gly Gly Asp Ser Leu Ser 290 295 300		
Glu Thr Lys Ser Asn Ile Asp Thr Tyr Leu Lys Asn Ile Glu Glu Arg 305 310 315 320		
Met Lys Phe Glu Gly Leu Glu Asp Gly Ala 325 330		

<210> 429

<211> 906

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(883)

<223> RXA01095

<400> 429

gaaaccccag gtcaaagcta ggggtgtggca ccctgatttc tttcgccatg tgtgttcggg 60

ataaccttaa acacagcatt ggttgaagg aggttggggc atg gtt gca aca gag	115
Met Val Ala Thr Glu	
1 5	

aac cgc atg ttg atg gaa atc gct gcg gaa ata tcg gct cgg gaa gca	163
Asn Arg Met Leu Met Glu Ile Ala Ala Glu Ile Ser Ala Arg Glu Ala	
10 15 20	

acg ctt ggt ttt caa gaa gtc aaa act aaa tct cga tca gca ggt ctc	211
Thr Leu Gly Phe Gln Glu Val Lys Thr Lys Ser Arg Ser Ala Gly Leu	
25 30 35	

acg gcg gct ttc gat att gct tca gtc ttt ttt tcg tct gga tgt aat	259
Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe Ser Ser Gly Cys Asn	
40 45 50	

gtc gta gtc gcc ttt gat cgt ttt gca tcc aat tgg tct gat cat tcg	307
Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn Trp Ser Asp His Ser	
55 60 65	

gat cat gtg gac tac gct gca cag gtt gcg ggt ttt ggc gca tca atg	355
---	-----

Asp	His	Val	Asp	Tyr	Ala	Ala	Gln	Val	Ala	Gly	Phe	Gly	Ala	Ser	Met	
70					75					80					85	
ctt	gca	tat	acg	gtg	cgc	agg	gga	cag	ttt	gat	acc	gca	gta	cgc	gat	403
Leu	Ala	Tyr	Thr	Val	Arg	Arg	Gly	Gln	Phe	Asp	Thr	Ala	Val	Arg	Asp	
				90					95					100		
atc	agg	gac	atc	aaa	tct	gaa	gta	gac	att	ccc	att	ctg	ctt	cat	gat	451
Ile	Arg	Asp	Ile	Lys	Ser	Glu	Val	Asp	Ile	Pro	Ile	Leu	Leu	His	Asp	
			105					110					115			
ccc	atc	atc	gat	ccg	tat	caa	atc	cac	gaa	gcc	cgc	gtc	atg	ggc	atc	499
Pro	Ile	Ile	Asp	Pro	Tyr	Gln	Ile	His	Glu	Ala	Arg	Val	Met	Gly	Ile	
		120					125					130				
gac	gct	ctt	caa	ttc	ccc	gta	tgg	gcg	atg	gaa	caa	gct	cga	ctg	gaa	547
Asp	Ala	Leu	Gln	Phe	Pro	Val	Trp	Ala	Met	Glu	Gln	Ala	Arg	Leu	Glu	
		135				140						145				
tct	ttg	gtg	gac	cgc	acc	gaa	tca	ttg	ggc	atg	aca	gcc	atc	gtg	tct	595
Ser	Leu	Val	Asp	Arg	Thr	Glu	Ser	Leu	Gly	Met	Thr	Ala	Ile	Val	Ser	
150				155						160				165		
gtg	cga	aac	cac	gaa	gaa	gcg	cat	cgt	gca	gtg	gac	gca	gga	gcg	aca	643
Val	Arg	Asn	His	Glu	Glu	Ala	His	Arg	Ala	Val	Asp	Ala	Gly	Ala	Thr	
			170					175						180		
gtg	gta	gca	att	gat	att	act	ggc	tat	acc	ggc	tca	ctc	act	ttg	cct	691
Val	Val	Ala	Ile	Asp	Ile	Thr	Gly	Tyr	Thr	Gly	Ser	Leu	Thr	Leu	Pro	
			185				190						195			
gaa	gcg	ttt	tcg	ggc	atc	acc	caa	ttc	atg	ccc	aaa	gag	gta	gcc	cgc	739
Glu	Ala	Phe	Ser	Gly	Ile	Thr	Gln	Phe	Met	Pro	Lys	Glu	Val	Ala	Arg	
		200					205					210				
att	gtg	ctc	gga	ggc	tgc	agc	agc	cct	aaa	gaa	ctc	atg	cgg	ttt	gca	787
Ile	Val	Leu	Gly	Gly	Cys	Ser	Ser	Pro	Lys	Glu	Leu	Met	Arg	Phe	Ala	
		215				220						225				
cga	cat	tct	gca	gac	gcc	atc	ttt	gtt	cca	cat	gca	gac	ctc	gcc	acc	835
Arg	His	Ser	Ala	Asp	Ala	Ile	Phe	Val	Pro	His	Ala	Asp	Leu	Ala	Thr	
230					235					240				245		
aca	aaa	tct	ctt	gtg	aca	gca	ggc	atg	cat	cca	gcg	tgc	cca	tcg	cgt	883
Thr	Lys	Ser	Leu	Val	Thr	Ala	Gly	Met	His	Pro	Ala	Cys	Pro	Ser	Arg	
			250					255						260		
tgaagaggtg	ctctgtgggc	agc														906

<210> 430

<211> 261

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Met	Val	Ala	Thr	Glu	Asn	Arg	Met	Leu	Met	Glu	Ile	Ala	Ala	Glu	Ile	
1				5					10					15		

Ser	Ala	Arg	Glu	Ala	Thr	Leu	Gly	Phe	Gln	Glu	Val	Lys	Thr	Lys	Ser	
		20						25					30			

Arg Ser Ala Gly Leu Thr Ala Ala Phe Asp Ile Ala Ser Val Phe Phe
 35 40 45
 Ser Ser Gly Cys Asn Val Val Val Ala Phe Asp Arg Phe Ala Ser Asn
 50 55 60
 Trp Ser Asp His Ser Asp His Val Asp Tyr Ala Ala Gln Val Ala Gly
 65 70 75 80
 Phe Gly Ala Ser Met Leu Ala Tyr Thr Val Arg Arg Gly Gln Phe Asp
 85 90 95
 Thr Ala Val Arg Asp Ile Arg Asp Ile Lys Ser Glu Val Asp Ile Pro
 100 105 110
 Ile Leu Leu His Asp Pro Ile Ile Asp Pro Tyr Gln Ile His Glu Ala
 115 120 125
 Arg Val Met Gly Ile Asp Ala Leu Gln Phe Pro Val Trp Ala Met Glu
 130 135 140
 Gln Ala Arg Leu Glu Ser Leu Val Asp Arg Thr Glu Ser Leu Gly Met
 145 150 155 160
 Thr Ala Ile Val Ser Val Arg Asn His Glu Glu Ala His Arg Ala Val
 165 170 175
 Asp Ala Gly Ala Thr Val Val Ala Ile Asp Ile Thr Gly Tyr Thr Gly
 180 185 190
 Ser Leu Thr Leu Pro Glu Ala Phe Ser Gly Ile Thr Gln Phe Met Pro
 195 200 205
 Lys Glu Val Ala Arg Ile Val Leu Gly Gly Cys Ser Ser Pro Lys Glu
 210 215 220
 Leu Met Arg Phe Ala Arg His Ser Ala Asp Ala Ile Phe Val Pro His
 225 230 235 240
 Ala Asp Leu Ala Thr Thr Lys Ser Leu Val Thr Ala Gly Met His Pro
 245 250 255
 Ala Cys Pro Ser Arg
 260

<210> 431

<211> 1545

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1522)

<223> RXA00955

<400> 431

gatggtgcac aaaaggcgct ttccttgctt gccgacggca ccacccaggc atggttggcc 60

aagcacgaag agatcgatta ctcagaaaag gagtcttcca atg act agt aat aat 115

	Met	Thr	Ser	Asn	Asn	
	1				5	
ctg ccc aca gtg ttg gaa agc atc gtc gag ggt cgt cgc gga cac ctg 163						
Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly Arg Arg Gly His Leu						
	10				20	
gag gaa att cgc gct cgc atc gct cac gtg gat gtg gat gcg ctt cca 211						
Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp Val Asp Ala Leu Pro						
	25				35	
aaa tcc acc cgt tct ctg ttt gat tcc ctc aac cag ggt agg gga ggg 259						
Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn Gln Gly Arg Gly Gly						
	40				50	
gcg cgt ttc atc atg gag tgc aag tcc gca tcg cct tct ttg gga atg 307						
Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser Pro Ser Leu Gly Met						
	55				65	
att cgt gag cac tac cag ccg ggt gaa atc gct cgc gtg tac tct cgc 355						
Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala Arg Val Tyr Ser Arg						
	70				80	85
tac gcc agc ggc att tcc gtg ctg tgc gag ccg gat cgt ttt ggt ggc 403						
Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro Asp Arg Phe Gly Gly						
	90				95	100
gat tac gat cac ctc gct acc gtt gcc gct acc tct cat ctt ccg gtg 451						
Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr Ser His Leu Pro Val						
	105				110	115
ctg tgc aaa gac ttc atc att gat cct gtc cag gta cac gcg gcg cgt 499						
Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln Val His Ala Ala Arg						
	120				125	130
tac ttt ggt gct gat gcc atc ctg ctc atg ctc tct gtg ctt gat gat 547						
Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu Ser Val Leu Asp Asp						
	135				140	145
gaa gag tac gca gca ctc gct gcc gag gct gcg cgt ttt gat ctg gat 595						
Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala Arg Phe Asp Leu Asp						
	150				155	160
atc ctc acc gag gtt att gat gag gag gaa gtc gcc cgc gcc atc aag 643						
Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val Ala Arg Ala Ile Lys						
	170				175	180
ctg ggt gcg aag atc ttt ggc gtc aac cac cgc aac ctg cat gat ctg 691						
Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg Asn Leu His Asp Leu						
	185				190	195
tcc att gat ttg gat cgt tca cgt cgc ctg tcc aag ctc att cca gca 739						
Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser Lys Leu Ile Pro Ala						
	200				205	210
gat gcc gtg ctc gtg tct gag tct ggc gtg cgc gat acc gaa acc gtc 787						
Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg Asp Thr Glu Thr Val						
	215				220	225
cgc cag cta ggt ggg cac tcc aat gca ttc ctc gtt ggc tcc cag ctg 835						
Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu Val Gly Ser Gln Leu						

230	235	240	245	
acc agc cag gaa aac gtc gat ctg gca gcc cgc gaa tta gtc tac ggc				883
Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg Glu Leu Val Tyr Gly				
250		255	260	
ccc aac aaa gtc tgc gga ctc acc tca cca agt gca gca caa acc gct				931
Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser Ala Ala Gln Thr Ala				
265		270	275	
cgc gca gcg ggt gcg gtc tac ggc ggg ctc atc ttc gaa gag gca tcg				979
Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile Phe Glu Glu Ala Ser				
280		285	290	
cca cgc aat gtt tca cgt gaa aca ttg caa aaa atc atc gcc gca gag				
1027				
Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys Ile Ile Ala Ala Glu				
295		300	305	
ccc aac ctg cgc tac gtc gcg gtc agc cgt cgc acc tcc ggg tac aag				
1075				
Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg Thr Ser Gly Tyr Lys				
310		315	320	325
gat ttg ctt gtc gac ggc atc ttc gcc gta caa atc cac gcc cca ctg				
1123				
Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln Ile His Ala Pro Leu				
	330	335	340	
cag gac agc gtc gaa gca gaa aag gca ttg atc gcc gcc gtt cgt gaa				
1171				
Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile Ala Ala Val Arg Glu				
	345	350	355	
gag gtt gga ccg cag gtc cag gtc tgg cgc gcg atc tcg atg tcc agc				
1219				
Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala Ile Ser Met Ser Ser				
	360	365	370	
ccc ttg ggg gct gaa gtg gca gct gcg gtg gag ggt gac gtc gat aag				
1267				
Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu Gly Asp Val Asp Lys				
	375	380	385	
cta att ctt gat gcc cat gaa ggt ggc agc ggg gaa gta ttc gac tgg				
1315				
Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly Glu Val Phe Asp Trp				
	390	395	400	405
gct acg gtg ccg gcc gct gtg aag gca aag tct ttg ctc gcg gga ggc				
1363				
Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser Leu Leu Ala Gly Gly				
	410	415	420	
atc tct ccg gac aac gct gcg cag gca ctc gct gtg ggc tgc gca ggt				
1411				
Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala Val Gly Cys Ala Gly				
	425	430	435	
ttg gac atc aac tct ggc gtg gaa tac ccc gcc ggt gca ggc acg tgg				
1459				

Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala Gly Ala Gly Thr Trp
 440 445 450

gct ggg gcg aaa gac gcc ggc gcg ctg ctg aaa att tta gcg acc atc
 1507

Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys Ile Leu Ala Thr Ile
 455 460 465

tcc aca ttc cat tac taaaggttta aataggatca tga

1545

Ser Thr Phe His Tyr

470

<210> 432

<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Met Thr Ser Asn Asn Leu Pro Thr Val Leu Glu Ser Ile Val Glu Gly
 1 5 10 15

Arg Arg Gly His Leu Glu Glu Ile Arg Ala Arg Ile Ala His Val Asp
 20 25 30

Val Asp Ala Leu Pro Lys Ser Thr Arg Ser Leu Phe Asp Ser Leu Asn
 35 40 45

Gln Gly Arg Gly Gly Ala Arg Phe Ile Met Glu Cys Lys Ser Ala Ser
 50 55 60

Pro Ser Leu Gly Met Ile Arg Glu His Tyr Gln Pro Gly Glu Ile Ala
 65 70 75 80

Arg Val Tyr Ser Arg Tyr Ala Ser Gly Ile Ser Val Leu Cys Glu Pro
 85 90 95

Asp Arg Phe Gly Gly Asp Tyr Asp His Leu Ala Thr Val Ala Ala Thr
 100 105 110

Ser His Leu Pro Val Leu Cys Lys Asp Phe Ile Ile Asp Pro Val Gln
 115 120 125

Val His Ala Ala Arg Tyr Phe Gly Ala Asp Ala Ile Leu Leu Met Leu
 130 135 140

Ser Val Leu Asp Asp Glu Glu Tyr Ala Ala Leu Ala Ala Glu Ala Ala
 145 150 155 160

Arg Phe Asp Leu Asp Ile Leu Thr Glu Val Ile Asp Glu Glu Glu Val
 165 170 175

Ala Arg Ala Ile Lys Leu Gly Ala Lys Ile Phe Gly Val Asn His Arg
 180 185 190

Asn Leu His Asp Leu Ser Ile Asp Leu Asp Arg Ser Arg Arg Leu Ser
 195 200 205

Lys Leu Ile Pro Ala Asp Ala Val Leu Val Ser Glu Ser Gly Val Arg
 210 215 220

Asp Thr Glu Thr Val Arg Gln Leu Gly Gly His Ser Asn Ala Phe Leu
 225 230 235 240
 Val Gly Ser Gln Leu Thr Ser Gln Glu Asn Val Asp Leu Ala Ala Arg
 245 250 255
 Glu Leu Val Tyr Gly Pro Asn Lys Val Cys Gly Leu Thr Ser Pro Ser
 260 265 270
 Ala Ala Gln Thr Ala Arg Ala Ala Gly Ala Val Tyr Gly Gly Leu Ile
 275 280 285
 Phe Glu Glu Ala Ser Pro Arg Asn Val Ser Arg Glu Thr Leu Gln Lys
 290 295 300
 Ile Ile Ala Ala Glu Pro Asn Leu Arg Tyr Val Ala Val Ser Arg Arg
 305 310 315 320
 Thr Ser Gly Tyr Lys Asp Leu Leu Val Asp Gly Ile Phe Ala Val Gln
 325 330 335
 Ile His Ala Pro Leu Gln Asp Ser Val Glu Ala Glu Lys Ala Leu Ile
 340 345 350
 Ala Ala Val Arg Glu Glu Val Gly Pro Gln Val Gln Val Trp Arg Ala
 355 360 365
 Ile Ser Met Ser Ser Pro Leu Gly Ala Glu Val Ala Ala Ala Val Glu
 370 375 380
 Gly Asp Val Asp Lys Leu Ile Leu Asp Ala His Glu Gly Gly Ser Gly
 385 390 395 400
 Glu Val Phe Asp Trp Ala Thr Val Pro Ala Ala Val Lys Ala Lys Ser
 405 410 415
 Leu Leu Ala Gly Gly Ile Ser Pro Asp Asn Ala Ala Gln Ala Leu Ala
 420 425 430
 Val Gly Cys Ala Gly Leu Asp Ile Asn Ser Gly Val Glu Tyr Pro Ala
 435 440 445
 Gly Ala Gly Thr Trp Ala Gly Ala Lys Asp Ala Gly Ala Leu Leu Lys
 450 455 460
 Ile Leu Ala Thr Ile Ser Thr Phe His Tyr
 465 470

<210> 433

<211> 494

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(471)

<223> RXA02814

<400> 433


```

gcc aaa aac cta gaa gaa cac tcc tac gtg gtc aac cac ctg cgc acc 48
Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

atc ctg gaa cca ctg tgc tca caa ttc gac gcc cca aca gtt cct gaa 96
Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

ctg acc aaa acc aac gaa atg tgg cac ctc gca aca ccc atc gtt ggc 144
Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

acc ctc aag tac cca cac atc acc gca cta gaa cta gcc ata cga aca 192
Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

cac ccc acc ccc gcg atc tgt ggc acc ccc acc gac gcc gcc gaa gcc 240
His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
  65          70          75          80

ctc atc atc gaa gcg gaa tcc ccc cga aac ttc tac gcc gga gca gcc 288
Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
          85          90          95

ggc tgg tgt gac tcc acc gga gac ggc gaa tac atg gta gcc atc cgc 336
Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
          100          105          110

tgc gcc gaa gta tcc gaa gac gga acc tgg gcc aga gca tgg gca ggc 384
Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
          115          120          125

gga ggc atc gtc gcc gaa tca gac gcc caa gaa gag ttt gat gaa acc 432
Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
          130          135          140

acc gcg aag ctc caa acc atc atg cgc tcg ctt ggt ttg tgagatgtgg 481
Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
          145          150          155

tcttaaaaca ccg 494

```

<210> 434

<211> 157

<212> PRT

<213> Corynebacterium glutamicum

<400> 434

```

Ala Lys Asn Leu Glu Glu His Ser Tyr Val Val Asn His Leu Arg Thr
  1          5          10          15

Ile Leu Glu Pro Leu Cys Ser Gln Phe Asp Ala Pro Thr Val Pro Glu
          20          25          30

Leu Thr Lys Thr Asn Glu Met Trp His Leu Ala Thr Pro Ile Val Gly
          35          40          45

Thr Leu Lys Tyr Pro His Ile Thr Ala Leu Glu Leu Ala Ile Arg Thr
          50          55          60

```

His Pro Thr Pro Ala Ile Cys Gly Thr Pro Thr Asp Ala Ala Glu Ala
 65 70 75 80
 Leu Ile Ile Glu Ala Glu Ser Pro Arg Asn Phe Tyr Ala Gly Ala Ala
 85 90 95
 Gly Trp Cys Asp Ser Thr Gly Asp Gly Glu Tyr Met Val Ala Ile Arg
 100 105 110
 Cys Ala Glu Val Ser Glu Asp Gly Thr Trp Ala Arg Ala Trp Ala Gly
 115 120 125
 Gly Gly Ile Val Ala Glu Ser Asp Ala Gln Glu Glu Phe Asp Glu Thr
 130 135 140
 Thr Ala Lys Leu Gln Thr Ile Met Arg Ser Leu Gly Leu
 145 150 155

<210> 435
 <211> 803
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(780)
 <223> RXA00229

<400> 435
 gag gcg aaa ggc ctc gcg cag gga cgt gcg acg gtg tac agg cgc atc 48
 Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15
 gac acg ctt ggg tcg cgt gct tcc ggg caa gat tta aat acg ctt ctc 96
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30
 gac gcc gcc ctc tac ctt ggc ttc agc ggc ctg aac atc act cac ccg 144
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45
 tac aag caa gca gta tta ccc ctg ctt ggc gaa gtc tcc gaa caa gcc 192
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60
 acc caa ctc ggc gca gtg aat act gtc gtt atg gac gcc acc ggc cac 240
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80
 acc acc ggc cac aac acc gac gtc tcc gga ttt ggc cgc gga atg gaa 288
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95
 gaa ggc ctc ccc aac gcc aag ctc gat tcc gtc gtg cag gtc ggc gcc 336
 Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 ggc ggc gta gaa aac gca gtg gca tac gcc ctg gtc acc cac ggt gtg 384
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125

cag aaa ctt cag gtc gct gac ctc gac act tcc cgc gcg cag gca ctg 432
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 gca gat gtc atc aac aac gca gtc ggc cgt gaa gcc gtc gtg gga gta 480
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 gac gcc cgc ggc atc gaa gac gtc atc gcc gcc gcc gac gga gta gtc 528
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 aac gca acc ccc atg gga atg cca gca cac ccc ggc acc gcc ttt gat 576
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 gtc agc tgc ctc acc aag gat cac tgg gtt ggc gac gtc gtg tac atg 624
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 ccc atc gaa act gaa ctt ctc aaa gcc gcc cgt gcc ctc ggc tgc gaa 672
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 acc ctc gac gga acc cgc atg gca atc cac caa gcc gtc gat gcc ttc 720
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 cga ctg ttc acc ggc ctc gaa ccc gac gtc tcc cgc atg cgg gaa act 768
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 ttc ctg tcc ctc taaaagagtc agtaaacct cga 803
 Phe Leu Ser Leu
 260

<210> 436

<211> 260

<212> PRT

<213> Corynebacterium glutamicum

<400> 436

Glu Ala Lys Gly Leu Ala Gln Gly Arg Ala Thr Val Tyr Arg Arg Ile
 1 5 10 15
 Asp Thr Leu Gly Ser Arg Ala Ser Gly Gln Asp Leu Asn Thr Leu Leu
 20 25 30
 Asp Ala Ala Leu Tyr Leu Gly Phe Ser Gly Leu Asn Ile Thr His Pro
 35 40 45
 Tyr Lys Gln Ala Val Leu Pro Leu Leu Gly Glu Val Ser Glu Gln Ala
 50 55 60
 Thr Gln Leu Gly Ala Val Asn Thr Val Val Met Asp Ala Thr Gly His
 65 70 75 80
 Thr Thr Gly His Asn Thr Asp Val Ser Gly Phe Gly Arg Gly Met Glu
 85 90 95

Glu Gly Leu Pro Asn Ala Lys Leu Asp Ser Val Val Gln Val Gly Ala
 100 105 110
 Gly Gly Val Glu Asn Ala Val Ala Tyr Ala Leu Val Thr His Gly Val
 115 120 125
 Gln Lys Leu Gln Val Ala Asp Leu Asp Thr Ser Arg Ala Gln Ala Leu
 130 135 140
 Ala Asp Val Ile Asn Asn Ala Val Gly Arg Glu Ala Val Val Gly Val
 145 150 155 160
 Asp Ala Arg Gly Ile Glu Asp Val Ile Ala Ala Ala Asp Gly Val Val
 165 170 175
 Asn Ala Thr Pro Met Gly Met Pro Ala His Pro Gly Thr Ala Phe Asp
 180 185 190
 Val Ser Cys Leu Thr Lys Asp His Trp Val Gly Asp Val Val Tyr Met
 195 200 205
 Pro Ile Glu Thr Glu Leu Leu Lys Ala Ala Arg Ala Leu Gly Cys Glu
 210 215 220
 Thr Leu Asp Gly Thr Arg Met Ala Ile His Gln Ala Val Asp Ala Phe
 225 230 235 240
 Arg Leu Phe Thr Gly Leu Glu Pro Asp Val Ser Arg Met Arg Glu Thr
 245 250 255
 Phe Leu Ser Leu
 260

<210> 437
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA02093

<400> 437
 ggcaggaatt tcccgaaaac ttccaccaat aatcaagcca tatcccacac aatcaggcat 60
 ttgtctttcc tttgtctcgc atgagtataa aatcactgtc atg gtc aac tac gtc 115
 Met Val Asn Tyr Val 5
 gac agg gaa aca acc ctg tgc atc tct ctc gct gct cgt cca tcc aac 163
 Asp Arg Glu Thr Leu Cys Ile Ser Leu Ala Ala Arg Pro Ser Asn
 10 15 20
 cat ggt gtt cgt ttc cac aac tgg ctt tac gct gaa ctt gga ttg aac 211
 His Gly Val Arg Phe His Asn Trp Leu Tyr Ala Glu Leu Gly Leu Asn
 25 30 35
 tac ctg tac aag gct gtt gcc cca gca gat atc acc gct gca gtc gca 259

Tyr	Leu	Tyr	Lys	Ala	Val	Ala	Pro	Ala	Asp	Ile	Thr	Ala	Ala	Val	Ala		
	40						45					50					
ggt	atc	cgt	ggt	ctg	aac	att	cgc	ggc	gca	ggt	gtc	tcc	atg	cca	tac	307	
Gly	Ile	Arg	Gly	Leu	Asn	Ile	Arg	Gly	Ala	Gly	Val	Ser	Met	Pro	Tyr		
	55					60					65						
aag	agc	gat	gtc	atc	cca	ctc	atc	gat	gag	ttg	cat	cct	tcc	gca	gag	355	
Lys	Ser	Asp	Val	Ile	Pro	Leu	Ile	Asp	Glu	Leu	His	Pro	Ser	Ala	Glu		
	70				75				80					85			
cgc	ata	cgt	tct	gtt	aac	acc	atc	gtc	aac	aat	gac	gga	cac	ctt	gtc	403	
Arg	Ile	Arg	Ser	Val	Asn	Thr	Ile	Val	Asn	Asn	Asp	Gly	His	Leu	Val		
				90					95					100			
gga	tac	aac	acc	gac	tac	act	gcg	gtg	tac	cac	ctc	ctt	gaa	gaa	cac	451	
Gly	Tyr	Asn	Thr	Asp	Tyr	Thr	Ala	Val	Tyr	His	Leu	Leu	Glu	Glu	His		
			105					110					115				
cgc	gtg	aac	ccc	aat	gca	cga	gta	gct	atc	aag	gga	tcc	ggc	ggc	atg	499	
Arg	Val	Asn	Pro	Asn	Ala	Arg	Val	Ala	Ile	Lys	Gly	Ser	Gly	Gly	Met		
		120					125					130					
gcc	aat	gct	gtt	gtt	gca	gct	ctt	gct	gag	tat	ggt	ctg	agt	ggc	acc	547	
Ala	Asn	Ala	Val	Val	Ala	Ala	Leu	Ala	Glu	Tyr	Gly	Leu	Ser	Gly	Thr		
	135					140					145						
gtc	gtt	gcc	cgc	aac	cac	acc	acc	ggt	tct	gcg	cta	gct	tcc	cgt	tac	595	
Val	Val	Ala	Arg	Asn	His	Thr	Thr	Gly	Ser	Ala	Leu	Ala	Ser	Arg	Tyr		
	150				155					160					165		
ggt	tgg	gaa	tac	tcc	gca	act	gtt	ccg	gaa	gac	gca	aaa	att	ttg	gtt	643	
Gly	Trp	Glu	Tyr	Ser	Ala	Thr	Val	Pro	Glu	Asp	Ala	Lys	Ile	Leu	Val		
				170					175					180			
aat	gta	acc	cca	atg	gga	atg	aat	gga	cct	gac	caa	gac	gtt	gta	tct	691	
Asn	Val	Thr	Pro	Met	Gly	Met	Asn	Gly	Pro	Asp	Gln	Asp	Val	Val	Ser		
			185					190					195				
ttt	ggt	gag	gat	gaa	gta	gac	cga	gcc	gac	gta	atc	ttt	gac	tgc	gta	739	
Phe	Gly	Glu	Asp	Glu	Val	Asp	Arg	Ala	Asp	Val	Ile	Phe	Asp	Cys	Val		
		200					205					210					
gca	ttc	ccc	gtc	gag	acc	cca	ctg	att	aag	ttg	gcc	aag	gaa	aag	ggt	787	
Ala	Phe	Pro	Val	Glu	Thr	Pro	Leu	Ile	Lys	Leu	Ala	Lys	Glu	Lys	Gly		
	215					220					225						
aag	caa	acc	atc	gac	ggc	gga	gaa	gtt	gcc	gct	ctt	cag	gca	gca	gag	835	
Lys	Gln	Thr	Ile	Asp	Gly	Gly	Glu	Val	Ala	Ala	Leu	Gln	Ala	Ala	Glu		
	230				235				240					245			
cag	ttc	cac	ctc	tac	acc	gga	gtt	ctt	cca	acc	aac	gac	cag	atc	att	883	
Gln	Phe	His	Leu	Tyr	Thr	Gly	Val	Leu	Pro	Thr	Asn	Asp	Gln	Ile	Ile		
				250				255						260			
gct	gcg	gag	gag	ttc	tcc	aag	taaattttctc	tcccctattt	tta							927	
Ala	Ala	Glu	Glu	Phe	Ser	Lys											
				265													

<210> 438

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 438

```

Met Val Asn Tyr Val Asp Arg Glu Thr Thr Leu Cys Ile Ser Leu Ala
  1              5              10              15

Ala Arg Pro Ser Asn His Gly Val Arg Phe His Asn Trp Leu Tyr Ala
      20              25              30

Glu Leu Gly Leu Asn Tyr Leu Tyr Lys Ala Val Ala Pro Ala Asp Ile
    35              40              45

Thr Ala Ala Val Ala Gly Ile Arg Gly Leu Asn Ile Arg Gly Ala Gly
    50              55              60

Val Ser Met Pro Tyr Lys Ser Asp Val Ile Pro Leu Ile Asp Glu Leu
    65              70              75              80

His Pro Ser Ala Glu Arg Ile Arg Ser Val Asn Thr Ile Val Asn Asn
      85              90              95

Asp Gly His Leu Val Gly Tyr Asn Thr Asp Tyr Thr Ala Val Tyr His
    100              105              110

Leu Leu Glu Glu His Arg Val Asn Pro Asn Ala Arg Val Ala Ile Lys
    115              120              125

Gly Ser Gly Gly Met Ala Asn Ala Val Val Ala Ala Leu Ala Glu Tyr
    130              135              140

Gly Leu Ser Gly Thr Val Val Ala Arg Asn His Thr Thr Gly Ser Ala
    145              150              155              160

Leu Ala Ser Arg Tyr Gly Trp Glu Tyr Ser Ala Thr Val Pro Glu Asp
      165              170              175

Ala Lys Ile Leu Val Asn Val Thr Pro Met Gly Met Asn Gly Pro Asp
    180              185              190

Gln Asp Val Val Ser Phe Gly Glu Asp Glu Val Asp Arg Ala Asp Val
    195              200              205

Ile Phe Asp Cys Val Ala Phe Pro Val Glu Thr Pro Leu Ile Lys Leu
    210              215              220

Ala Lys Glu Lys Gly Lys Gln Thr Ile Asp Gly Gly Glu Val Ala Ala
    225              230              235              240

Leu Gln Ala Ala Glu Gln Phe His Leu Tyr Thr Gly Val Leu Pro Thr
    245              250              255

Asn Asp Gln Ile Ile Ala Ala Glu Glu Phe Ser Lys
    260              265

```

<210> 439

<211> 951

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(928)

<223> RXA02791

<400> 439

```

accgtgttca acgacacctt cgaagagcac gaagccgaca ttgagcaagc tttgaacagt 60

ggcgttctag acagcaaccg ataaggatca gcgaataaaa ttg ggt tct cac atc 115
                                   Leu Gly Ser His Ile
                                   1 5

act cac cgg gcg gcc gta ctc ggc tca ccc atc gag cat tcc aaa tcc 163
Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile Glu His Ser Lys Ser
                                   10 15 20

cca gtc ctc cac aac acc ggc tat aaa gcc ctc gga ctg gac caa tgg 211
Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu Gly Leu Asp Gln Trp
                                   25 30 35

gaa tac gac cgc ttt gag tgc acc ggc gac atg ctc ccc ggc atc gtc 259
Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met Leu Pro Gly Ile Val
                                   40 45 50

tcc ggc gct gat gaa acc tac tgc gga ttc tcc gtc acc atg ccg tct 307
Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser Val Thr Met Pro Ser
                                   55 60 65

aaa ttc gca gct ctt gaa ttc gcc gac gaa gta acc gaa cgc gcc tgc 355
Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val Thr Glu Arg Ala Cys
                                   70 75 80 85

gcc atc ggc tcc gca aac acc ttg ctg cgc acg gcc acc gga tgg cgc 403
Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr Ala Thr Gly Trp Arg
                                   90 95 100

gcc gac aac acc gac gtc gac ggc atc agg gga gct ctc ggt gaa ctc 451
Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly Ala Leu Gly Glu Leu
                                   105 110 115

ctc ggc ggc gca tca ctg gcc ggc aaa cac gcc atc gtc atc ggc tcc 499
Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala Ile Val Ile Gly Ser
                                   120 125 130

ggc ggc acc gca cgc ccc gcc atc tgg gca ctc atc gaa gcc ggg gtc 547
Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu Ile Glu Ala Gly Val
                                   135 140 145

gcc cgg atc acg gtg ctc aac cgc tcc gat cgc acc gcc gaa ctg caa 595
Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg Thr Ala Glu Leu Gln
                                   150 155 160 165

acg ctt ttc gac gaa acc ccc acc acc ttg gcc tac gcc ccg ctc gag 643
Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala Tyr Ala Pro Leu Glu
                                   170 175 180

cat ctc cac atc gaa gcc gac gtc gta gtc tct aca gtg ccc tcc gca 691
His Leu His Ile Glu Ala Asp Val Val Val Ser Thr Val Pro Ser Ala
                                   185 190 195

```

gca atc gca ggc ctc gaa gac acc ctt gcg atc gcc cca gtc ctc gac 739
 Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile Ala Pro Val Leu Asp
 200 205 210

 gtc atc tac gac ccc tgg cca aca cca ctc gta gaa gtc aca cga gcc 787
 Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val Glu Val Thr Arg Ala
 215 220 225

 aaa ggc ctc aaa gct gtc gga ggc cac gtc atg ctg gca cac cag tcc 835
 Lys Gly Leu Lys Ala Val Gly Gly His Val Met Leu Ala His Gln Ser
 230 235 240 245

 tac gga cag ttt gaa caa ttc acc gga atg gat gca ccc cgc gat gcc 883
 Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp Ala Pro Arg Asp Ala
 250 255 260

 atg cgt gag gct ttg gaa gag tct tta ggc atc tca gaa gaa cac 928
 Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile Ser Glu Glu His
 265 270 275

 taagtccccg ccacctctc aac 951

<210> 440
 <211> 276
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 440
 Leu Gly Ser His Ile Thr His Arg Ala Ala Val Leu Gly Ser Pro Ile
 1 5 10 15

 Glu His Ser Lys Ser Pro Val Leu His Asn Thr Gly Tyr Lys Ala Leu
 20 25 30

 Gly Leu Asp Gln Trp Glu Tyr Asp Arg Phe Glu Cys Thr Gly Asp Met
 35 40 45

 Leu Pro Gly Ile Val Ser Gly Ala Asp Glu Thr Tyr Cys Gly Phe Ser
 50 55 60

 Val Thr Met Pro Ser Lys Phe Ala Ala Leu Glu Phe Ala Asp Glu Val
 65 70 75 80

 Thr Glu Arg Ala Cys Ala Ile Gly Ser Ala Asn Thr Leu Leu Arg Thr
 85 90 95

 Ala Thr Gly Trp Arg Ala Asp Asn Thr Asp Val Asp Gly Ile Arg Gly
 100 105 110

 Ala Leu Gly Glu Leu Leu Gly Gly Ala Ser Leu Ala Gly Lys His Ala
 115 120 125

 Ile Val Ile Gly Ser Gly Gly Thr Ala Arg Pro Ala Ile Trp Ala Leu
 130 135 140

 Ile Glu Ala Gly Val Ala Arg Ile Thr Val Leu Asn Arg Ser Asp Arg
 145 150 155 160

 Thr Ala Glu Leu Gln Thr Leu Phe Asp Glu Thr Pro Thr Thr Leu Ala
 165 170 175

Tyr Ala Pro Leu Glu His Leu His Ile Glu Ala Asp Val Val Val Ser
 180 185 190
 Thr Val Pro Ser Ala Ala Ile Ala Gly Leu Glu Asp Thr Leu Ala Ile
 195 200 205
 Ala Pro Val Leu Asp Val Ile Tyr Asp Pro Trp Pro Thr Pro Leu Val
 210 215 220
 Glu Val Thr Arg Ala Lys Gly Leu Lys Ala Val Gly Gly His Val Met
 225 230 235 240
 Leu Ala His Gln Ser Tyr Gly Gln Phe Glu Gln Phe Thr Gly Met Asp
 245 250 255
 Ala Pro Arg Asp Ala Met Arg Glu Ala Leu Glu Glu Ser Leu Gly Ile
 260 265 270
 Ser Glu Glu His
 275

<210> 441
 <211> 693
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(670)
 <223> RXA01699

<400> 441
 ctgcagaaat tcggcgggtga ctccctgagc gaaaccaaga gcaacattga cacctacctc 60
 aaaaacattg aggaacgaat gaaattcgaa ggttttagagg atg gag cgt aat gaa 115
 Met Glu Arg Asn Glu
 1 5
 gtg aat gat caa att cac tta gat cat caa tca gat gac acc tct gaa 163
 Val Asn Asp Gln Ile His Leu Asp His Gln Ser Asp Asp Thr Ser Glu
 10 15 20
 tgc tcc tgc ccg atc gtg gtt ctt gtg ggt ttg cca gga gct gga aaa 211
 Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu Pro Gly Ala Gly Lys
 25 30 35
 tcc acc att gga cgt cga tta gcg cgc gcc tta aac act gaa ctc gtc 259
 Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu Asn Thr Glu Leu Val
 40 45 50
 gac tcc gac gaa ctg att gag cgc gcc acc gga aaa gcc tgt ggc gcc 307
 Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly Lys Ala Cys Gly Ala
 55 60 65
 gtg ttc agc gag ctc ggc gag cca gcc ttc cgc gag ctc gag gcc atc 355
 Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg Glu Leu Glu Ala Ile
 70 75 80 85
 cac gtg gcc gaa gca ctg aaa tcc tcc gga gtg gtg agc ttg gga ggc 403

His Val Ala Glu Ala Leu Lys Ser Ser Gly Val Val Ser Leu Gly Gly
 90 95 100

 gga tct gtg ctg aca gaa tcc acc cgt gaa ctg ctc aaa ggc cag gac 451
 Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu Leu Lys Gly Gln Asp
 105 110 115

 gtg gtc tgg atc gac gtg cca gta gaa gaa ggc atc agg cgc acc gca 499
 Val Val Trp Ile Asp Val Pro Val Glu Glu Gly Ile Arg Arg Thr Ala
 120 125 130

 aac gag cgt tcc cgc ccc gtg ctg caa gcc gcc gac ccc gcc gag cac 547
 Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala Asp Pro Ala Glu His
 135 140 145

 tac cgc aac ctg gtg aaa gtg cgc acc ccg ttg tac gaa gag gtg gca 595
 Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu Tyr Glu Glu Val Ala
 150 155 160 165

 acc tac cga ctt cgc acc aac aac cgc agc ccc cag caa gtg gtg gca 643
 Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro Gln Gln Val Val Ala
 170 175 180

 gca gtg ttg cat cat cta gaa atc gat taattaaacc gggcacctga 690
 Ala Val Leu His His Leu Glu Ile Asp
 185 190

 tta 693

<210> 442

<211> 190

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 442

Met Glu Arg Asn Glu Val Asn Asp Gln Ile His Leu Asp His Gln Ser
 1 5 10 15

 Asp Asp Thr Ser Glu Cys Ser Cys Pro Ile Val Val Leu Val Gly Leu
 20 25 30

 Pro Gly Ala Gly Lys Ser Thr Ile Gly Arg Arg Leu Ala Arg Ala Leu
 35 40 45

 Asn Thr Glu Leu Val Asp Ser Asp Glu Leu Ile Glu Arg Ala Thr Gly
 50 55 60

 Lys Ala Cys Gly Ala Val Phe Ser Glu Leu Gly Glu Pro Ala Phe Arg
 65 70 75 80

 Glu Leu Glu Ala Ile His Val Ala Glu Ala Leu Lys Ser Ser Gly Val
 85 90 95

 Val Ser Leu Gly Gly Gly Ser Val Leu Thr Glu Ser Thr Arg Glu Leu
 100 105 110

 Leu Lys Gly Gln Asp Val Val Trp Ile Asp Val Pro Val Glu Glu Gly
 115 120 125

 Ile Arg Arg Thr Ala Asn Glu Arg Ser Arg Pro Val Leu Gln Ala Ala

130	135	140	
Asp Pro Ala Glu His Tyr Arg Asn Leu Val Lys Val Arg Thr Pro Leu 145 150 155 160			
Tyr Glu Glu Val Ala Thr Tyr Arg Leu Arg Thr Asn Asn Arg Ser Pro 165 170 175			
Gln Gln Val Val Ala Ala Val Leu His His Leu Glu Ile Asp 180 185 190			
<210> 443			
<211> 959			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (97)..(936)			
<223> RXA00952			
<400> 443			
catcctcgtc tccctatccg gccgtggcga caaggacgtt gaccacgtgc gccgcaccct 60			
cgaagaaaat ccagaactga tcctgaagga caaccgatg agc cgt tac gac gat 114			
		Met Ser Arg Tyr Asp Asp	
		1 5	
ctt ttt gca cgc ctc gac acg gca ggg gag ggc gcc ttt gtt ccc ttc 162			
Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu Gly Ala Phe Val Pro Phe			
	10	15	20
atc atg ctg agc gac cct tca cca gag gag gct ttc cag atc atc tcc 210			
Ile Met Leu Ser Asp Pro Ser Pro Glu Glu Ala Phe Gln Ile Ile Ser			
	25	30	35
aca gca atc gaa gct ggc gca gat gca ctg gaa ctt ggc gta cct ttc 258			
Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu Glu Leu Gly Val Pro Phe			
	40	45	50
tcc gac cca gtt gcc gat ggc ccc acc gtc gcg gaa tcc cac ctc cgc 306			
Ser Asp Pro Val Ala Asp Gly Pro Thr Val Ala Glu Ser His Leu Arg			
	55	60	70
gca ctc gac ggc ggc gcc acc gta gac agc gca ctc gag cag atc aag 354			
Ala Leu Asp Gly Gly Ala Thr Val Asp Ser Ala Leu Glu Gln Ile Lys			
	75	80	85
cgc gtg cgc gca gcc tac cca gag gtt ccc atc gga atg ctc atc tac 402			
Arg Val Arg Ala Ala Tyr Pro Glu Val Pro Ile Gly Met Leu Ile Tyr			
	90	95	100
ggc aac gtt cct ttc acc cgt ggc ttg gat cgc ttc tac caa gag ttc 450			
Gly Asn Val Pro Phe Thr Arg Gly Leu Asp Arg Phe Tyr Gln Glu Phe			
	105	110	115
gct gaa gct ggc gca gac tcc atc ctc ctg cca gac gtc cca gtc cga 498			
Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu Pro Asp Val Pro Val Arg			
	120	125	130

gaa ggc gca ccg ttt tct gca gca gct gca gca gcc gga att gat ccc 546
 Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala Ala Gly Ile Asp Pro
 135 140 145 150

 att tac atc gct ccg gcc aac gcc agc gag aaa acc ctc gag ggt gtc 594
 Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu Lys Thr Leu Glu Gly Val
 155 160 165

 tcc gcc gca tca aag ggc tac atc tac gcc atc tcc cgc gac ggc gtc 642
 Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala Ile Ser Arg Asp Gly Val
 170 175 180

 acc ggc acc gaa cgt gaa tca tcc acc gac ggc ctg tcc gca gtg gtg 690
 Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp Gly Leu Ser Ala Val Val
 185 190 195

 gac aac atc aag aaa ttt gat ggc gca ccc atc ctc ttg ggc ttc ggc 738
 Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro Ile Leu Leu Gly Phe Gly
 200 205 210

 atc tca tcc cct cag cac gtg gca gac gcg att gca gcg ggt gct tcc 786
 Ile Ser Ser Pro Gln His Val Ala Asp Ala Ile Ala Ala Gly Ala Ser
 215 220 225 230

 ggt gcg atc acg ggt tcc gcg atc acc aag atc att gct tcc cac tgc 834
 Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys Ile Ile Ala Ser His Cys
 235 240 245

 gaa ggt gag cac ccg aac ccg tcc acc att cga gat atg gac ggt ttg 882
 Glu Gly Glu His Pro Asn Pro Ser Thr Ile Arg Asp Met Asp Gly Leu
 250 255 260

 aag aag gat ctc act gag ttc atc tct gcg atg aag gca gcg acc aag 930
 Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala Met Lys Ala Ala Thr Lys
 265 270 275

 aag gtt taggccttta aatgtggcaa tgt 959
 Lys Val
 280

<210> 444

<211> 280

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Met Ser Arg Tyr Asp Asp Leu Phe Ala Arg Leu Asp Thr Ala Gly Glu
 1 5 10 15

 Gly Ala Phe Val Pro Phe Ile Met Leu Ser Asp Pro Ser Pro Glu Glu
 20 25 30

 Ala Phe Gln Ile Ile Ser Thr Ala Ile Glu Ala Gly Ala Asp Ala Leu
 35 40 45

 Glu Leu Gly Val Pro Phe Ser Asp Pro Val Ala Asp Gly Pro Thr Val
 50 55 60

 Ala Glu Ser His Leu Arg Ala Leu Asp Gly Gly Ala Thr Val Asp Ser
 65 70 75 80

Ala Leu Glu Gln Ile Lys Arg Val Arg Ala Ala Tyr Pro Glu Val Pro
85 90 95

Ile Gly Met Leu Ile Tyr Gly Asn Val Pro Phe Thr Arg Gly Leu Asp
100 105 110

Arg Phe Tyr Gln Glu Phe Ala Glu Ala Gly Ala Asp Ser Ile Leu Leu
115 120 125

Pro Asp Val Pro Val Arg Glu Gly Ala Pro Phe Ser Ala Ala Ala Ala
130 135 140

Ala Ala Gly Ile Asp Pro Ile Tyr Ile Ala Pro Ala Asn Ala Ser Glu
145 150 155 160

Lys Thr Leu Glu Gly Val Ser Ala Ala Ser Lys Gly Tyr Ile Tyr Ala
165 170 175

Ile Ser Arg Asp Gly Val Thr Gly Thr Glu Arg Glu Ser Ser Thr Asp
180 185 190

Gly Leu Ser Ala Val Val Asp Asn Ile Lys Lys Phe Asp Gly Ala Pro
195 200 205

Ile Leu Leu Gly Phe Gly Ile Ser Ser Pro Gln His Val Ala Asp Ala
210 215 220

Ile Ala Ala Gly Ala Ser Gly Ala Ile Thr Gly Ser Ala Ile Thr Lys
225 230 235 240

Ile Ile Ala Ser His Cys Glu Gly Glu His Pro Asn Pro Ser Thr Ile
245 250 255

Arg Asp Met Asp Gly Leu Lys Lys Asp Leu Thr Glu Phe Ile Ser Ala
260 265 270

Met Lys Ala Ala Thr Lys Lys Val
275 280

<210> 445
<211> 1237
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1237)
<223> RXN00956

<400> 445
gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaagggttt aaataggatc atg act gaa aaa gaa 115
Met Thr Glu Lys Glu
1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag	211
Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu	
25 30 35	
aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc	259
Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu	
40 45 50	
ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa	307
Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu	
55 60 65	
tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc	355
Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile	
70 75 80 85	
ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac	403
Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn	
90 95 100	
cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc	451
Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg	
105 110 115	
atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc	499
Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu	
120 125 130	
gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag	547
Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys	
135 140 145	
gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc	595
Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly	
150 155 160 165	
gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc	643
Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala	
170 175 180	
gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac	691
Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His	
185 190 195	
tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg	739
Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val	
200 205 210	
cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta	787
Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu	
215 220 225	
gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt	835
Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly	
230 235 240 245	
ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt	883
Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly	
250 255 260	

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc ggc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac ggc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc gaa gta
 1237
 Ala Lys Thr Ala Glu Val
 375

<210> 446

<211> 379

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 446

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
 1 5 10 15

Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
 20 25 30

Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45

Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60

Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80

Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly

				85				90				95				
Ala	His	Lys	Thr	Asn	Gln	Val	Ile	Gly	Gln	Val	Leu	Leu	Ala	Lys	Arg	
100								105				110				
Met	Gly	Lys	Thr	Arg	Ile	Ile	Ala	Glu	Thr	Gly	Ala	Gly	Gln	His	Gly	
115								120				125				
Thr	Ala	Thr	Ala	Leu	Ala	Cys	Ala	Leu	Met	Gly	Leu	Glu	Cys	Val	Val	
130								135				140				
Tyr	Met	Gly	Ala	Lys	Asp	Val	Ala	Arg	Gln	Gln	Pro	Asn	Val	Tyr	Arg	
145												155				
Met	Gln	Leu	His	Gly	Ala	Lys	Val	Ile	Pro	Val	Glu	Ser	Gly	Ser	Gly	
				165								175				
Thr	Leu	Lys	Asp	Ala	Val	Asn	Glu	Ala	Leu	Arg	Asp	Trp	Thr	Ala	Thr	
				180								185				
Phe	His	Glu	Ser	His	Tyr	Leu	Leu	Gly	Thr	Pro	Ala	Gly	Pro	His	Pro	
195								200				205				
Phe	Pro	Thr	Ile	Val	Arg	Glu	Phe	His	Lys	Val	Ile	Ser	Glu	Glu	Ala	
210								215				220				
Lys	Ala	Gln	Met	Leu	Glu	Arg	Thr	Gly	Lys	Leu	Pro	Asp	Val	Val	Val	
				230								235				
Ala	Cys	Val	Gly	Gly	Gly	Ser	Asn	Ala	Ile	Gly	Met	Phe	Ala	Asp	Phe	
				245								250				
Ile	Asp	Asp	Glu	Gly	Val	Glu	Leu	Val	Gly	Ala	Glu	Pro	Ala	Gly	Glu	
				260								265				
Gly	Leu	Asp	Ser	Gly	Lys	His	Gly	Ala	Thr	Ile	Thr	Asn	Gly	Gln	Ile	
				275								280				
Gly	Ile	Leu	His	Gly	Thr	Arg	Ser	Tyr	Leu	Met	Arg	Asn	Ser	Asp	Gly	
290								295				300				
Gln	Val	Glu	Glu	Ser	Tyr	Ser	Ile	Ser	Ala	Gly	Leu	Asp	Tyr	Pro	Gly	
305								310				315				
Val	Gly	Pro	Gln	His	Ala	His	Leu	His	Ala	Thr	Gly	Arg	Ala	Thr	Tyr	
				325								330				
Val	Gly	Ile	Thr	Asp	Ala	Glu	Ala	Leu	Gln	Ala	Phe	Gln	Tyr	Leu	Ala	
				340								345				
Arg	Tyr	Glu	Gly	Ile	Ile	Pro	Ala	Leu	Glu	Ser	Ser	His	Ala	Phe	Ala	
355								360				365				
Tyr	Ala	Leu	Lys	Arg	Ala	Lys	Thr	Ala	Glu	Val						
370								375								

```
<210> 447
<211> 1231
<212> DNA
<213> Corynebacterium glutamicum
```


<220>

<221> CDS

<222> (101)..(1231)

<223> FRXA00956

<400> 447

gccggtgcag gcacgtgggc tggggcgaaa gacgccggcg cgctgctgaa aatttttagcg 60

accatctcca cattccatta ctaaaggttt aaataggatc atg act gaa aaa gaa 115
 Met Thr Glu Lys Glu
 1 5

aac ttg ggc ggc tcc acg ctg ctg cct gca tac ttc ggt gaa ttc ggc 163
 Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr Phe Gly Glu Phe Gly
 10 15 20

ggc cag ttc gtc gcg gaa tcc ctc ctg cct gct ctc gac cag ctg gag 211
 Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala Leu Asp Gln Leu Glu
 25 30 35

aag gcc ttc gtt gac gcg acc aac agc cca gag ttc cgc gaa gaa ctc 259
 Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu Phe Arg Glu Glu Leu
 40 45 50

ggc ggc tac ctc cgc gat tac ctc ggc cgc cca acc ccg ctg acc gaa 307
 Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro Thr Pro Leu Thr Glu
 55 60 65

tgc tcc aac ctg cca ctc gca ggc gaa ggc aaa ggc ttt gcg cgg atc 355
 Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys Gly Phe Ala Arg Ile
 70 75 80 85

ttc ctc aag cgc gaa gac ctc gtc cac ggc ggt gca cac aaa act aac 403
 Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly Ala His Lys Thr Asn
 90 95 100

cag gtg atc ggc cag gtg ctg ctt gcc aag cgc atg ggc aaa acc cgc 451
 Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg Met Gly Lys Thr Arg
 105 110 115

atc atc gca gag acc ggc gca ggc cag cac ggc acc gcc acc gct ctc 499
 Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly Thr Ala Thr Ala Leu
 120 125 130

gca tgt gcg ctc atg ggc ctc gag tgc gtt gtc tac atg ggc gcc aag 547
 Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val Tyr Met Gly Ala Lys
 135 140 145

gac gtt gcc cgc cag cag ccc aac gtc tac cgc atg cag ctg cac ggc 595
 Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg Met Gln Leu His Gly
 150 155 160 165

gcg aag gtc atc ccc gtg gaa tct ggt tcc ggc acc ctg aag gac gcc 643
 Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly Thr Leu Lys Asp Ala
 170 175 180

gtg aat gaa gcg ctg cgc gat tgg acc gca acc ttc cac gag tcc cac 691
 Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr Phe His Glu Ser His
 185 190 195

tac ctt ctc ggc acc ccc gcc ggc ccg cac cca ttc cca acc atc gtg 739
 Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro Phe Pro Thr Ile Val
 200 205 210

cgt gaa ttc cac aag gtg atc tct gag gaa gcc aag gca cag atg cta 787
 Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala Lys Ala Gln Met Leu
 215 220 225

gag cgc acc ggc aag ctt ccc gac gtt gtg gtc gcc tgt gtc ggt ggt 835
 Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val Ala Cys Val Gly Gly
 230 235 240 245

ggc tcc aac gcc atc ggc atg ttc gca gac ttc att gac gat gaa ggt 883
 Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe Ile Asp Asp Glu Gly
 250 255 260

gta gag ctc gtc ggc gct gag cca gcc ggt gaa ggc ctc gac tcc gcc 931
 Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu Gly Leu Asp Ser Gly
 265 270 275

aag cac ggc gca acc atc acc aac ggt cag atc ggc atc ctg cac gcc 979
 Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile Gly Ile Leu His Gly
 280 285 290

acc cgt tcc tac ctg atg cgc aac tcc gac ggc caa gtg gaa gag tcc
 1027
 Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly Gln Val Glu Glu Ser
 295 300 305

tac tcc atc tcc gcc gga ctt gat tac cca ggc gtc ggc cca cag cac
 1075
 Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly Val Gly Pro Gln His
 310 315 320 325

gca cac ctg cac gcc acc ggc cgc gcc acc tac gtt ggt atc acc gac
 1123
 Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr Val Gly Ile Thr Asp
 330 335 340

gcc gaa gcc ctc caa gca ttc cag tac ctc gcc cgc tac gaa ggc atc
 1171
 Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala Arg Tyr Glu Gly Ile
 345 350 355

atc ccc gca ctg gaa tcc tca cac gcg ttc gcc tac gca ctc aag cgc
 1219
 Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala Tyr Ala Leu Lys Arg
 360 365 370

gcc aag acc gcc
 1231
 Ala Lys Thr Ala
 375

<210> 448

<211> 377

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

Met Thr Glu Lys Glu Asn Leu Gly Gly Ser Thr Leu Leu Pro Ala Tyr
 1 5 10 15
 Phe Gly Glu Phe Gly Gly Gln Phe Val Ala Glu Ser Leu Leu Pro Ala
 20 25 30
 Leu Asp Gln Leu Glu Lys Ala Phe Val Asp Ala Thr Asn Ser Pro Glu
 35 40 45
 Phe Arg Glu Glu Leu Gly Gly Tyr Leu Arg Asp Tyr Leu Gly Arg Pro
 50 55 60
 Thr Pro Leu Thr Glu Cys Ser Asn Leu Pro Leu Ala Gly Glu Gly Lys
 65 70 75 80
 Gly Phe Ala Arg Ile Phe Leu Lys Arg Glu Asp Leu Val His Gly Gly
 85 90 95
 Ala His Lys Thr Asn Gln Val Ile Gly Gln Val Leu Leu Ala Lys Arg
 100 105 110
 Met Gly Lys Thr Arg Ile Ile Ala Glu Thr Gly Ala Gly Gln His Gly
 115 120 125
 Thr Ala Thr Ala Leu Ala Cys Ala Leu Met Gly Leu Glu Cys Val Val
 130 135 140
 Tyr Met Gly Ala Lys Asp Val Ala Arg Gln Gln Pro Asn Val Tyr Arg
 145 150 155 160
 Met Gln Leu His Gly Ala Lys Val Ile Pro Val Glu Ser Gly Ser Gly
 165 170 175
 Thr Leu Lys Asp Ala Val Asn Glu Ala Leu Arg Asp Trp Thr Ala Thr
 180 185 190
 Phe His Glu Ser His Tyr Leu Leu Gly Thr Pro Ala Gly Pro His Pro
 195 200 205
 Phe Pro Thr Ile Val Arg Glu Phe His Lys Val Ile Ser Glu Glu Ala
 210 215 220
 Lys Ala Gln Met Leu Glu Arg Thr Gly Lys Leu Pro Asp Val Val Val
 225 230 235 240
 Ala Cys Val Gly Gly Gly Ser Asn Ala Ile Gly Met Phe Ala Asp Phe
 245 250 255
 Ile Asp Asp Glu Gly Val Glu Leu Val Gly Ala Glu Pro Ala Gly Glu
 260 265 270
 Gly Leu Asp Ser Gly Lys His Gly Ala Thr Ile Thr Asn Gly Gln Ile
 275 280 285
 Gly Ile Leu His Gly Thr Arg Ser Tyr Leu Met Arg Asn Ser Asp Gly
 290 295 300
 Gln Val Glu Glu Ser Tyr Ser Ile Ser Ala Gly Leu Asp Tyr Pro Gly
 305 310 315 320
 Val Gly Pro Gln His Ala His Leu His Ala Thr Gly Arg Ala Thr Tyr

325	330	335	
Val Gly Ile Thr Asp Ala Glu Ala Leu Gln Ala Phe Gln Tyr Leu Ala			
340	345	350	
Arg Tyr Glu Gly Ile Ile Pro Ala Leu Glu Ser Ser His Ala Phe Ala			
355	360	365	
Tyr Ala Leu Lys Arg Ala Lys Thr Ala			
370	375		
<210> 449			
<211> 1401			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(1378)			
<223> RXA00064			
<400> 449			
tcccctaataaa cgtctagagt agtggcttga ggtcactgct ctttttttgt gccctttttt 60 ggctcgtcta ttttgcacc acatgcggag gtacgcagtt atg agt tca gtt tcg 115 <div style="display: flex; justify-content: space-between; width: 100%;"> Met Ser Ser Val Ser 1 5 </div>			
ctg cag gat ttt gat gca gag cga att ggt ttg ttc cac gag gac att 163 Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu Phe His Glu Asp Ile <div style="display: flex; justify-content: space-between; width: 100%;"> 10 15 20 </div>			
aag cgc aag ttt gat gag ctc aag tca aaa aat ctg aag ctg gat ctt 211 Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn Leu Lys Leu Asp Leu <div style="display: flex; justify-content: space-between; width: 100%;"> 25 30 35 </div>			
act cgc ggt aag cct tcg tcg gag cag ttg gat ttc gct gat gag ttg 259 Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp Phe Ala Asp Glu Leu <div style="display: flex; justify-content: space-between; width: 100%;"> 40 45 50 </div>			
ttg gcg ttg cct ggt aag ggt gat ttc aag gct gcg gat ggt act gat 307 Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala Ala Asp Gly Thr Asp <div style="display: flex; justify-content: space-between; width: 100%;"> 55 60 65 </div>			
gtc cgt aac tat ggc ggg ctg gat ggc atc gtt gat att cgc cag att 355 Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val Asp Ile Arg Gln Ile <div style="display: flex; justify-content: space-between; width: 100%;"> 70 75 80 85 </div>			
tgg gcg gat ttg ctg ggt gtt cct gtg gag cag gtc ttg gcg ggg gat 403 Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln Val Leu Ala Gly Asp <div style="display: flex; justify-content: space-between; width: 100%;"> 90 95 100 </div>			
gct tcg agc ttg aac atc atg ttt gat gtg atc agc tgg tcg tac att 451 Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile Ser Trp Ser Tyr Ile <div style="display: flex; justify-content: space-between; width: 100%;"> 105 110 115 </div>			
ttc ggt aac aat gat tcg gtt cag cct tgg tcg aag gaa gaa acc gtt 499 Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser Lys Glu Glu Thr Val <div style="display: flex; justify-content: space-between; width: 100%;"> 120 125 130 </div>			

aag tgg att tgc cct gtt ccg ggc tat gat cgc cat ttc tcc atc acg 547
Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg His Phe Ser Ile Thr
135 140 145

gag cgt ttc ggc ttt gag atg att tct gtg cca atg aat gaa gac ggc 595
Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro Met Asn Glu Asp Gly
150 155 160 165

cct gat atg gat gct gtt gag gaa ttg gtg aag aat ccg cag gtt aag 643
Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys Asn Pro Gln Val Lys
170 175 180

ggc atg tgg gtt gtt ccg gtg ttt tct aac ccg act ggt ttc acg gtg 691
Gly Met Trp Val Val Pro Val Phe Ser Asn Pro Thr Gly Phe Thr Val
185 190 195

aca gaa gac gtc gca aag cgt cta agc gca atg gaa acc gca gct ccg 739
Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met Glu Thr Ala Ala Pro
200 205 210

gac ttc cgc gtt gtg tgg gat aat gcc tac gcc gtt cat acg ctg acc 787
Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala Val His Thr Leu Thr
215 220 225

gat gaa ttc cct gag gtt atc gat atc gtc ggg ctt ggt gag gcc gct 835
Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly Leu Gly Glu Ala Ala
230 235 240 245

ggc aac ccg aac cgt ttc tgg gcg ttc act tct act tcg aag atc act 883
Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser Thr Ser Lys Ile Thr
250 255 260

ctc gcg ggt gcg ggc gtg tcg ttc ttc ctc acc tct gcg gag aac cgc 931
Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr Ser Ala Glu Asn Arg
265 270 275

aag tgg tac acc ggc cat gcg ggt atc cgt ggc att ggc cct aac aag 979
Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly Ile Gly Pro Asn Lys
280 285 290

gtc aat cag ttg gct cat gcg cgt tac ttt ggc gat gct gag gga gtg
1027
Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly Asp Ala Glu Gly Val
295 300 305

cgc gcg gtg atg cgt aag cat gct gcg tcg ttg gct ccg aag ttc aac
1075
Arg Ala Val Met Arg Lys His Ala Ala Ser Leu Ala Pro Lys Phe Asn
310 315 320 325

aag gtt ctg gag att ctg gat tct cgc ctt gct gag tac ggt gtc gcg
1123
Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala Glu Tyr Gly Val Ala
330 335 340

cag tgg act gtc cct gcg ggc ggt tac ttc att tcc ctt gat gtg gtt
1171
Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile Ser Leu Asp Val Val
345 350 355

cct ggt acg gcg tct cgc gtg gct gag ttg gct aag gaa gcc ggc atc
 1219
 Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala Lys Glu Ala Gly Ile
 360 365 370

gcg ttg acg ggt gcg ggt tct tct tac ccg ctg cgt cag gat ccg gag
 1267
 Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu Arg Gln Asp Pro Glu
 375 380 385

aac aaa aat ctc cgt ttg gca ccg tcg ctg cct cca gtt gag gaa ctt
 1315
 Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro Pro Val Glu Glu Leu
 390 395 400 405

gag gtt gcc atg gat ggc gtg gct acc tgt gtg ctg ttg gca gca gcg
 1363
 Glu Val Ala Met Asp Gly Val Ala Thr Cys Val Leu Leu Ala Ala Ala
 410 415 420

gag cat tac gct aac taaaagtgaac tacagcggag aca
 1401
 Glu His Tyr Ala Asn
 425

<210> 450

<211> 426

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 450

Met Ser Ser Val Ser Leu Gln Asp Phe Asp Ala Glu Arg Ile Gly Leu
 1 5 10 15

Phe His Glu Asp Ile Lys Arg Lys Phe Asp Glu Leu Lys Ser Lys Asn
 20 25 30

Leu Lys Leu Asp Leu Thr Arg Gly Lys Pro Ser Ser Glu Gln Leu Asp
 35 40 45

Phe Ala Asp Glu Leu Leu Ala Leu Pro Gly Lys Gly Asp Phe Lys Ala
 50 55 60

Ala Asp Gly Thr Asp Val Arg Asn Tyr Gly Gly Leu Asp Gly Ile Val
 65 70 75 80

Asp Ile Arg Gln Ile Trp Ala Asp Leu Leu Gly Val Pro Val Glu Gln
 85 90 95

Val Leu Ala Gly Asp Ala Ser Ser Leu Asn Ile Met Phe Asp Val Ile
 100 105 110

Ser Trp Ser Tyr Ile Phe Gly Asn Asn Asp Ser Val Gln Pro Trp Ser
 115 120 125

Lys Glu Glu Thr Val Lys Trp Ile Cys Pro Val Pro Gly Tyr Asp Arg
 130 135 140

His Phe Ser Ile Thr Glu Arg Phe Gly Phe Glu Met Ile Ser Val Pro
 145 150 155 160

Met Asn Glu Asp Gly Pro Asp Met Asp Ala Val Glu Glu Leu Val Lys
 165 170 175
 Asn Pro Gln Val Lys Gly Met Trp Val Val Pro Val Phe Ser Asn Pro
 180 185 190
 Thr Gly Phe Thr Val Thr Glu Asp Val Ala Lys Arg Leu Ser Ala Met
 195 200 205
 Glu Thr Ala Ala Pro Asp Phe Arg Val Val Trp Asp Asn Ala Tyr Ala
 210 215 220
 Val His Thr Leu Thr Asp Glu Phe Pro Glu Val Ile Asp Ile Val Gly
 225 230 235 240
 Leu Gly Glu Ala Ala Gly Asn Pro Asn Arg Phe Trp Ala Phe Thr Ser
 245 250 255
 Thr Ser Lys Ile Thr Leu Ala Gly Ala Gly Val Ser Phe Phe Leu Thr
 260 265 270
 Ser Ala Glu Asn Arg Lys Trp Tyr Thr Gly His Ala Gly Ile Arg Gly
 275 280 285
 Ile Gly Pro Asn Lys Val Asn Gln Leu Ala His Ala Arg Tyr Phe Gly
 290 295 300
 Asp Ala Glu Gly Val Arg Ala Val Met Arg Lys His Ala Ala Ser Leu
 305 310 315 320
 Ala Pro Lys Phe Asn Lys Val Leu Glu Ile Leu Asp Ser Arg Leu Ala
 325 330 335
 Glu Tyr Gly Val Ala Gln Trp Thr Val Pro Ala Gly Gly Tyr Phe Ile
 340 345 350
 Ser Leu Asp Val Val Pro Gly Thr Ala Ser Arg Val Ala Glu Leu Ala
 355 360 365
 Lys Glu Ala Gly Ile Ala Leu Thr Gly Ala Gly Ser Ser Tyr Pro Leu
 370 375 380
 Arg Gln Asp Pro Glu Asn Lys Asn Leu Arg Leu Ala Pro Ser Leu Pro
 385 390 395 400
 Pro Val Glu Glu Leu Glu Val Ala Met Asp Gly Val Ala Thr Cys Val
 405 410 415
 Leu Leu Ala Ala Ala Glu His Tyr Ala Asn
 420 425

<210> 451

<211> 1143

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101) .. (1120)

<223> RXN00448

<400> 451

```

ccattttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60

catagagata accgtagtag gtatgtgcc aactgtgcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                               10                               15                               20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                               25                               30                               35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                               40                               45                               50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                               55                               60                               65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg ctt ctc gac 355
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser Leu Leu Asp
70                               75                               80                               85

gcc gtc cac acc cac gca cca aac aac ggc ttc acc gac gtc gta tcc 403
Ala Val His Thr His Ala Pro Asn Asn Gly Phe Thr Asp Val Val Ser
                               90                               95                               100

gta aaa acc gcc gtc tac gac gca gta aaa gcc cgc aac atg caa cac 451
Val Lys Thr Ala Val Tyr Asp Ala Val Lys Ala Arg Asn Met Gln His
                               105                               110                               115

cgt tat gtg gga tcc cac ccc atg gca ggc acc gcc aac tcc ggc tgg 499
Arg Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp
120                               125                               130

agc gca tcc atg gac gga ctg ttc aaa cga gca gta tgg gtg gtc acc 547
Ser Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr
135                               140                               145

ttc gac cag ctt ttc gac ggc acc gac atc aac tcc acc tgg atc agc 595
Phe Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser
150                               155                               160                               165

atc tgg aaa gac gtc gtc caa atg gca ctc gcc gtg ggc gct gaa gtt 643
Ile Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val
170                               175                               180

gtc cca tcc cga gtt ggc cca cac gat gca gca gca gca cga gtg tct 691
Val Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Ala Arg Val Ser
185                               190                               195

cat tta aca cac atc ctg gct gaa acc ctc gcc atc gtc ggt gac aac 739
His Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn
200                               205                               210

```


ggt ggc gca ctg tct ctc tct tta gcc gct ggc agc tac cgc gac tcc 787
 Gly Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser
 215 220 225
 acc cgc gtt gca ggc acc gac cca gga ctc gtc cgc gcc atg tgt gaa 835
 Thr Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala M t Cys Glu
 230 235 240 245
 agc aac gcc ggc cca ctg gtc aaa gcc ctc gac gaa gca ctg gcg atc 883
 Ser Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile
 250 255 260
 ctc cac gaa gcc cgc gaa ggc ctc acc gca gaa cag cca aac atc gag 931
 Leu His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu
 265 270 275
 caa ctt gcc gac aac ggc tac cga tcc cgc atc cgc tac gaa gcc cgc 979
 Gln Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg
 280 285 290
 tcc ggc cag cga cgc gcc aaa gaa tcc gtt agc cct acc atc acc tca
 1027
 Ser Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser
 295 300 305
 tcc agg cca gtg ctc cgt ctc cac ccg ggc aca cca aac tgg gag aag
 1075
 Ser Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys
 310 315 320 325
 cag ctc atc cac gct gaa acc ctc ggc gca cgg atc gaa gtg ttc
 1120
 Gln Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 330 335 340
 tagttttatc ggctgatgat tct
 1143

<210> 452

<211> 340

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 452

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
 1 5 10 15
 Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
 20 25 30
 Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
 35 40 45
 Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
 50 55 60
 Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
 65 70 75 80
 Asp Ser Leu Leu Asp Ala Val His Thr His Ala Pro Asn Asn Gly Phe

85					90					95					
Thr	Asp	Val	Val	Ser	Val	Lys	Thr	Ala	Val	Tyr	Asp	Ala	Val	Lys	Ala
		100						105					110		
Arg	Asn	Met	Gln	His	Arg	Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr
		115					120					125			
Ala	Asn	Ser	Gly	Trp	Ser	Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala
		130					135					140			
Val	Trp	Val	Val	Thr	Phe	Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn
		145				150					155				160
Ser	Thr	Trp	Ile	Ser	Ile	Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala
			165					170						175	
Val	Gly	Ala	Glu	Val	Val	Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala
			180					185					190		
Ala	Ala	Arg	Val	Ser	His	Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala
		195					200					205			
Ile	Val	Gly	Asp	Asn	Gly	Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly
		210				215					220				
Ser	Tyr	Arg	Asp	Ser	Thr	Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val
		225				230					235				240
Arg	Ala	Met	Cys	Glu	Ser	Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp
			245					250						255	
Glu	Ala	Leu	Ala	Ile	Leu	His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu
			260					265					270		
Gln	Pro	Asn	Ile	Glu	Gln	Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile
		275					280					285			
Arg	Tyr	Glu	Ala	Arg	Ser	Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser
		290				295					300				
Pro	Thr	Ile	Thr	Ser	Ser	Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr
		305				310					315				320
Pro	Asn	Trp	Glu	Lys	Gln	Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg
			325						330					335	
Ile	Glu	Val	Phe												
			340												

<210> 453

<211> 689

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(666)

<223> FRXA00448

<400> 453

tat	gtg	gga	tcc	cac	ccc	atg	gca	ggc	acc	gcc	aac	tcc	ggc	tgg	agc	48
Tyr	Val	Gly	Ser	His	Pro	Met	Ala	Gly	Thr	Ala	Asn	Ser	Gly	Trp	Ser	
1				5					10					15		
gca	tcc	atg	gac	gga	ctg	ttc	aaa	cga	gca	gta	tgg	gtg	gtc	acc	ttc	96
Ala	Ser	Met	Asp	Gly	Leu	Phe	Lys	Arg	Ala	Val	Trp	Val	Val	Thr	Phe	
			20					25					30			
gac	cag	ctt	ttc	gac	ggc	acc	gac	atc	aac	tcc	acc	tgg	atc	agc	atc	144
Asp	Gln	Leu	Phe	Asp	Gly	Thr	Asp	Ile	Asn	Ser	Thr	Trp	Ile	Ser	Ile	
		35					40					45				
tgg	aaa	gac	gtc	gtc	caa	atg	gca	ctc	gcc	gtg	ggc	gct	gaa	gtt	gtc	192
Trp	Lys	Asp	Val	Val	Gln	Met	Ala	Leu	Ala	Val	Gly	Ala	Glu	Val	Val	
	50					55					60					
cca	tcc	cga	gtt	ggc	cca	cac	gat	gca	gca	gca	gca	cga	gtg	tct	cat	240
Pro	Ser	Arg	Val	Gly	Pro	His	Asp	Ala	Ala	Ala	Ala	Arg	Val	Ser	His	
	65				70					75					80	
tta	aca	cac	atc	ctg	gct	gaa	acc	ctc	gcc	atc	gtc	ggc	gac	aac	ggc	288
Leu	Thr	His	Ile	Leu	Ala	Glu	Thr	Leu	Ala	Ile	Val	Gly	Asp	Asn	Gly	
			85						90					95		
ggc	gca	ctg	tct	ctc	tct	tta	gcc	gct	ggc	agc	tac	cgc	gac	tcc	acc	336
Gly	Ala	Leu	Ser	Leu	Ser	Leu	Ala	Ala	Gly	Ser	Tyr	Arg	Asp	Ser	Thr	
			100					105					110			
cgc	gtt	gca	ggc	acc	gac	cca	gga	ctc	gtc	cgc	gcc	atg	tgt	gaa	agc	384
Arg	Val	Ala	Gly	Thr	Asp	Pro	Gly	Leu	Val	Arg	Ala	Met	Cys	Glu	Ser	
		115					120					125				
aac	gcc	ggc	cca	ctg	gtc	aaa	gcc	ctc	gac	gaa	gca	ctg	gcg	atc	ctc	432
Asn	Ala	Gly	Pro	Leu	Val	Lys	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Ile	Leu	
	130					135					140					
cac	gaa	gcc	cgc	gaa	ggc	ctc	acc	gca	gaa	cag	cca	aac	atc	gag	caa	480
His	Glu	Ala	Arg	Glu	Gly	Leu	Thr	Ala	Glu	Gln	Pro	Asn	Ile	Glu	Gln	
	145				150					155					160	
ctt	gcc	gac	aac	ggc	tac	cga	tcc	cgc	atc	cgc	tac	gaa	gcc	cgc	tcc	528
Leu	Ala	Asp	Asn	Gly	Tyr	Arg	Ser	Arg	Ile	Arg	Tyr	Glu	Ala	Arg	Ser	
			165						170					175		
ggc	cag	cga	cgc	gcc	aaa	gaa	tcc	gtt	agc	cct	acc	atc	acc	tca	tcc	576
Gly	Gln	Arg	Arg	Ala	Lys	Glu	Ser	Val	Ser	Pro	Thr	Ile	Thr	Ser	Ser	
			180					185					190			
agg	cca	gtg	ctc	cgt	ctc	cac	ccg	ggc	aca	cca	aac	tgg	gag	aag	cag	624
Arg	Pro	Val	Leu	Arg	Leu	His	Pro	Gly	Thr	Pro	Asn	Trp	Glu	Lys	Gln	
		195					200					205				
ctc	atc	cac	gct	gaa	acc	ctc	ggc	gca	cgg	atc	gaa	gtg	ttc			666
Leu	Ile	His	Ala	Glu	Thr	Leu	Gly	Ala	Arg	Ile	Glu	Val	Phe			
	210					215					220					
tag	ttttatc	ggctgatgat	tct													689

<210> 454

<211> 222

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 454

Tyr Val Gly Ser His Pro Met Ala Gly Thr Ala Asn Ser Gly Trp Ser
 1 5 10 15

Ala Ser Met Asp Gly Leu Phe Lys Arg Ala Val Trp Val Val Thr Phe
 20 25 30

Asp Gln Leu Phe Asp Gly Thr Asp Ile Asn Ser Thr Trp Ile Ser Ile
 35 40 45

Trp Lys Asp Val Val Gln Met Ala Leu Ala Val Gly Ala Glu Val Val
 50 55 60

Pro Ser Arg Val Gly Pro His Asp Ala Ala Ala Arg Val Ser His
 65 70 75 80

Leu Thr His Ile Leu Ala Glu Thr Leu Ala Ile Val Gly Asp Asn Gly
 85 90 95

Gly Ala Leu Ser Leu Ser Leu Ala Ala Gly Ser Tyr Arg Asp Ser Thr
 100 105 110

Arg Val Ala Gly Thr Asp Pro Gly Leu Val Arg Ala Met Cys Glu Ser
 115 120 125

Asn Ala Gly Pro Leu Val Lys Ala Leu Asp Glu Ala Leu Ala Ile Leu
 130 135 140

His Glu Ala Arg Glu Gly Leu Thr Ala Glu Gln Pro Asn Ile Glu Gln
 145 150 155 160

Leu Ala Asp Asn Gly Tyr Arg Ser Arg Ile Arg Tyr Glu Ala Arg Ser
 165 170 175

Gly Gln Arg Arg Ala Lys Glu Ser Val Ser Pro Thr Ile Thr Ser Ser
 180 185 190

Arg Pro Val Leu Arg Leu His Pro Gly Thr Pro Asn Trp Glu Lys Gln
 195 200 205

Leu Ile His Ala Glu Thr Leu Gly Ala Arg Ile Glu Val Phe
 210 215 220

<210> 455

<211> 346

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(346)

<223> FRXA00452

<400> 455

ccatttacct tcaactaagg tagccgtaac tgcaaagctc aggccatcct cttcagtggt 60

```

catagagata accgtagtag gtatgtgccca cacttgtcag gtg act acc aaa gac 115
                               Val Thr Thr Lys Asp
                               1                               5

att tcc cgc cca gta tgc atc ctg ggc ctc ggc ctc atc ggc gga tcc 163
Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly Leu Ile Gly Gly Ser
                10                15                20

ctc ctc cgc gac ctc cat gca gcc aac cac tcc gtc ttc ggc tac aac 211
Leu Leu Arg Asp Leu His Ala Ala Asn His Ser Val Phe Gly Tyr Asn
                25                30                35

cgc tca cgc tcc ggc gct aaa tca gcc gtc gac gaa ggc ttc gac gtt 259
Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp Glu Gly Phe Asp Val
                40                45                50

tcc gcc gat ctt gaa gca acc ctc cag cgt gca gcc gcc gaa gat gcg 307
Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala Ala Ala Glu Asp Ala
                55                60                65

ctc atc gtc ctc gcg gtc ccc atg acc gca atc gat tcg 346
Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile Asp Ser
    70                75                80

```

<210> 456

<211> 82

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 456

```

Val Thr Thr Lys Asp Ile Ser Arg Pro Val Cys Ile Leu Gly Leu Gly
    1                5                10                15

Leu Ile Gly Gly Ser Leu Leu Arg Asp Leu His Ala Ala Asn His Ser
    20                25                30

Val Phe Gly Tyr Asn Arg Ser Arg Ser Gly Ala Lys Ser Ala Val Asp
    35                40                45

Glu Gly Phe Asp Val Ser Ala Asp Leu Glu Ala Thr Leu Gln Arg Ala
    50                55                60

Ala Ala Glu Asp Ala Leu Ile Val Leu Ala Val Pro Met Thr Ala Ile
    65                70                75                80

Asp Ser

```

<210> 457

<211> 1248

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1225)

<223> RXA00584

<400> 457

```

tagttgtgcc acctaaaacg cgaacagaac cggagtcgag cagcacctcc ccgcaagggt 60
agaggggctg cttttttgtt tcctaaattc accccatccc atg cat agc cct gaa 115
                                         Met His Ser Pro Glu
                                         1                               5
agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca 163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser
                        10                        15                        20
acc agc aac aag cgc gtc gtg gct ttc cac gag ctg cct agc cct aca 211
Thr Ser Asn Lys Arg Val Val Ala Phe His Glu Leu Pro Ser Pro Thr
                        25                        30                        35
gat ctc atc gcc gca aac cca ctg aca cca aag cag gct tcc aag gtg 259
Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys Gln Ala Ser Lys Val
                        40                        45                        50
gag cag gat cgc cag gac atc gct gat atc ttc gct ggc gac gat gac 307
Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe Ala Gly Asp Asp Asp
                        55                        60                        65
cgc ctc gtt gtc gtt gtg gga cct tgc tca gtt cac gat cct gaa gca 355
Arg Leu Val Val Val Val Gly Pro Cys Ser Val His Asp Pro Glu Ala
                        70                        75                        80                        85
gcc atc gat tac gca aac cgc ctg gct ccg ctg gca aag cgc ctt gat 403
Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu Ala Lys Arg Leu Asp
                        90                        95                        100
cag gac ctc aag att gtc atg cgc gtg tac ttc gag aag cct cgc acc 451
Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe Glu Lys Pro Arg Thr
                        105                        110                        115
atc gtc gga tgg aag gga ttg atc aat gat cct cac ctc aac gaa acc 499
Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro His Leu Asn Glu Thr
                        120                        125                        130
tac gac atc cca gag ggc ttg cgc att gcg cgc aaa gtg ctt atc gac 547
Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg Lys Val Leu Ile Asp
                        135                        140                        145
gtt gtg aac ctt gat ctc cca gtc ggc tgc gaa ttc ctc gaa cca aac 595
Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu Phe Leu Glu Pro Asn
                        150                        155                        160                        165
agc cct cag tac tac gcc gac act gtc gca tgg gga gca atc ggc gct 643
Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp Gly Ala Ile Gly Ala
                        170                        175                        180
cgt acc acc gaa tct cag gtg cac cgc cag ctg gct tct ggg atg tct 691
Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu Ala Ser Gly Met Ser
                        185                        190                        195
atg cca att ggt ttc aag aac gga act gac gga aac atc cag gtt gca 739
Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly Asn Ile Gln Val Ala
                        200                        205                        210
gtc gac gcg gta cag gct gcc cag aac cca cac ttc ttc ttc gga acc 787
Val Asp Ala Val Gln Ala Ala Gln Asn Pro His Phe Phe Phe Gly Thr
                        215                        220                        225

```

tcc gac gac ggc gcg ctg agc gtc gtg gag acc gca ggc aac agc aac 835
 Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr Ala Gly Asn Ser Asn
 230 235 240 245

tcc cac atc att ttg cgc ggc ggt acc tcc ggc ccg aat cat gat gca 883
 Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly Pro Asn His Asp Ala
 250 255 260

gct tcg gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
 265 270 275

atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
 280 285 290

gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa
 1027
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
 295 300 305

gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag
 1075
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
 310 315 320 325

aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg
 1123
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
 330 335 340

tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc
 1171
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
 345 350 355

gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca
 1219
 Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg Glu Arg Arg Ala Ala
 360 365 370

gcc aag taattaaggg cgctagactg tta
 1248
 Ala Lys
 375

<210> 458

<211> 375

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 458

Met His Ser Pro Glu Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu
 1 5 10 15

Glu Asn Ala Ala Ser Thr Ser Asn Lys Arg Val Val Ala Phe His Glu
 20 25 30

Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys

35					40					45					
Gln	Ala	Ser	Lys	Val	Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe
50					55					60					
Ala	Gly	Asp	Asp	Asp	Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val
65					70					75					80
His	Asp	Pro	Glu	Ala	Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu
				85					90					95	
Ala	Lys	Arg	Leu	Asp	Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe
			100					105					110		
Glu	Lys	Pro	Arg	Thr	Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro
		115					120					125			
His	Leu	Asn	Glu	Thr	Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg
	130					135					140				
Lys	Val	Leu	Ile	Asp	Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu
145				150						155					160
Phe	Leu	Glu	Pro	Asn	Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp
				165					170					175	
Gly	Ala	Ile	Gly	Ala	Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu
			180					185					190		
Ala	Ser	Gly	Met	Ser	Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly
		195					200					205			
Asn	Ile	Gln	Val	Ala	Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His
	210					215					220				
Phe	Phe	Phe	Gly	Thr	Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr
225						230					235				240
Ala	Gly	Asn	Ser	Asn	Ser	His	Ile	Ile	Leu	Arg	Gly	Gly	Thr	Ser	Gly
				245					250					255	
Pro	Asn	His	Asp	Ala	Ala	Ser	Val	Glu	Ala	Val	Val	Glu	Lys	Leu	Gly
			260					265					270		
Glu	Asn	Ala	Arg	Leu	Met	Ile	Asp	Ala	Ser	His	Ala	Asn	Ser	Gly	Lys
		275					280					285			
Asp	His	Ile	Arg	Gln	Val	Glu	Val	Val	Arg	Glu	Ile	Ala	Glu	Gln	Ile
	290					295					300				
Ser	Gly	Gly	Ser	Glu	Ala	Val	Ala	Gly	Ile	Met	Ile	Glu	Ser	Phe	Leu
305						310					315				320
Val	Gly	Gly	Ala	Gln	Asn	Leu	Asp	Pro	Ala	Lys	Leu	Arg	Ile	Asn	Gly
				325					330					335	
Gly	Glu	Gly	Leu	Val	Tyr	Gly	Gln	Ser	Val	Thr	Asp	Lys	Cys	Ile	Asp
			340					345					350		
Ile	Asp	Thr	Thr	Ile	Asp	Leu	Leu	Ala	Glu	Leu	Ala	Ala	Ala	Val	Arg
		355					360					365			

Glu Arg Arg Ala Ala Ala Lys
370 375

<210> 459

<211> 1983

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1960)

<223> RXA00579

<400> 459

```

tcgtctaagt ttttctttga gttttcatat gtagaaggca tcgtcggcctt cggcctggcg 60

gtgcttttct cgttgttttg tggttttgtc agaggatgtc atg cgc gtt tta att 115
                                         Met Arg Val Leu Ile
                                         1 5

att gat aat tat gat tct ttc acg ttt aat ctc gcc acc tat gtg gaa 163
Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu Ala Thr Tyr Val Glu
                        10 15 20

gag gtt acg ggt cag gca cct gtg gtg gtg cct aat gat caa gaa ata 211
Glu Val Thr Gly Gln Ala Pro Val Val Val Pro Asn Asp Gln Glu Ile
                        25 30 35

gat gag atg ctt ttc gac gcc gtc atc ctc tca cct ggc ccg ggc cac 259
Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser Pro Gly Pro Gly His
                        40 45 50

gcc ggc gtt gcg gct gat ttt ggt atc tgt gca ggc gtc att gag cgt 307
Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala Gly Val Ile Glu Arg
                        55 60 65

gca cgc gtt ccg att ttg ggt gtg tgt tta ggc cac cag ggc att gcg 355
Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly His Gln Gly Ile Ala
                        70 75 80 85

ttg gcc tat ggc ggt gat gtt gat ttg gcg ccc agg ccg gtc cac ggt 403
Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro Arg Pro Val His Gly
                        90 95 100

gag gtt tcg cag atc acc cat gat ggt tca ggt tta ttt gca ggc atc 451
Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly Leu Phe Ala Gly Ile
                        105 110 115

cct gaa acg ttt gag gcg gtg cgt tat cac tcg atg gtg gca acc cgc 499
Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser Met Val Ala Thr Arg
                        120 125 130

ttg ccg gag tca ttg aaa gct aca gct acc agc gat gat ggt ttg atc 547
Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser Asp Asp Gly Leu Ile
                        135 140 145

atg gca ttg gca cat gaa gtg ctt ccg cag tgg ggt gtg caa ttt cat 595
Met Ala Leu Ala His Glu Val Leu Pro Gln Trp Gly Val Gln Phe His
                        150 155 160 165

```

ccg gaa tct att ggt gga caa ttc ggc cat cag atc att aag aac ttc 643
 Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln Ile Ile Lys Asn Phe
 170 175 180

ctt aat tta gcg cgc aca tat cgc tgg caa ctc acg gag aaa act att 691
 Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu Thr Glu Lys Thr Ile
 185 190 195

ccg ctc agc gtt gat tca gca gcg gtt ttt gaa aca ttc ttt gcc cat 739
 Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu Thr Phe Phe Ala His
 200 205 210

tcc tcc cat gct ttt tgg ctc gat gat gcc caa gga acc agc tat ctt 787
 Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln Gly Thr Ser Tyr Leu
 215 220 225

ggt gat gcc agc ggt cct ctc gca cgc aca aaa acc cat aat gtc ggc 835
 Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys Thr His Asn Val Gly
 230 235 240 245

gag ggg gat ttc ttc acc tgg cta aag gag gat ctc gcc gcc aac tca 883
 Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp Leu Ala Ala Asn Ser
 250 255 260

gtt gcg ccc ggt caa ggt ttt cgt ctt ggc tgg gtt ggt tac gtt ggt 931
 Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp Val Gly Tyr Val Gly
 265 270 275

tat gag ctt aaa gcg gaa gct ggc gca cgg gct gcg cac act tcg agt 979
 Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala Ala His Thr Ser Ser
 280 285 290

ctt ccg gat gcg cac ctc att ttt gcc gat cgc gcc atc gca gtg gaa
 1027
 Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg Ala Ile Ala Val Glu
 295 300 305

tcg gat cag gtt cgg ttg ctg gcg ttg ggg gag cag gac gag tgg ttt
 1075
 Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu Gln Asp Glu Trp Phe
 310 315 320 325

gaa gaa acc atc aag aag ctg cat aat ctt gtc gcc ccg cgg ata cct
 1123
 Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val Ala Pro Arg Ile Pro
 330 335 340

gcg tcc gga cac ctc gct ttg cag gtt cga gat tcc aaa gat gag tat
 1171
 Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp Ser Lys Asp Glu Tyr
 345 350 355

ctc gac aaa att cgc aga gcc cag gag ctg att act cgc ggc gaa tcg
 1219
 Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile Thr Arg Gly Glu Ser
 360 365 370

tat gaa atc tgc ctg acc aca aaa ctt cag ggc acc act gat gtg gcc
 1267
 Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly Thr Thr Asp Val Ala

375	380	385
cct ctg gct gcc tat cta gca ctg cgt ggg gcc aat ccc acc gca tat		
1315		
Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala Asn Pro Thr Ala Tyr		
390	395	400 405
ggg gcg tat ctt cag ctg ggg gat acc tct att ttg agt tcc tcg ccg		
1363		
Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile Leu Ser Ser Ser Pro		
	410	415 420
gag cgg ttc atc acc att gat tcg gca ggg tat gtg gaa tca aag ccc		
1411		
Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr Val Glu Ser Lys Pro		
	425	430 435
att aaa ggc acc agg ccg cgt ggg cga aca gcg caa gaa gac caa gaa		
1459		
Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala Gln Glu Asp Gln Glu		
	440	445 450
atc att gct gag ctg cgc agt aat cct aaa gat cgt gca gaa aac ttg		
1507		
Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp Arg Ala Glu Asn Leu		
	455	460 465
atg atc gtg gat ttg gtc cgc aac gac tta gcc cgc ggc gct ttg ccc		
1555		
Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala Arg Gly Ala Leu Pro		
470	475	480 485
acc aca gtt aaa aca tcc aag ctt ttc gac gtc gaa acc tac gcc aca		
1603		
Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val Glu Thr Tyr Ala Thr		
	490	495 500
gtc cac caa ctt gtc agc acc gtc tct gca gag ttg ggg cca cgc agt		
1651		
Val His Gln Leu Val Ser Thr Val Ser Ala Glu Leu Gly Pro Arg Ser		
	505	510 515
ccg att gag tgc gtg cgc gca gca ttc ccc ggt ggt tcg atg act ggt		
1699		
Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly Gly Ser Met Thr Gly		
	520	525 530
gcc cca aag ctg cgc acc atg gag atc atc gat gag ctg gag gca gct		
1747		
Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp Glu Leu Glu Ala Ala		
	535	540 545
cct cgc ggt att tac tca ggt ggc ttg gga tat ttt tcc ctc gac ggc		
1795		
Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr Phe Ser Leu Asp Gly		
550	555	560 565
gca gtt gat ctc tcc atg gtg atc aga act ctc gtc atc cag aac aat		
1843		
Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu Val Ile Gln Asn Asn		
	570	575 580

cac gtg gag tac gga gtg ggc ggt gca ctt ctt gct ctg tct gat ccg
1891

His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu Ala Leu Ser Asp Pro
585 590 595

gag gct gag tgg gag gaa atc cgc gtt aaa tca cgg cct ctg ctg aat
1939

Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser Arg Pro Leu Leu Asn
600 605 610

ttg ttt ggg gtt gaa ttc cca tgacgtacct cgtgtgggac ggt
1983

Leu Phe Gly Val Glu Phe Pro
615 620

<210> 460

<211> 620

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 460

Met Arg Val Leu Ile Ile Asp Asn Tyr Asp Ser Phe Thr Phe Asn Leu
1 5 10 15

Ala Thr Tyr Val Glu Glu Val Thr Gly Gln Ala Pro Val Val Val Pro
20 25 30

Asn Asp Gln Glu Ile Asp Glu Met Leu Phe Asp Ala Val Ile Leu Ser
35 40 45

Pro Gly Pro Gly His Ala Gly Val Ala Ala Asp Phe Gly Ile Cys Ala
50 55 60

Gly Val Ile Glu Arg Ala Arg Val Pro Ile Leu Gly Val Cys Leu Gly
65 70 75 80

His Gln Gly Ile Ala Leu Ala Tyr Gly Gly Asp Val Asp Leu Ala Pro
85 90 95

Arg Pro Val His Gly Glu Val Ser Gln Ile Thr His Asp Gly Ser Gly
100 105 110

Leu Phe Ala Gly Ile Pro Glu Thr Phe Glu Ala Val Arg Tyr His Ser
115 120 125

Met Val Ala Thr Arg Leu Pro Glu Ser Leu Lys Ala Thr Ala Thr Ser
130 135 140

Asp Asp Gly Leu Ile Met Ala Leu Ala His Glu Val Leu Pro Gln Trp
145 150 155 160

Gly Val Gln Phe His Pro Glu Ser Ile Gly Gly Gln Phe Gly His Gln
165 170 175

Ile Ile Lys Asn Phe Leu Asn Leu Ala Arg Thr Tyr Arg Trp Gln Leu
180 185 190

Thr Glu Lys Thr Ile Pro Leu Ser Val Asp Ser Ala Ala Val Phe Glu
195 200 205

Thr Phe Phe Ala His Ser Ser His Ala Phe Trp Leu Asp Asp Ala Gln
 210 215 220
 Gly Thr Ser Tyr Leu Gly Asp Ala Ser Gly Pro Leu Ala Arg Thr Lys
 225 230 235 240
 Thr His Asn Val Gly Glu Gly Asp Phe Phe Thr Trp Leu Lys Glu Asp
 245 250 255
 Leu Ala Ala Asn Ser Val Ala Pro Gly Gln Gly Phe Arg Leu Gly Trp
 260 265 270
 Val Gly Tyr Val Gly Tyr Glu Leu Lys Ala Glu Ala Gly Ala Arg Ala
 275 280 285
 Ala His Thr Ser Ser Leu Pro Asp Ala His Leu Ile Phe Ala Asp Arg
 290 295 300
 Ala Ile Ala Val Glu Ser Asp Gln Val Arg Leu Leu Ala Leu Gly Glu
 305 310 315 320
 Gln Asp Glu Trp Phe Glu Glu Thr Ile Lys Lys Leu His Asn Leu Val
 325 330 335
 Ala Pro Arg Ile Pro Ala Ser Gly His Leu Ala Leu Gln Val Arg Asp
 340 345 350
 Ser Lys Asp Glu Tyr Leu Asp Lys Ile Arg Arg Ala Gln Glu Leu Ile
 355 360 365
 Thr Arg Gly Glu Ser Tyr Glu Ile Cys Leu Thr Thr Lys Leu Gln Gly
 370 375 380
 Thr Thr Asp Val Ala Pro Leu Ala Ala Tyr Leu Ala Leu Arg Gly Ala
 385 390 395 400
 Asn Pro Thr Ala Tyr Gly Ala Tyr Leu Gln Leu Gly Asp Thr Ser Ile
 405 410 415
 Leu Ser Ser Ser Pro Glu Arg Phe Ile Thr Ile Asp Ser Ala Gly Tyr
 420 425 430
 Val Glu Ser Lys Pro Ile Lys Gly Thr Arg Pro Arg Gly Arg Thr Ala
 435 440 445
 Gln Glu Asp Gln Glu Ile Ile Ala Glu Leu Arg Ser Asn Pro Lys Asp
 450 455 460
 Arg Ala Glu Asn Leu Met Ile Val Asp Leu Val Arg Asn Asp Leu Ala
 465 470 475 480
 Arg Gly Ala Leu Pro Thr Thr Val Lys Thr Ser Lys Leu Phe Asp Val
 485 490 495
 Glu Thr Tyr Ala Thr Val His Gln Leu Val Ser Thr Val Ser Ala Glu
 500 505 510
 Leu Gly Pro Arg Ser Pro Ile Glu Cys Val Arg Ala Ala Phe Pro Gly
 515 520 525

Gly Ser Met Thr Gly Ala Pro Lys Leu Arg Thr Met Glu Ile Ile Asp
 530 535 540

Glu Leu Glu Ala Ala Pro Arg Gly Ile Tyr Ser Gly Gly Leu Gly Tyr
 545 550 555 560

Phe Ser Leu Asp Gly Ala Val Asp Leu Ser Met Val Ile Arg Thr Leu
 565 570 575

Val Ile Gln Asn Asn His Val Glu Tyr Gly Val Gly Gly Ala Leu Leu
 580 585 590

Ala Leu Ser Asp Pro Glu Ala Glu Trp Glu Glu Ile Arg Val Lys Ser
 595 600 605

Arg Pro Leu Leu Asn Leu Phe Gly Val Glu Phe Pro
 610 615 620

<210> 461
 <211> 747
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(724)
 <223> RXA00958

<400> 461
 attctaattcc tcaatctgaa gccgatgaga cggtgcacaa ggcgtatgcc gtgttgaatg 60

ccattgcgct tgctgctggg tccactttgg aggtcatccg atg aca cac gtt gtt 115
 Met Thr His Val Val
 1 5

ctc att gat aat cac gat tct ttt gtc tac aac ctg gtg gat gcg ttc 163
 Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn Leu Val Asp Ala Phe
 10 15 20

gcc gtg gcc ggt tat aag tgc acg gtg ttc cgc aat acg gtg cca gtg 211
 Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg Asn Thr Val Pro Val
 25 30 35

gaa acc att ttg gca gcc aac ccg gac ctg atc tgc ctt tca cct gga 259
 Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile Cys Leu Ser Pro Gly
 40 45 50

cct ggt tac cct gcc gat gcg ggc aac atg atg gcg ctg atc gag cgc 307
 Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met Ala Leu Ile Glu Arg
 55 60 65

aca ctc ggc cag att cct tta ctg ggt att tgc ctc ggc tac cag gca 355
 Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys Leu Gly Tyr Gln Ala
 70 75 80 85

ctc atc gaa tac cac ggc ggc aag gtt gag cct tgt ggc cct gtg cac 403
 Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro Cys Gly Pro Val His
 90 95 100

ggc acc acc gac aac atg atc ctt act gat gca ggt gtg cag agc cct 451

Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala Gly Val Gln Ser Pro
 105 110 115
 gtt ttt gca ggt ctt gcc act gat gtt gag cct gat cat cca gaa atc 499
 Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro Asp His Pro Glu Ile
 120 125 130
 cca ggc cgc aag gtt cca att ggc cgt tat cac tca ctg ggc tgc gtg 547
 Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His Ser Leu Gly Cys Val
 135 140 145
 gtt gcc cca gac ggt att gaa tca cta ggt acc tgt tcc tcg gag att 595
 Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr Cys Ser Ser Glu Ile
 150 155 160 165
 ggt gat gtc atc atg gcg gca cgc acc acc gat gga aag gcc att ggc 643
 Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp Gly Lys Ala Ile Gly
 170 175 180
 ctg cag ttt cac cct gag tca gtg cta agc cca acg ggt cct gtc att 691
 Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro Thr Gly Pro Val Ile
 185 190 195
 ttg tcc cgc tgt gtc gaa cag ctt ctc gcg aac taataaaaaaa aggatttgat 744
 Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn
 200 205
 tca 747

<210> 462

<211> 208

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 462

Met Thr His Val Val Leu Ile Asp Asn His Asp Ser Phe Val Tyr Asn
 1 5 10 15
 Leu Val Asp Ala Phe Ala Val Ala Gly Tyr Lys Cys Thr Val Phe Arg
 20 25 30
 Asn Thr Val Pro Val Glu Thr Ile Leu Ala Ala Asn Pro Asp Leu Ile
 35 40 45
 Cys Leu Ser Pro Gly Pro Gly Tyr Pro Ala Asp Ala Gly Asn Met Met
 50 55 60
 Ala Leu Ile Glu Arg Thr Leu Gly Gln Ile Pro Leu Leu Gly Ile Cys
 65 70 75 80
 Leu Gly Tyr Gln Ala Leu Ile Glu Tyr His Gly Gly Lys Val Glu Pro
 85 90 95
 Cys Gly Pro Val His Gly Thr Thr Asp Asn Met Ile Leu Thr Asp Ala
 100 105 110
 Gly Val Gln Ser Pro Val Phe Ala Gly Leu Ala Thr Asp Val Glu Pro
 115 120 125
 Asp His Pro Glu Ile Pro Gly Arg Lys Val Pro Ile Gly Arg Tyr His

130	135	140
Ser Leu Gly Cys Val Val Ala Pro Asp Gly Ile Glu Ser Leu Gly Thr		
145	150	155
Cys Ser Ser Glu Ile Gly Asp Val Ile Met Ala Ala Arg Thr Thr Asp		
	165	170
Gly Lys Ala Ile Gly Leu Gln Phe His Pro Glu Ser Val Leu Ser Pro		
	180	185
Thr Gly Pro Val Ile Leu Ser Arg Cys Val Glu Gln Leu Leu Ala Asn		
	195	200
		205

<210> 463

<211> 469

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(469)

<223> RXN03007

<400> 463

cagtttcacc ctgagtcagt gctaagccca acgggtcctg tcattttgtc ccgctgtgtc 60

gaacagcttc tcgcgaacta ataaaaaaag gattttgattc atg act tct cca gca	115
Met Thr Ser Pro Ala	
1 5	

aca ctg aaa gtt ctc aac gcc tac ttg gat aac ccc act cca acc ctg	163
Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn Pro Thr Pro Thr Leu	
10 15 20	

gag gag gca att gag gtg ttc acc ccg ctg acc gtg ggt gaa tac gat	211
Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr Val Gly Glu Tyr Asp	
25 30 35	

gac gtg cac atc gca gcg ctg ctt gcc acc atc cgt act cgc ggt gag	259
Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile Arg Thr Arg Gly Glu	
40 45 50	

cag ttc gct gat att gcc ggc gct gcc aag gcg ttc ctc gcg gcg gct	307
Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala Phe Leu Ala Ala Ala	
55 60 65	

cgt ccg ttc ccg att act ggc gca ggt ttg cta gat tcc gct ggt act	355
Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu Asp Ser Ala Gly Thr	
70 75 80 85	

ggt ggc gac ggt gcc aac acc atc aac atc acc acc ggc gca tcc ctg	403
Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr Thr Gly Ala Ser Leu	
90 95 100	

atc gca gca tcc ggt gga gtg aag ctg gtt aag cac ggc aac cgt tcg	451
Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys His Gly Asn Arg Ser	

105 110 115

gtg agc tcc aag tcc ggc 469
Val Ser Ser Lys Ser Gly
120

<210> 464
<211> 123
<212> PRT
<213> *Corynebacterium glutamicum*

<400> 464
Met Thr Ser Pro Ala Thr Leu Lys Val Leu Asn Ala Tyr Leu Asp Asn
1 5 10 15
Pro Thr Pro Thr Leu Glu Glu Ala Ile Glu Val Phe Thr Pro Leu Thr
20 25 30
Val Gly Glu Tyr Asp Asp Val His Ile Ala Ala Leu Leu Ala Thr Ile
35 40 45
Arg Thr Arg Gly Glu Gln Phe Ala Asp Ile Ala Gly Ala Ala Lys Ala
50 55 60
Phe Leu Ala Ala Ala Arg Pro Phe Pro Ile Thr Gly Ala Gly Leu Leu
65 70 75 80
Asp Ser Ala Gly Thr Gly Gly Asp Gly Ala Asn Thr Ile Asn Ile Thr
85 90 95
Thr Gly Ala Ser Leu Ile Ala Ala Ser Gly Gly Val Lys Leu Val Lys
100 105 110
His Gly Asn Arg Ser Val Ser Ser Lys Ser Gly
115 120

<210> 465
<211> 564
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101)..(541)
<223> RXN02918

<400> 465
agattgtcgc ttttccatt tctccgggtt ttctggaact ttttgggcgt atgctgggaa 60
tgattctatt attgccaaat cagaaagcag gagagacccg atg agc gaa atc cta 115
Met Ser Glu Ile Leu
1 5
gaa acc tat tgg gca ccc cac ttt gga aaa acc gaa gaa gcc aca gca 163
Glu Thr Tyr Trp Ala Pro His Phe Gly Lys Thr Glu Glu Ala Thr Ala
10 15 20
ctc gtt tca tac ctg gca caa gct tcc ggc gat ccc att gag gtt cac 211
Leu Val Ser Tyr Leu Ala Gln Ala Ser Gly Asp Pro Ile Glu Val His

25										30										35										
acc	ctg	ttc	ggg	gat	tta	ggt	tta	gac	gga	ctc	tct	gga	aac	tac	acc	259														
Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu	Ser	Gly	Asn	Tyr	Thr															
40						45						50																		
gac	act	gag	att	gac	ggc	tac	ggc	gac	gca	ttc	ctg	ctg	gtt	gca	gcg	307														
Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe	Leu	Leu	Val	Ala	Ala															
55						60						65																		
cta	tcc	gtg	ttg	atg	gct	gaa	aac	aaa	gca	aca	ggt	ggc	gtg	aat	ctg	355														
Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr	Gly	Gly	Val	Asn	Leu															
70						75						80			85															
ggt	gag	ctt	ggg	gga	gct	gat	aaa	tcg	atc	cgg	ctg	cat	gtt	gaa	tcc	403														
Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg	Leu	His	Val	Glu	Ser															
			90						95						100															
aag	gag	aac	acc	caa	atc	aac	acc	gca	ttg	aag	tat	ttt	gcg	ctc	tcc	451														
Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys	Tyr	Phe	Ala	Leu	Ser															
			105						110						115															
cca	gaa	gac	cac	gca	gca	gca	gat	cgc	ttc	gat	gag	gat	gac	ctg	tct	499														
Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp	Glu	Asp	Asp	Leu	Ser															
			120			125						130																		
gag	ctt	gcc	aac	ttg	agt	gaa	gag	ctg	cgc	gga	cag	ctg	gac			541														
Glu	Leu	Ala	Asn	Leu	Ser	Glu	Glu	Leu	Arg	Gly	Gln	Leu	Asp																	
135						140						145																		
taattgtctc ccatttaagg agt															564															

<210> 466

<211> 147

<212> PRT

<213> Corynebacterium glutamicum

<400> 466

Met	Ser	Glu	Ile	Leu	Glu	Thr	Tyr	Trp	Ala	Pro	His	Phe	Gly	Lys	Thr
1				5					10					15	
Glu	Glu	Ala	Thr	Ala	Leu	Val	Ser	Tyr	Leu	Ala	Gln	Ala	Ser	Gly	Asp
			20					25					30		
Pro	Ile	Glu	Val	His	Thr	Leu	Phe	Gly	Asp	Leu	Gly	Leu	Asp	Gly	Leu
			35				40					45			
Ser	Gly	Asn	Tyr	Thr	Asp	Thr	Glu	Ile	Asp	Gly	Tyr	Gly	Asp	Ala	Phe
	50					55					60				
Leu	Leu	Val	Ala	Ala	Leu	Ser	Val	Leu	Met	Ala	Glu	Asn	Lys	Ala	Thr
65					70					75					80
Gly	Gly	Val	Asn	Leu	Gly	Glu	Leu	Gly	Gly	Ala	Asp	Lys	Ser	Ile	Arg
			85					90						95	
Leu	His	Val	Glu	Ser	Lys	Glu	Asn	Thr	Gln	Ile	Asn	Thr	Ala	Leu	Lys
			100					105					110		
Tyr	Phe	Ala	Leu	Ser	Pro	Glu	Asp	His	Ala	Ala	Ala	Asp	Arg	Phe	Asp

115	120	125	
Glu Asp Asp Leu Ser Glu Leu Ala Asn Leu Ser		Glu Glu Leu Arg Gly	
130	135	140	
Gln Leu Asp			
145			
<210> 467			
<211> 735			
<212> DNA			
<213> Corynebacterium glutamicum			
<220>			
<221> CDS			
<222> (101)..(712)			
<223> RXN01116			
<400> 467			
tgccaggaat ttacgtcaac cgcgtcgtcc acgttggacc gcaggaaacc ggaatcgaaa	60		
acaggacggt gtctaactaa tgacttggga tcataaccaa atg gca gcc cgc gtt	115		
	Met Ala Ala Arg Val		
	1	5	
gcc cag gaa ctt gaa gac ggc cag tac gtc aac ctc ggc atc ggc atg	163		
Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn Leu Gly Ile Gly Met			
10	15	20	
cct aca ctt atc ccc ggc tac ctg cct gag gga cta gag gtt atc ctt	211		
Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly Leu Glu Val Ile Leu			
25	30	35	
cac tcc gaa aac ggt gtg ctg ggc gtt gga cct tac cca act gaa gag	259		
His Ser Glu Asn Gly Val Leu Gly Val Gly Pro Tyr Pro Thr Glu Glu			
40	45	50	
gaa ctt gat cct gag ctg atc aac gcc ggc aag gaa acc atc acg gtt	307		
Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys Glu Thr Ile Thr Val			
55	60	65	
gca cct ggc gca tcc tac ttc tcc tct tct gat tct ttc gcc atg atc	355		
Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp Ser Phe Ala Met Ile			
70	75	80	85
cgc tcc aag tct gtc gac gtt gca gtc ttg ggc gtt atg gaa gtc tcc	403		
Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly Val Met Glu Val Ser			
90	95	100	
cag tac ggc gac ctg gcc aac tgg atg att ccc ggc aag ctg gtc aag	451		
Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro Gly Lys Leu Val Lys			
105	110	115	
ggg atg ggt ggc gca atg gat ctg gtg cac ggc gca tcc aag atc atc	499		
Gly Met Gly Gly Ala Met Asp Leu Val His Gly Ala Ser Lys Ile Ile			
120	125	130	
gcc atg acc gat cac atc acc aag aag ggc gct ccg aag atc ctt aag	547		
Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala Pro Lys Ile Leu Lys			
135	140	145	

gag tgt cgc ctc cca ctg act ggc gcg aag tgc gtg gac atg att gtc 595
 Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys Val Asp Met Ile Val
 150 155 160 165
 acc acc cac gct gtg ttc tct gtg gac cct gaa gaa ggc ctc acg ctc 643
 Thr Thr His Ala Val Phe Ser Val Asp Pro Glu Glu Gly Leu Thr Leu
 170 175 180
 atc gag tgc gcc gac ggt gtc acc gtt gag gaa ctc cgc gaa atc acc 691
 Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu Leu Arg Glu Ile Thr
 185 190 195
 gaa gcc gat ttc aaa gtt gct taagcaaacg ctgcgcaatt aag 735
 Glu Ala Asp Phe Lys Val Ala
 200

<210> 468

<211> 204

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 468

Met Ala Ala Arg Val Ala Gln Glu Leu Glu Asp Gly Gln Tyr Val Asn
 1 5 10 15
 Leu Gly Ile Gly Met Pro Thr Leu Ile Pro Gly Tyr Leu Pro Glu Gly
 20 25 30
 Leu Glu Val Ile Leu His Ser Glu Asn Gly Val Leu Gly Val Gly Pro
 35 40 45
 Tyr Pro Thr Glu Glu Glu Leu Asp Pro Glu Leu Ile Asn Ala Gly Lys
 50 55 60
 Glu Thr Ile Thr Val Ala Pro Gly Ala Ser Tyr Phe Ser Ser Ser Asp
 65 70 75 80
 Ser Phe Ala Met Ile Arg Ser Lys Ser Val Asp Val Ala Val Leu Gly
 85 90 95
 Val Met Glu Val Ser Gln Tyr Gly Asp Leu Ala Asn Trp Met Ile Pro
 100 105 110
 Gly Lys Leu Val Lys Gly Met Gly Gly Ala Met Asp Leu Val His Gly
 115 120 125
 Ala Ser Lys Ile Ile Ala Met Thr Asp His Ile Thr Lys Lys Gly Ala
 130 135 140
 Pro Lys Ile Leu Lys Glu Cys Arg Leu Pro Leu Thr Gly Ala Lys Cys
 145 150 155 160
 Val Asp Met Ile Val Thr Thr His Ala Val Phe Ser Val Asp Pro Glu
 165 170 175
 Glu Gly Leu Thr Leu Ile Glu Cys Ala Asp Gly Val Thr Val Glu Glu
 180 185 190
 Leu Arg Glu Ile Thr Glu Ala Asp Phe Lys Val Ala

195

200

```
<210> 469
<211> 876
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>  
<221> CDS  
<222> (101) .. (853)  
<223> RXN01115
```

<400> 469															
ctcaccgcat gcagcgtgaa aacactcagt acggactggc caccatgtgc atcgggtggcg 60															
gccagggtct tgcagctgtc tttgaaaagg agaactaaaa atg gct att ttg cac 115															
Met Ala Ile Leu His 5															
1															
agc gtt tcc tac gga act tcc gac aac acc ttg gtg ttc att ggc tcg 163															
Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu Val Phe Ile Gly Ser 20															
10 15															
ttg ggt tcc acc acc gac atg tgg ctg cca cag ctg gat gcc ttg cat 211															
Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln Leu Asp Ala Leu His 35															
25 30															
aag gat ttc cgc gtc atc gct gtt gat cac cgc gga cat ggt ctg tct 259															
Lys Asp Phe Arg Val Ile Ala Val Asp His Arg Gly His Gly Leu Ser 50															
40 45															
gaa ctc atc gaa ggc acc ccc act gtg gcg gat ctg gcg cag gat gtg 307															
Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp Leu Ala Gln Asp Val 65															
55 60															
ctg gat acc ctc gat gac ctg ggt gtc gga aac ttc ggc gtc atc gga 355															
Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn Phe Gly Val Ile Gly 85															
70 75 80															
cta tct ctc ggc gga gcg gtt gca caa tac ttg gcg gcc acc tct gat 403															
Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu Ala Ala Thr Ser Asp 100															
90 95															
cgt gtc acc aag gca gca ttc atg tgt acc gct gca aaa ttc ggc gag 451															
Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala Ala Lys Phe Gly Glu 115															
105 110															
ccc cag ggc tgg cta gat cgc gcc gca gcg tgc cgc gaa aac ggc act 499															
Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys Arg Glu Asn Gly Thr 130															
120 125															
ggg tct ctg tcc gaa gct gtg atc cag cgc tgg ttc tcc ccc act tgg 547															
Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp Phe Ser Pro Thr Trp 145															
135 140															
ttg gag aac aac cca gcg tcc cgc gag cac ttc gaa gcc atg gtt gcc 595															
Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe Glu Ala Met Val Ala 165															
150 155 160															
ggc acc cca tct gag ggt tac gcg ctg tgc tgc gag gcg ttg gca acc 643															

Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys Glu Ala Leu Ala Thr
 170 175 180
 tgg gat ttc acc gat cgc ctg gga gaa atc acc gtg cca gtg ctc acc 691
 Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr Val Pro Val Leu Thr
 185 190 195
 atc gca ggt gcc gat gac ccc tcc act cct cca gca acc gtg cag atc 739
 Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro Ala Thr Val Gln Ile
 200 205 210
 att gcc gat ggc gtt ggc ggc gag tcc cgc gca gag gtc cta agc cca 787
 Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala Glu Val Leu Ser Pro
 215 220 225
 gcc gcg cac gta cca acc gtg gaa cgt cca aac gag gta aat gaa ctg 835
 Ala Ala His Val Pro Thr Val Glu Arg Pro Asn Glu Val Asn Glu Leu
 230 235 240 245
 cta gca cag cat ttc gct taatgttgta ggcatgttca caa 876
 Leu Ala Gln His Phe Ala
 250

<210> 470

<211> 251

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 470

Met Ala Ile Leu His Ser Val Ser Tyr Gly Thr Ser Asp Asn Thr Leu
 1 5 10 15
 Val Phe Ile Gly Ser Leu Gly Ser Thr Thr Asp Met Trp Leu Pro Gln
 20 25 30
 Leu Asp Ala Leu His Lys Asp Phe Arg Val Ile Ala Val Asp His Arg
 35 40 45
 Gly His Gly Leu Ser Glu Leu Ile Glu Gly Thr Pro Thr Val Ala Asp
 50 55 60
 Leu Ala Gln Asp Val Leu Asp Thr Leu Asp Asp Leu Gly Val Gly Asn
 65 70 75 80
 Phe Gly Val Ile Gly Leu Ser Leu Gly Gly Ala Val Ala Gln Tyr Leu
 85 90 95
 Ala Ala Thr Ser Asp Arg Val Thr Lys Ala Ala Phe Met Cys Thr Ala
 100 105 110
 Ala Lys Phe Gly Glu Pro Gln Gly Trp Leu Asp Arg Ala Ala Ala Cys
 115 120 125
 Arg Glu Asn Gly Thr Gly Ser Leu Ser Glu Ala Val Ile Gln Arg Trp
 130 135 140
 Phe Ser Pro Thr Trp Leu Glu Asn Asn Pro Ala Ser Arg Glu His Phe
 145 150 155 160
 Glu Ala Met Val Ala Gly Thr Pro Ser Glu Gly Tyr Ala Leu Cys Cys

	165		170		175
Glu Ala Leu Ala Thr Trp Asp Phe Thr Asp Arg Leu Gly Glu Ile Thr	180		185		190
Val Pro Val Leu Thr Ile Ala Gly Ala Asp Asp Pro Ser Thr Pro Pro	195		200		205
Ala Thr Val Gln Ile Ile Ala Asp Gly Val Gly Gly Glu Ser Arg Ala	210		215		220
Glu Val Leu Ser Pro Ala Ala His Val Pro Thr Val Glu Arg Pro Asn	225		230		235
					240
Glu Val Asn Glu Leu Leu Ala Gln His Phe Ala	245		250		

<210> 471

<211> 1284

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1261)

<223> RXS00116

<400> 471

```

cgcggcacgc acgctggggg caagcgtcga caagcacaaa ctttttgctt aattgaatcc 60
tttgcgcacc aatcaatggg ggatcaaata tagtagctgc atg agt aat gac ttc 115
                                         Met Ser Asn Asp Phe
                                         1                               5

gtc gtt tct agg ctt aga ccc ttt ggt gaa acg att ttt gca acc atg 163
Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr Ile Phe Ala Thr Met
                        10                        15                        20

acc cag cga gct gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt 211
Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe
                        25                        30                        35

cct gat gag gat ggt cct cgt cgg atg tta gag atc gcg tcg gag cag 259
Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln
                        40                        45                        50

att ctc ggg gga aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg 307
Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser
                        55                        60                        65

ttg agg gca gct gtg gct cgt gat cat ttg gag agg ttt gat ctg gag 355
Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu
                        70                        75                        80                        85

tac aac cct gat tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg 403
Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala
                        90                        95                        100

att acg gcg act gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc 451
Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile

```

105						110						115						
gtt	ttg	gaa	ccg	tat	tac	gat	gcg	tat	gcg	gcg	gct	att	gcg	ttg	gcg	499		
Val	Leu	Glu	Pro	Tyr	Tyr	Asp	Ala	Tyr	Ala	Ala	Ala	Ile	Ala	Leu	Ala			
120						125						130						
ggg	gcg	acg	cgg	gtg	gcg	gtt	cct	ttg	cag	gag	gtg	gag	aac	tcg	tgg	547		
Gly	Ala	Thr	Arg	Val	Ala	Val	Pro	Leu	Gln	Glu	Val	Glu	Asn	Ser	Trp			
135						140						145						
gat	gtg	gat	gtc	gat	aag	ttg	cat	gcg	gcg	gtg	act	aag	aag	acg	cgg	595		
Asp	Val	Asp	Val	Asp	Lys	Leu	His	Ala	Ala	Val	Thr	Lys	Lys	Thr	Arg			
150						155						160						
atg	att	atc	gtt	aat	tcg	ccg	cat	aat	ccg	acg	ggg	tcg	gtg	ttt	tct	643		
Met	Ile	Ile	Val	Asn	Ser	Pro	His	Asn	Pro	Thr	Gly	Ser	Val	Phe	Ser			
170						175						180						
aag	aag	gcg	ttg	aag	cag	ttg	gcg	ggg	gtt	gct	cgt	gcg	tat	gac	ttg	691		
Lys	Lys	Ala	Leu	Lys	Gln	Leu	Ala	Gly	Val	Ala	Arg	Ala	Tyr	Asp	Leu			
185						190						195						
ttg	gtg	ttg	tca	gat	gag	gtg	tat	gag	cat	ctt	gtt	ttt	gat	gat	cag	739		
Leu	Val	Leu	Ser	Asp	Glu	Val	Tyr	Glu	His	Leu	Val	Phe	Asp	Asp	Gln			
200						205						210						
aag	cat	gtg	agt	gtc	gcg	aag	ctg	ccc	ggg	atg	tgg	gat	cgc	acg	gtg	787		
Lys	His	Val	Ser	Val	Ala	Lys	Leu	Pro	Gly	Met	Trp	Asp	Arg	Thr	Val			
215						220						225						
acg	gtg	tcg	tcg	gcg	gcg	aaa	acg	ttc	aat	gtg	act	ggg	tgg	aag	acg	835		
Thr	Val	Ser	Ser	Ala	Ala	Lys	Thr	Phe	Asn	Val	Thr	Gly	Trp	Lys	Thr			
230						235						240						
ggg	tgg	gcg	ttg	gca	ccg	gag	ccg	ttg	ttg	gag	gcg	gtg	ttg	aag	gcg	883		
Gly	Trp	Ala	Leu	Ala	Pro	Glu	Pro	Leu	Leu	Glu	Ala	Val	Leu	Lys	Ala			
250						255						260						
aag	cag	ttt	atg	tct	tat	gtg	ggg	gct	aca	cct	ttt	cag	ccg	gct	gtg	931		
Lys	Gln	Phe	Met	Ser	Tyr	Val	Gly	Ala	Thr	Pro	Phe	Gln	Pro	Ala	Val			
265						270						275						
gcg	cat	gcg	att	gaa	cat	gag	cag	aag	tgg	gtg	tca	aag	atg	tct	aag	979		
Ala	His	Ala	Ile	Glu	His	Glu	Gln	Lys	Trp	Val	Ser	Lys	Met	Ser	Lys			
280						285						290						
ggg	ctt	gag	ctc	aag	cgg	gat	att	ttg	cgt	act	gcg	tta	gat	aag	gcg			
1027																		
Gly	Leu	Glu	Leu	Lys	Arg	Asp	Ile	Leu	Arg	Thr	Ala	Leu	Asp	Lys	Ala			
295						300						305						
ggg	ctg	aag	act	cat	gac	agt	atg	ggc	acg	tat	ttc	atc	gtt	gcg	gat			
1075																		
Gly	Leu	Lys	Thr	His	Asp	Ser	Met	Gly	Thr	Tyr	Phe	Ile	Val	Ala	Asp			
310						315						320						
att	ggg	gat	cgt	gat	ggg	gcg	gag	ttc	tgt	ttt	gag	ttg	att	gag	aag			
1123																		
Ile	Gly	Asp	Arg	Asp	Gly	Ala	Glu	Phe	Cys	Phe	Glu	Leu	Ile	Glu	Lys			
330						335						340						

gtt ggg gtg gcg gcg att ccg gtg cag gcg ttt gtg gat cat ccg aag
 1171
 Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe Val Asp His Pro Lys
 345 350 355

aag tgg tcg tcg aag gtt cgt ttt gcg ttt tgc aaa aaa gaa gag acg
 1219
 Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys Lys Lys Glu Glu Thr
 360 365 370

ctc cgc gaa gct gcg gag cgt ctc aag ggg att aag aaa cta
 1261
 Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile Lys Lys Leu
 375 380 385

tagtttgaac aggttggttg ggg
 1284

<210> 472

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ser Asn Asp Phe Val Val Ser Arg Leu Arg Pro Phe Gly Glu Thr
 1 5 10 15

Ile Phe Ala Thr Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn
 20 25 30

Leu Gly Gln Gly Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu
 35 40 45

Ile Ala Ser Glu Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly
 50 55 60

Arg Gly Asp Ala Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu
 65 70 75 80

Arg Phe Asp Leu Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val
 85 90 95

Gly Ala Thr Glu Ala Ile Thr Ala Thr Val Leu Gly Leu Val Glu Pro
 100 105 110

Gly Asp Glu Val Ile Val Leu Glu Pro Tyr Tyr Asp Ala Tyr Ala Ala
 115 120 125

Ala Ile Ala Leu Ala Gly Ala Thr Arg Val Ala Val Pro Leu Gln Glu
 130 135 140

Val Glu Asn Ser Trp Asp Val Asp Val Asp Lys Leu His Ala Ala Val
 145 150 155 160

Thr Lys Lys Thr Arg Met Ile Ile Val Asn Ser Pro His Asn Pro Thr
 165 170 175

Gly Ser Val Phe Ser Lys Lys Ala Leu Lys Gln Leu Ala Gly Val Ala
 180 185 190

Arg Ala Tyr Asp Leu Leu Val Leu Ser Asp Glu Val Tyr Glu His Leu
 195 200 205
 Val Phe Asp Asp Gln Lys His Val Ser Val Ala Lys Leu Pro Gly Met
 210 215 220
 Trp Asp Arg Thr Val Thr Val Ser Ser Ala Ala Lys Thr Phe Asn Val
 225 230 235 240
 Thr Gly Trp Lys Thr Gly Trp Ala Leu Ala Pro Glu Pro Leu Leu Glu
 245 250 255
 Ala Val Leu Lys Ala Lys Gln Phe Met Ser Tyr Val Gly Ala Thr Pro
 260 265 270
 Phe Gln Pro Ala Val Ala His Ala Ile Glu His Glu Gln Lys Trp Val
 275 280 285
 Ser Lys Met Ser Lys Gly Leu Glu Leu Lys Arg Asp Ile Leu Arg Thr
 290 295 300
 Ala Leu Asp Lys Ala Gly Leu Lys Thr His Asp Ser Met Gly Thr Tyr
 305 310 315 320
 Phe Ile Val Ala Asp Ile Gly Asp Arg Asp Gly Ala Glu Phe Cys Phe
 325 330 335
 Glu Leu Ile Glu Lys Val Gly Val Ala Ala Ile Pro Val Gln Ala Phe
 340 345 350
 Val Asp His Pro Lys Lys Trp Ser Ser Lys Val Arg Phe Ala Phe Cys
 355 360 365
 Lys Lys Glu Glu Thr Leu Arg Glu Ala Ala Glu Arg Leu Lys Gly Ile
 370 375 380
 Lys Lys Leu
 385

<210> 473
 <211> 607
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(607)
 <223> FRXA00116

<400> 473
 ttgcgcacc aatcaatggg ggatcaaata tagtagctgc atgagtaatg acttcgtcgt 60
 ttctaggctt agaccctttg gtgaaacgat ttttgcaacc atg acc cag cga gct 115
 Met Thr Gln Arg Ala
 1 5
 gtt gag gcg ggt gca atc aat ctt ggt cag ggc ttt cct gat gag gat 163
 Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly Phe Pro Asp Glu Asp
 10 15 20

```

ggt cct cgt cgg atg tta gag atc gcg tcg gag cag att ctc ggg gga    211
Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu Gln Ile Leu Gly Gly
                25                      30                      35

aat aat cag tat tcg gcg ggg cgt ggg gat gct tcg ttg agg gca gct    259
Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala Ser Leu Arg Ala Ala
                40                      45                      50

gtg gct cgt gat cat ttg gag agg ttt gat ctg gag tac aac cct gat    307
Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu Glu Tyr Asn Pro Asp
                55                      60                      65

tcg gag gtg ttg atc acg gtg ggg gcc act gag gcg att acg gcg act    355
Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu Ala Ile Thr Ala Thr
                70                      75                      80                      85

gtg ttg ggt ttg gtg gag cct ggg gat gaa gtg atc gtt ttg gaa ccg    403
Val Leu Gly Leu Val Glu Pro Gly Asp Glu Val Ile Val Leu Glu Pro
                90                      95                      100

tat tac gat gcg tat gcg gcg gct att gcg ttg gcg ggg gcg acg cgg    451
Tyr Tyr Asp Ala Tyr Ala Ala Ala Ile Ala Leu Ala Gly Ala Thr Arg
                105                      110                      115

gtg gcg gtt cct ttg cag gag gtg gag aac tcg tgg gat gtg gat gtc    499
Val Ala Val Pro Leu Gln Glu Val Glu Asn Ser Trp Asp Val Asp Val
                120                      125                      130

gat aag ttg cat gcg gcg gtg act aag aag acg cgg atg att atc gtt    547
Asp Lys Leu His Ala Ala Val Thr Lys Lys Thr Arg Met Ile Ile Val
                135                      140                      145

aat tcg ccg cat aat ccg acg ggt tcg gtg ttt tct aag aag gcg ttg    595
Asn Ser Pro His Asn Pro Thr Gly Ser Val Phe Ser Lys Lys Ala Leu
                150                      155                      160                      165

aag cag ttg gcg
Lys Gln Leu Ala
                                                607

```

<210> 474

<211> 169

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 474

```

Met Thr Gln Arg Ala Val Glu Ala Gly Ala Ile Asn Leu Gly Gln Gly
  1                      5                      10                      15

Phe Pro Asp Glu Asp Gly Pro Arg Arg Met Leu Glu Ile Ala Ser Glu
                20                      25                      30

Gln Ile Leu Gly Gly Asn Asn Gln Tyr Ser Ala Gly Arg Gly Asp Ala
                35                      40                      45

Ser Leu Arg Ala Ala Val Ala Arg Asp His Leu Glu Arg Phe Asp Leu
                50                      55                      60

Glu Tyr Asn Pro Asp Ser Glu Val Leu Ile Thr Val Gly Ala Thr Glu
                65                      70                      75                      80

```

[illegible]

<210> 475
<211> 843
<212> DNA
<213> *Corynebacterium glutamicum*

```
<220>  
<221> CDS  
<222> (101) .. (820)  
<223> RXS00391
```

<400> 475																	
atctt	gtaga	tccc	accgca	attct	gtggag	atctc	gagga	cgcaat	ctct	ggaag	aaaac	60					
tttcctcccc atccctgtac aagataaaac ccgtgcacag												ttg	ctg	cgc	gat	tct	115
												Leu	Leu	Arg	Asp	Ser	5
												1					
caa	cga	gtt	ggc	ctc	gcc	atc	gat	cct	tcg	atc	gct	ttg	gtg	atg	gcc	163	
Gln	Arg	Val	Gly	Leu	Ala	Ile	Asp	Pro	Ser	Ile	Ala	Leu	Val	Met	Ala		
				10					15					20			
act	tct	ggt	tct	aca	ggt	acc	ccg	aag	ggc	gct	cag	ctc	act	ccg	ttg	211	
Thr	Ser	Gly	Ser	Thr	Gly	Thr	Pro	Lys	Gly	Ala	Gln	Leu	Thr	Pro	Leu		
				25					30					35			
aat	ttg	gtg	agt	tcc	gcc	gat	gct	acg	cat	cag	ttt	tta	ggt	ggc	gaa	259	
Asn	Leu	Val	Ser	Ser	Ala	Asp	Ala	Thr	His	Gln	Phe	Leu	Gly	Gly	Glu		
				40					45					50			
ggc	cag	tg	gtg	ttg	ctt	gcc	atg	cca	gca	cac	cac	att	gca	ggc	atg	307	
Gly	Gln	Trp	Leu	Leu	Ala	Met	Pro	Ala	His	His	Ile	Ala	Gly	Met	Gln		
				55					60					65			
gtg	ctt	ctt	cga	agc	ctc	att	gct	gga	gtt	gag	cca	cta	gct	att	gat	355	
Val	Leu	Leu	Arg	Ser	Leu	Ile	Ala	Gly	Val	Glu	Pro	Leu	Ala	Ile	Asp		
				70					75					80			
ctc	agc	aca	ggt	ttt	cac	att	gac	gct	ttc	gca	ggc	gcc	gcg	gca	gaa	403	
Leu	Ser	Thr	Gly	Phe	His	Ile	Asp	Ala	Phe	Ala	Gly	Ala	Ala	Ala	Glu		
				90					95					100			

ctg aaa aat acc ggc gac cgc gtc tat aca tcc ttg act cca atg cag 451
 Leu Lys Asn Thr Gly Asp Arg Val Tyr Thr Ser Leu Thr Pro Met Gln
 105 110 115

 tta ctt aaa gca atg gac tcc ttg caa ggc att gaa gcc ctg aaa ctt 499
 Leu Leu Lys Ala Met Asp Ser Leu Gln Gly Ile Glu Ala Leu Lys Leu
 120 125 130

 ttt gat gtc att ctt gtt ggc ggt gct gca ttg tct aag cag gcc cga 547
 Phe Asp Val Ile Leu Val Gly Gly Ala Ala Leu Ser Lys Gln Ala Arg
 135 140 145

 att tct gcg gag cag cta gac atc aac att gtc acc acc tac ggc tcc 595
 Ile Ser Ala Glu Gln Leu Asp Ile Asn Ile Val Thr Thr Tyr Gly Ser
 150 155 160 165

 tca gag act tca ggt ggc tgc gtt tat gat ggc aag ccc att ccc ggc 643
 Ser Glu Thr Ser Gly Gly Cys Val Tyr Asp Gly Lys Pro Ile Pro Gly
 170 175 180

 gcg aaa gtc cgt att tcg gat gag cgc att gag ttg ggt ggc ccg atg 691
 Ala Lys Val Arg Ile Ser Asp Glu Arg Ile Glu Leu Gly Gly Pro Met
 185 190 195

 att gcg cag ggc tac aga aat gca cct gaa cat ccg gat ttc gcc aac 739
 Ile Ala Gln Gly Tyr Arg Asn Ala Pro Glu His Pro Asp Phe Ala Asn
 200 205 210

 gag ggt tgg ttt acc acc tct gat tca ggt gaa ctc cac gac ggg att 787
 Glu Gly Trp Phe Thr Thr Ser Asp Ser Gly Glu Leu His Asp Gly Ile
 215 220 225

 ctc acc gtg act ggt cgc gtg gat acc cgt cat tgattccggt ggattgaagt 840
 Leu Thr Val Thr Gly Arg Val Asp Thr Arg His
 230 235 240

 tgc 843

<210> 476
 <211> 240
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 476
 Leu Leu Arg Asp Ser Gln Arg Val Gly Leu Ala Ile Asp Pro Ser Ile
 1 5 10 15

 Ala Leu Val Met Ala Thr Ser Gly Ser Thr Gly Thr Pro Lys Gly Ala
 20 25 30

 Gln Leu Thr Pro Leu Asn Leu Val Ser Ser Ala Asp Ala Thr His Gln
 35 40 45

 Phe Leu Gly Gly Glu Gly Gln Trp Leu Leu Ala Met Pro Ala His His
 50 55 60

 Ile Ala Gly Met Gln Val Leu Leu Arg Ser Leu Ile Ala Gly Val Glu
 65 70 75 80

 Pro Leu Ala Ile Asp Leu Ser Thr Gly Phe His Ile Asp Ala Phe Ala

85										90					95				
Gly	Ala	Ala	Ala	Glu	Leu	Lys	Asn	Thr	Gly	Asp	Arg	Val	Tyr	Thr	Ser				
			100						105					110					
Leu	Thr	Pro	Met	Gln	Leu	Leu	Lys	Ala	Met	Asp	Ser	Leu	Gln	Gly	Ile				
		115					120					125							
Glu	Ala	Leu	Lys	Leu	Phe	Asp	Val	Ile	Leu	Val	Gly	Gly	Ala	Ala	Leu				
		130				135					140								
Ser	Lys	Gln	Ala	Arg	Ile	Ser	Ala	Glu	Gln	Leu	Asp	Ile	Asn	Ile	Val				
145					150					155					160				
Thr	Thr	Tyr	Gly	Ser	Ser	Glu	Thr	Ser	Gly	Gly	Cys	Val	Tyr	Asp	Gly				
			165						170					175					
Lys	Pro	Ile	Pro	Gly	Ala	Lys	Val	Arg	Ile	Ser	Asp	Glu	Arg	Ile	Glu				
			180					185					190						
Leu	Gly	Gly	Pro	Met	Ile	Ala	Gln	Gly	Tyr	Arg	Asn	Ala	Pro	Glu	His				
		195					200					205							
Pro	Asp	Phe	Ala	Asn	Glu	Gly	Trp	Phe	Thr	Thr	Ser	Asp	Ser	Gly	Glu				
	210					215					220								
Leu	His	Asp	Gly	Ile	Leu	Thr	Val	Thr	Gly	Arg	Val	Asp	Thr	Arg	His				
225					230					235					240				

<210> 477

<211> 1017

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(994)

<223> RXS00393

<400> 477

tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60

aattgcgcga	tcgagtatgt	gatggggaaa	gatagagggt	atg	tct	cac	acg	gaa	115
				Met	Ser	His	Thr	Glu	
				1				5	

ccc	cag	ccg	aat	tct	gta	act	ttg	tcc	gat	tgg	att	caa	ggc	gca	cgc	163
Pro	Gln	Pro	Asn	Ser	Val	Thr	Leu	Ser	Asp	Trp	Ile	Gln	Gly	Ala	Arg	
			10						15					20		

ccg	cgt	acc	tgg	gca	aat	gcg	ttc	gcg	cct	gtc	att	gcc	ggg	tca	ggg	211
Pro	Arg	Thr	Trp	Ala	Asn	Ala	Phe	Ala	Pro	Val	Ile	Ala	Gly	Ser	Gly	
			25				30						35			

gtc	gcc	gct	ttt	cat	gat	ggg	ttt	gtg	tgg	tgg	aag	gcc	ttg	ctg	gcg	259
Val	Ala	Ala	Phe	His	Asp	Gly	Phe	Val	Trp	Trp	Lys	Ala	Leu	Leu	Ala	
			40				45					50				

ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat	307
Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp	
55 60 65	
tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg	355
Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu	
70 75 80 85	
cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg	403
Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala	
90 95 100	
gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc	451
Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser	
105 110 115	
ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg	499
Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu	
120 125 130	
ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg	547
Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly	
135 140 145	
ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg	595
Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met	
150 155 160 165	
gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc	643
Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala	
170 175 180	
gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac	691
Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn	
185 190 195	
aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc	739
Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu	
200 205 210	
gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg	787
Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu	
215 220 225	
att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg	835
Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp	
230 235 240 245	
cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca	883
Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala	
250 255 260	
ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccc gtc atc	931
Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Val Ile	
265 270 275	
ggc tca aca ggg cgc gcc atg gcg ttg tgg gcc gtg ctc acg ggc ctg	979
Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala Val Leu Thr Gly Leu	
280 285 290	

gca tta gcg ttt agc taaaacgctt ttcgacgctc ccc
 1017
 Ala Leu Ala Phe Ser
 295

<210> 478
 <211> 298
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 478
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15
 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60
 Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp

260 265 270
 Leu Ile Pro Val Ile Gly Ser Thr Gly Arg Ala Met Ala Leu Trp Ala
 275 280 285
 Val Leu Thr Gly Leu Ala Leu Ala Phe Ser
 290 295
 <210> 479
 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
 <221> CDS
 <222> (101)..(982)
 <223> FRXA00393
 <400> 479
 tctattcatt tcacaatagc gtttcacact ccccatagc ctgccgaacg tatttcaagc 60
 aattgcgcga tcgagtatgt gatggggaaa gatagaggtt atg tct cac acg gaa 115
 Met Ser His Thr Glu
 1 5
 ccc cag ccg aat tct gta act ttg tcc gat tgg att caa ggc gca cgc 163
 Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp Ile Gln Gly Ala Arg
 10 15 20
 ccg cgt acc tgg gca aat gcg ttc gcg cct gtc att gcc ggt tca ggt 211
 Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val Ile Ala Gly Ser Gly
 25 30 35
 gtc gcc gct ttt cat gat ggt ttt gtg tgg tgg aag gcc ttg ctg gcg 259
 Val Ala Ala Phe His Asp Gly Phe Val Trp Trp Lys Ala Leu Leu Ala
 40 45 50
 ctt gtc gtg gcg tgg gct ttg atc atc ggt gtg aat tac gcc aat gat 307
 Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val Asn Tyr Ala Asn Asp
 55 60 65
 tac tct gat ggc att cgt ggc acc gat gaa gac cgc acc ggt cct ctg 355
 Tyr Ser Asp Gly Ile Arg Gly Thr Asp Glu Asp Arg Thr Gly Pro Leu
 70 75 80 85
 cga ctc act ggt tct ggg ttg gct gag ccg aag aaa gtg aaa gct gcg 403
 Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys Lys Val Lys Ala Ala
 90 95 100
 gcg ttt att tct ttc ggt atc gca ggt gtc gcc ggc acc gcg ctg agc 451
 Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala Gly Thr Ala Leu Ser
 105 110 115
 ctg ttg agc gcg tgg tgg ctg atc ctc atc ggc atc ctg tgt gtg ctg 499
 Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly Ile Leu Cys Val Leu
 120 125 130
 ggc gcg tgg ttc tac acc ggc ggt aaa aat cct tat ggt tac cgc ggg 547
 Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro Tyr Gly Tyr Arg Gly
 135 140 145

ctc ggc gag att gct gtg ttc atc ttc ttc ggc ctc gtc gcg gtc atg 595
 Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly Leu Val Ala Val Met
 150 155 160 165
 gga acg cag ttc acc caa acc ggt tcc gtc agc tgg gcc ggt ttg gcc 643
 Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser Trp Ala Gly Leu Ala
 170 175 180
 gcc gca gtt ggc gtg ggg tcg atg tct gct ggc gtg aac ttg gcc aac 691
 Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly Val Asn Leu Ala Asn
 185 190 195
 aat att cgc gat att cca acc gat agc aag acc gga aaa att acc ctc 739
 Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr Gly Lys Ile Thr Leu
 200 205 210
 gcg gtc cgc ctg ggc gat gcg ggt gct cgt aag ctg ttc ctc gcg ctg 787
 Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys Leu Phe Leu Ala Leu
 215 220 225
 att tcc acg ccg ttc atc atg tcc atc tgc ctg gcg ttt gtc gcc tgg 835
 Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu Ala Phe Val Ala Trp
 230 235 240 245
 cca gcg ctg atc gcg atc atc gtt ttc ccg ctg gca ctg aaa gcc gca 883
 Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu Ala Leu Lys Ala Ala
 250 255 260
 ggg ccg atc cgc aac aac gcc acc ggc aag gat ctc atc ccg tca tcg 931
 Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp Leu Ile Pro Ser Ser
 265 270 275
 gct caa cag ggc gcg cca tgg cgt tgt ggg ccg tgc tca cgg gcc tgg 979
 Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro Cys Ser Arg Ala Trp
 280 285 290

cat tagcgttttag ctaaaacgct ttt
 1005
 His

<210> 480
 <211> 294
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 480
 Met Ser His Thr Glu Pro Gln Pro Asn Ser Val Thr Leu Ser Asp Trp
 1 5 10 15
 Ile Gln Gly Ala Arg Pro Arg Thr Trp Ala Asn Ala Phe Ala Pro Val
 20 25 30
 Ile Ala Gly Ser Gly Val Ala Ala Phe His Asp Gly Phe Val Trp Trp
 35 40 45
 Lys Ala Leu Leu Ala Leu Val Val Ala Trp Ala Leu Ile Ile Gly Val
 50 55 60

Asn Tyr Ala Asn Asp Tyr Ser Asp Gly Il Arg Gly Thr Asp Glu Asp
 65 70 75 80
 Arg Thr Gly Pro Leu Arg Leu Thr Gly Ser Gly Leu Ala Glu Pro Lys
 85 90 95
 Lys Val Lys Ala Ala Ala Phe Ile Ser Phe Gly Ile Ala Gly Val Ala
 100 105 110
 Gly Thr Ala Leu Ser Leu Leu Ser Ala Trp Trp Leu Ile Leu Ile Gly
 115 120 125
 Ile Leu Cys Val Leu Gly Ala Trp Phe Tyr Thr Gly Gly Lys Asn Pro
 130 135 140
 Tyr Gly Tyr Arg Gly Leu Gly Glu Ile Ala Val Phe Ile Phe Phe Gly
 145 150 155 160
 Leu Val Ala Val Met Gly Thr Gln Phe Thr Gln Thr Gly Ser Val Ser
 165 170 175
 Trp Ala Gly Leu Ala Ala Ala Val Gly Val Gly Ser Met Ser Ala Gly
 180 185 190
 Val Asn Leu Ala Asn Asn Ile Arg Asp Ile Pro Thr Asp Ser Lys Thr
 195 200 205
 Gly Lys Ile Thr Leu Ala Val Arg Leu Gly Asp Ala Gly Ala Arg Lys
 210 215 220
 Leu Phe Leu Ala Leu Ile Ser Thr Pro Phe Ile Met Ser Ile Cys Leu
 225 230 235 240
 Ala Phe Val Ala Trp Pro Ala Leu Ile Ala Ile Ile Val Phe Pro Leu
 245 250 255
 Ala Leu Lys Ala Ala Gly Pro Ile Arg Asn Asn Ala Thr Gly Lys Asp
 260 265 270
 Leu Ile Pro Ser Ser Ala Gln Gln Gly Ala Pro Trp Arg Cys Gly Pro
 275 280 285
 Cys Ser Arg Ala Trp His
 290

<210> 481

<211> 987

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> RXS00446

<400> 481

tgctacgaag ttatctagta atgaagttag tttttcccct ctcccggcag cagttgatgc 60

 ggtgacggag gctacttggg gggctaatacg gtacccggat atg ggt gcg gtt gag 115
 Met Gly Ala Val Glu

																1	5
ctc	cgt	gag	gct	ctt	gca	gag	cat	tta	gag	gtt	gag	ttt	gac	cag	gtc	163	
Leu	Arg	Glu	Ala	Leu	Ala	Glu	His	Leu	Glu	Val	Glu	Phe	Asp	Gln	Val		
				10					15					20			
acg	gta	ggc	tgc	ggc	tcg	tct	gcg	ctg	tgt	caa	cag	ctg	gtt	cag	gca	211	
Thr	Val	Gly	Cys	Gly	Ser	Ser	Ala	Leu	Cys	Gln	Gln	Leu	Val	Gln	Ala		
				25					30					35			
acg	tgc	gct	cag	ggc	gat	gag	gtc	att	ttt	cca	tgg	cgc	agc	ttt	gag	259	
Thr	Cys	Ala	Gln	Gly	Asp	Glu	Val	Ile	Phe	Pro	Trp	Arg	Ser	Phe	Glu		
				40					45					50			
gct	tat	cca	att	ttc	gcg	cag	gtc	gcg	ggc	gcc	act	cct	gtt	gcc	att	307	
Ala	Tyr	Pro	Ile	Phe	Ala	Gln	Val	Ala	Gly	Ala	Thr	Pro	Val	Ala	Ile		
				55					60					65			
ccg	ctg	act	gct	gat	cag	aat	cat	gat	ctt	gat	gcg	atg	gca	gcc	gcg	355	
Pro	Leu	Thr	Ala	Asp	Gln	Asn	His	Asp	Leu	Asp	Ala	Met	Ala	Ala	Ala		
				70					75					80			
atc	act	gat	aag	acc	cgc	ctc	att	ttc	atc	tgc	aac	ccc	aac	aat	cct	403	
Ile	Thr	Asp	Lys	Thr	Arg	Leu	Ile	Phe	Ile	Cys	Asn	Pro	Asn	Asn	Pro		
				90					95					100			
tcg	ggc	acc	acc	atc	acc	cag	gcg	cag	ttt	gat	aat	ttc	atg	gaa	aag	451	
Ser	Gly	Thr	Thr	Ile	Thr	Gln	Ala	Gln	Phe	Asp	Asn	Phe	Met	Glu	Lys		
				105					110					115			
gtt	cca	aac	gat	gtc	gtt	gtt	ggg	ctg	gat	gag	gct	tat	ttt	gag	ttc	499	
Val	Pro	Asn	Asp	Val	Val	Val	Gly	Leu	Asp	Glu	Ala	Tyr	Phe	Glu	Phe		
				120					125					130			
aac	cgc	gcg	gac	gac	acc	cca	gtt	gcc	act	gag	gaa	atc	cac	cgc	cac	547	
Asn	Arg	Ala	Asp	Asp	Thr	Pro	Val	Ala	Thr	Glu	Glu	Ile	His	Arg	His		
				135					140					145			
gac	aac	gtg	att	ggc	ttg	cgc	acg	ttc	tcc	aag	gcg	tat	ggc	ctg	gcg	595	
Asp	Asn	Val	Ile	Gly	Leu	Arg	Thr	Phe	Ser	Lys	Ala	Tyr	Gly	Leu	Ala		
				150					155					160			
ggc	ttg	cgt	gtt	ggc	tac	gcc	ttc	gga	aac	gca	gag	atc	atc	gca	gcg	643	
Gly	Leu	Arg	Val	Gly	Tyr	Ala	Phe	Gly	Asn	Ala	Glu	Ile	Ile	Ala	Ala		
				170					175					180			
atg	aat	aag	gtg	gct	att	cct	ttc	gcg	gtg	aat	tca	gca	gct	cag	gcg	691	
Met	Asn	Lys	Val	Ala	Ile	Pro	Phe	Ala	Val	Asn	Ser	Ala	Ala	Gln	Ala		
				185					190					195			
gca	gcg	ctt	gcg	agt	ttg	aat	tct	gcc	gat	gag	ttg	atg	gaa	cgg	gtg	739	
Ala	Ala	Leu	Ala	Ser	Leu	Asn	Ser	Ala	Asp	Glu	Leu	Met	Glu	Arg	Val		
				200					205					210			
gag	gaa	acc	gtc	gaa	aag	cgt	gat	gct	gtg	gtg	tca	gcg	ctt	ggc	gct	787	
Glu	Glu	Thr	Val	Glu	Lys	Arg	Asp	Ala	Val	Val	Ser	Ala	Leu	Gly	Ala		
				215					220					225			
gcg	ccg	acg	cag	gcc	aat	ttc	gtc	tgg	ctg	ccg	ggc	gag	ggc	gcc	gct	835	
Ala	Pro	Thr	Gln	Ala	Asn	Phe	Val	Trp	Leu	Pro	Gly	Glu	Gly	Ala	Ala		
				230					235					240			
														245			

gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att cgc gcg ttc 883
 Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile Arg Ala Phe
 250 255 260

ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa act gac aag 931
 Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu Thr Asp Lys
 265 270 275

ctg ctg cgc gcg tgg gag gcc atc aat gct ggg tagtctttgg cgttttgcgg 984
 Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 280 285

tgc 987

<210> 482

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 482

Met Gly Ala Val Glu Leu Arg Glu Ala Leu Ala Glu His Leu Glu Val
 1 5 10 15

Glu Phe Asp Gln Val Thr Val Gly Cys Gly Ser Ser Ala Leu Cys Gln
 20 25 30

Gln Leu Val Gln Ala Thr Cys Ala Gln Gly Asp Glu Val Ile Phe Pro
 35 40 45

Trp Arg Ser Phe Glu Ala Tyr Pro Ile Phe Ala Gln Val Ala Gly Ala
 50 55 60

Thr Pro Val Ala Ile Pro Leu Thr Ala Asp Gln Asn His Asp Leu Asp
 65 70 75 80

Ala Met Ala Ala Ala Ile Thr Asp Lys Thr Arg Leu Ile Phe Ile Cys
 85 90 95

Asn Pro Asn Asn Pro Ser Gly Thr Thr Ile Thr Gln Ala Gln Phe Asp
 100 105 110

Asn Phe Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu
 115 120 125

Ala Tyr Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu
 130 135 140

Glu Ile His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys
 145 150 155 160

Ala Tyr Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala
 165 170 175

Glu Ile Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn
 180 185 190

Ser Ala Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu
 195 200 205

Leu Met Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val
 210 215 220
 Ser Ala Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro
 225 230 235 240
 Gly Glu Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile
 245 250 255
 Val Ile Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala
 260 265 270
 Glu Glu Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 275 280 285

<210> 483
 <211> 545
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1) .. (522)
 <223> FRXA00446

<400> 483
 atg gaa aag gtt cca aac gat gtc gtt gtt ggg ctg gat gag gct tat 48
 Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15
 ttt gag ttc aac cgc gcg gac gac acc cca gtt gcc act gag gaa atc 96
 Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Ile
 20 25 30
 cac cgc cac gac aac gtg att ggt ttg cgc acg ttc tcc aag gcg tat 144
 His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45
 ggc ctg gcg ggc ttg cgt gtt ggt tac gcc ttc gga aac gca gag atc 192
 Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60
 atc gca gcg atg aat aag gtg gct att cct ttc gcg gtg aat tca gca 240
 Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80
 gct cag gcg gca gcg ctt gcg agt ttg aat tct gcc gat gag ttg atg 288
 Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95
 gaa cgg gtg gag gaa acc gtc gaa aag cgt gat gct gtg gtg tca gcg 336
 Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110
 ctt ggt gct gcg ccg acg cag gcc aat ttc gtc tgg ctg ccg ggc gag 384
 Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

ggc gcc gct gag ttg gcg gct aaa ttg gcc gag cac ggc atc gtg att 432
 Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

cgc gcg ttc ccc gag ggt gcg cgc att tcg gtg acc aac gcc gag gaa 480
 Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

act gac aag ctg ctg cgc gcg tgg gag gcc atc aat gct ggg 522
 Thr Asp Lys Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

tagtctttgg cgttttgcgg tgc 545

<210> 484

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

Met Glu Lys Val Pro Asn Asp Val Val Val Gly Leu Asp Glu Ala Tyr
 1 5 10 15

Phe Glu Phe Asn Arg Ala Asp Asp Thr Pro Val Ala Thr Glu Glu Ile
 20 25 30

His Arg His Asp Asn Val Ile Gly Leu Arg Thr Phe Ser Lys Ala Tyr
 35 40 45

Gly Leu Ala Gly Leu Arg Val Gly Tyr Ala Phe Gly Asn Ala Glu Ile
 50 55 60

Ile Ala Ala Met Asn Lys Val Ala Ile Pro Phe Ala Val Asn Ser Ala
 65 70 75 80

Ala Gln Ala Ala Ala Leu Ala Ser Leu Asn Ser Ala Asp Glu Leu Met
 85 90 95

Glu Arg Val Glu Glu Thr Val Glu Lys Arg Asp Ala Val Val Ser Ala
 100 105 110

Leu Gly Ala Ala Pro Thr Gln Ala Asn Phe Val Trp Leu Pro Gly Glu
 115 120 125

Gly Ala Ala Glu Leu Ala Ala Lys Leu Ala Glu His Gly Ile Val Ile
 130 135 140

Arg Ala Phe Pro Glu Gly Ala Arg Ile Ser Val Thr Asn Ala Glu Glu
 145 150 155 160

Thr Asp Lys Leu Leu Arg Ala Trp Glu Ala Ile Asn Ala Gly
 165 170

<210> 485

<211> 1230

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1207)

<223> RXS00618

<400> 485

```

gctgcattag agggtcgtat ctcgatctaa aagcagtagc cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
                                         Met Gln Met Leu Asp
                                         1           5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
                        10                        15                        20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
                        25                        30                        35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
                        40                        45                        50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
                        55                        60                        65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
                        70                        75                        80                        85

ggt gga ttc gtg gca tcg ttt atc gcc acc ttg gat cac ggg gat tat 403
Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu Asp His Gly Asp Tyr
                        90                        95                        100

gtg gca atg cct acc ccg ggg tac ccg gca tat cgc aat att ctg gaa 451
Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr Arg Asn Ile Leu Glu
                        105                        110                        115

tct ttg ggg gcg aag gtt ctg aac ctg cgc tgt act gca gag act cgt 499
Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys Thr Ala Glu Thr Arg
                        120                        125                        130

ttc cag cca acc gct caa atg ttg gag gaa ctg cca cac aag ccg aag 547
Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu Pro His Lys Pro Lys
                        135                        140                        145

gct gtt att gtc acc agc cca gga aac cca acg ggc acc atc att gat 595
Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr Gly Thr Ile Ile Asp
150                        155                        160                        165

ccg gaa gag cta gag cgc atc gcc aag tgg tgc gat gac aat gat gct 643
Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys Asp Asp Asn Asp Ala
                        170                        175                        180

gtt ctt atc tct gat gag gac tac cac ggc atg agc ttt ggt cgt ccg 691
Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met Ser Phe Gly Arg Pro
                        185                        190                        195

ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt acc 739

```


Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly Thr
 200 205 210
 ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc atc 787
 Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile Ile
 215 220 225
 gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct ctt 835
 Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser Leu
 230 235 240 245
 tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc ttc 883
 Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala Phe
 250 255 260
 act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat cgc 931
 Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr Arg
 265 270 275
 gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt ggc 979
 Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu Gly
 280 285 290
 act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt tct
 1027
 Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val Ser
 295 300 305
 gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat gaa
 1075
 Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp Glu
 310 315 320 325
 gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa ggc
 1123
 Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu Gly
 330 335 340
 cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc att
 1171
 His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr Ile
 345 350 355
 gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac
 1217
 Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 360 365
 taggttagtt tcg
 1230

<210> 486

<211> 369

<212> PRT

<213> Corynebacterium glutamicum

<400> 486

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30
 Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45
 Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60
 His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80
 Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr Leu
 85 90 95
 Asp His Gly Asp Tyr Val Ala Met Pro Thr Pro Gly Tyr Pro Ala Tyr
 100 105 110
 Arg Asn Ile Leu Glu Ser Leu Gly Ala Lys Val Leu Asn Leu Arg Cys
 115 120 125
 Thr Ala Glu Thr Arg Phe Gln Pro Thr Ala Gln Met Leu Glu Glu Leu
 130 135 140
 Pro His Lys Pro Lys Ala Val Ile Val Thr Ser Pro Gly Asn Pro Thr
 145 150 155 160
 Gly Thr Ile Ile Asp Pro Glu Glu Leu Glu Arg Ile Ala Lys Trp Cys
 165 170 175
 Asp Asp Asn Asp Ala Val Leu Ile Ser Asp Glu Asp Tyr His Gly Met
 180 185 190
 Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala
 195 200 205
 Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg
 210 215 220
 Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn
 225 230 235 240
 Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala
 245 250 255
 Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His
 260 265 270
 Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro
 275 280 285
 Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu
 290 295 300
 Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu
 305 310 315 320
 Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe
 325 330 335
 Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser

340	345	350
Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys		
355	360	365
Lys		
<210> 487		
<211> 657		
<212> DNA		
<213> <i>Corynebacterium glutamicum</i>		
<220>		
<221> CDS		
<222> (101)..(634)		
<223> FRXA00618		
<400> 487		
cccaacgggc accatcattg atccggaaga gctagagcgc atcgccaagt ggtgcgatga 60		
caatgatgct gttcttatct ctgatgagga ctaccacggc atg agc ttt ggt cgt 115		
		Met Ser Phe Gly Arg
		1 5
ccg ctg gca act gcg cat cag ttt tcc aag aac gcc atc gtg gtg ggt 163		
Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn Ala Ile Val Val Gly		
	10	15 20
acc ttg tcc aag tac ttc tcc atg acg ggt tgg cgc gtg ggt tgg atc 211		
Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp Arg Val Gly Trp Ile		
	25	30 35
atc gtt cca gat gag ctg gtc aca ccg att gaa aac ctg cag gct tct 259		
Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu Asn Leu Gln Ala Ser		
	40	45 50
ctt tcc ttg tgt gct cct gcc atc ggg cag gct gcg gga cgc gca gcc 307		
Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala Ala Gly Arg Ala Ala		
	55	60 65
ttc act ttg gag gct ggg gcc gaa ctt gat gcc cac gtt gaa gcg tat 355		
Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala His Val Glu Ala Tyr		
	70	75 80 85
cgc gag gcc cgg gag gtg ttc gtc gat aag ctc cct gaa atc ggg ctt 403		
Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu Pro Glu Ile Gly Leu		
	90	95 100
ggc act ttc gcc gac ccg gat ggc ggc ctg tat ttg tgg gtc gat gtt 451		
Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr Leu Trp Val Asp Val		
	105	110 115
tct gca tac acc gat gat tca gag gaa tgg gca ttg cgt ttg ctc gat 499		
Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala Leu Arg Leu Leu Asp		
	120	125 130
gaa gcg ggc gtg gcc gtc gcg ccg ggt gtt gat ttt gat cct gag gaa 547		
Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp Phe Asp Pro Glu Glu		
	135	140 145

ggc cac aag tgg att cgt ttg agc ctg tgc gcg tca aag gaa gac acc 595
 Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala Ser Lys Glu Asp Thr
 150 155 160 165

att gaa ggt gtg cgc aaa atc gga gaa ttc atc aaa aaa tagcagcgac 644
 Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile Lys Lys
 170 175

taggttagtt tcg 657

<210> 488

<211> 178

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

Met Ser Phe Gly Arg Pro Leu Ala Thr Ala His Gln Phe Ser Lys Asn
 1 5 10 15

Ala Ile Val Val Gly Thr Leu Ser Lys Tyr Phe Ser Met Thr Gly Trp
 20 25 30

Arg Val Gly Trp Ile Ile Val Pro Asp Glu Leu Val Thr Pro Ile Glu
 35 40 45

Asn Leu Gln Ala Ser Leu Ser Leu Cys Ala Pro Ala Ile Gly Gln Ala
 50 55 60

Ala Gly Arg Ala Ala Phe Thr Leu Glu Ala Gly Ala Glu Leu Asp Ala
 65 70 75 80

His Val Glu Ala Tyr Arg Glu Ala Arg Glu Val Phe Val Asp Lys Leu
 85 90 95

Pro Glu Ile Gly Leu Gly Thr Phe Ala Asp Pro Asp Gly Gly Leu Tyr
 100 105 110

Leu Trp Val Asp Val Ser Ala Tyr Thr Asp Asp Ser Glu Glu Trp Ala
 115 120 125

Leu Arg Leu Leu Asp Glu Ala Gly Val Ala Val Ala Pro Gly Val Asp
 130 135 140

Phe Asp Pro Glu Glu Gly His Lys Trp Ile Arg Leu Ser Leu Cys Ala
 145 150 155 160

Ser Lys Glu Asp Thr Ile Glu Gly Val Arg Lys Ile Gly Glu Phe Ile
 165 170 175

Lys Lys

<210> 489

<211> 385

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(385)

<223> FRXA00627

<400> 489

gctgcattag agggctcgat ctcgatctaa aagcagtagc cagataggct tgtctcttat 60

gaagccaagc actagaagca atgttcagcc gtttcgcgtc atg cag atg ttg gac 115
 Met Gln Met Leu Asp
 1 5

cga gtc cac cgt cgc agg cgc gaa ggc aaa gac acc tta atg ttc tgc 163
 Arg Val His Arg Arg Arg Glu Gly Lys Asp Thr Leu Met Phe Cys
 10 15 20

gct ggc cag ccg tca act ggt gcg cca gaa gca gtc atc gaa gaa gca 211
 Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala Val Ile Glu Glu Ala
 25 30 35

gag atc gct ctt cgc tcg ggt cct ttg gga tac acc gag gtg att ggt 259
 Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr Thr Glu Val Ile Gly
 40 45 50

gat cgt gag ttc cgt gaa cgc atc gcc gat tgg cac tct gct act tat 307
 Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp His Ser Ala Thr Tyr
 55 60 65

gac gta gac acc aac cct gac aat gtt att gtc acc acc ggt tct tca 355
 Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val Thr Thr Gly Ser Ser
 70 75 80 85

ggt gga ttc gtg gca tcg ttt atc gcc acc 385
 Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 90 95

<210> 490

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

Met Gln Met Leu Asp Arg Val His Arg Arg Arg Arg Glu Gly Lys Asp
 1 5 10 15

Thr Leu Met Phe Cys Ala Gly Gln Pro Ser Thr Gly Ala Pro Glu Ala
 20 25 30

Val Ile Glu Glu Ala Glu Ile Ala Leu Arg Ser Gly Pro Leu Gly Tyr
 35 40 45

Thr Glu Val Ile Gly Asp Arg Glu Phe Arg Glu Arg Ile Ala Asp Trp
 50 55 60

His Ser Ala Thr Tyr Asp Val Asp Thr Asn Pro Asp Asn Val Ile Val
 65 70 75 80

Thr Thr Gly Ser Ser Gly Gly Phe Val Ala Ser Phe Ile Ala Thr
 85 90 95

<210> 491
 <211> 1221
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(1198)
 <223> RXS01105

<400> 491
 ttgtcatcaa ctttgccaac gccgaagatc ttccagcgca cggcgaagca atccgtgcac 60
 gctttgaaaa cctccccacc accgacgagg cctaagaaaa atg acc aaa att act 115
 Met Thr Lys Ile Thr
 1 5
 ttg agc gat ttg cca ttg cgt gaa gaa ctg cgc ggt gag cac gct tac 163
 Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg Gly Glu His Ala Tyr
 10 15 20
 ggc gca ccc cag ctc aac gtt gat att cgc ctc aac acc aac gaa aac 211
 Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu Asn Thr Asn Glu Asn
 25 30 35
 cct tac cca ccg tca gag gca ttg gtc gct gac ttg gtt gcc acc gtg 259
 Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp Leu Val Ala Thr Val
 40 45 50
 gat aag atc gcc acc gag ctg aac cgc tac cca gag cgc gat gct gtg 307
 Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro Glu Arg Asp Ala Val
 55 60 65
 gaa ctg cgt gat gag ttg gct gcg tac atc acc aag caa acc ggc gtg 355
 Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr Lys Gln Thr Gly Val
 70 75 80 85
 gct gtc acc agg gat aac ctg tgg gct gcc aat ggt tcc aat gaa att 403
 Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn Gly Ser Asn Glu Ile
 90 95 100
 ctg cag cag ctg ctg cag gct ttt ggt gga cct gga cgc acc gcg ttg 451
 Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro Gly Arg Thr Ala Leu
 105 110 115
 gga ttc caa ccc agc tat tcc atg cac cca att ttg gct aaa ggc acc 499
 Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile Leu Ala Lys Gly Thr
 120 125 130
 cac act gaa ttc att gcg gtg tcc cga ggt gct gat ttc cgc atc gat 547
 His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala Asp Phe Arg Ile Asp
 135 140 145
 atg gat gtg gcg ctg gaa gaa att cgt gca aag cag cct gac att gtt 595
 Met Asp Val Ala Leu Glu Ile Arg Ala Lys Gln Pro Asp Ile Val
 150 155 160 165
 ttt gtc acc acc ccg aac aac ccg acc ggt gat gtg acc tcg ctg gac 643
 Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp Val Thr Ser Leu Asp
 170 175 180

gat gtt gag cgc atc atc aac gtt gcc cca ggc atc gtg atc gtg gat 691
Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly Ile Val Ile Val Asp
185 190 195

gaa gct tat gcg gaa ttc tcc cca tca cct tca gca acc act ctt ctg 739
Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser Ala Thr Thr Leu Leu
200 205 210

gag aag tac cca acc aag ctg gtg gtg tcc cgc acc atg agt aag gct 787
Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg Thr Met Ser Lys Ala
215 220 225

ttt gat ttc gca ggt gga cgc ctc ggc tac ttc gtg gcc aac cca gcg 835
Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe Val Ala Asn Pro Ala
230 235 240 245

ttt atc gac gcc gtg atg cta gtc cgc ctt ccg tat cat ctt tca gcg 883
Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro Tyr His Leu Ser Ala
250 255 260

ctg agc caa gca gcc gca atc gta gcg ctg cgt cac tcc gct gac acg 931
Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg His Ser Ala Asp Thr
265 270 275

ctg gga acc gtc gaa aag ctc tct gta gag cgt gtt cgc gtg gca gca 979
Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg Val Arg Val Ala Ala
280 285 290

cgc ttg gag gaa ctg ggc tac gct gtg gtt cca agt gag tcc aac ttt
1027
Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro Ser Glu Ser Asn Phe
295 300 305

gtg ttc ttt gga gat ttc tcc gat cag cac gcg gca tgg cag gca ttt
1075
Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala Ala Trp Gln Ala Phe
310 315 320 325

ttg gat agg gga gtg ctc atc cgc gat gtg gga atc gct ggg cac ttg
1123
Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly Ile Ala Gly His Leu
330 335 340

cgc act acc att ggt gtg cct gag gaa aat gat gcg ttt ttg gac gca
1171
Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp Ala Phe Leu Asp Ala
345 350 355

gct gca gag atc atc aag ctg aac ctg taagagagaa gaatttttca
1218
Ala Ala Glu Ile Ile Lys Leu Asn Leu
360 365

tga
1221

<210> 492

<211> 366

<212> PRT

<213> Corynebacterium glutamicum

<400> 492

```

Met Thr Lys Ile Thr Leu Ser Asp Leu Pro Leu Arg Glu Glu Leu Arg
 1           5           10           15

Gly Glu His Ala Tyr Gly Ala Pro Gln Leu Asn Val Asp Ile Arg Leu
          20           25           30

Asn Thr Asn Glu Asn Pro Tyr Pro Pro Ser Glu Ala Leu Val Ala Asp
      35           40           45

Leu Val Ala Thr Val Asp Lys Ile Ala Thr Glu Leu Asn Arg Tyr Pro
 50           55           60

Glu Arg Asp Ala Val Glu Leu Arg Asp Glu Leu Ala Ala Tyr Ile Thr
 65           70           75           80

Lys Gln Thr Gly Val Ala Val Thr Arg Asp Asn Leu Trp Ala Ala Asn
          85           90           95

Gly Ser Asn Glu Ile Leu Gln Gln Leu Leu Gln Ala Phe Gly Gly Pro
      100           105           110

Gly Arg Thr Ala Leu Gly Phe Gln Pro Ser Tyr Ser Met His Pro Ile
      115           120           125

Leu Ala Lys Gly Thr His Thr Glu Phe Ile Ala Val Ser Arg Gly Ala
      130           135           140

Asp Phe Arg Ile Asp Met Asp Val Ala Leu Glu Glu Ile Arg Ala Lys
      145           150           155           160

Gln Pro Asp Ile Val Phe Val Thr Thr Pro Asn Asn Pro Thr Gly Asp
          165           170           175

Val Thr Ser Leu Asp Asp Val Glu Arg Ile Ile Asn Val Ala Pro Gly
      180           185           190

Ile Val Ile Val Asp Glu Ala Tyr Ala Glu Phe Ser Pro Ser Pro Ser
      195           200           205

Ala Thr Thr Leu Leu Glu Lys Tyr Pro Thr Lys Leu Val Val Ser Arg
      210           215           220

Thr Met Ser Lys Ala Phe Asp Phe Ala Gly Gly Arg Leu Gly Tyr Phe
      225           230           235           240

Val Ala Asn Pro Ala Phe Ile Asp Ala Val Met Leu Val Arg Leu Pro
          245           250           255

Tyr His Leu Ser Ala Leu Ser Gln Ala Ala Ala Ile Val Ala Leu Arg
      260           265           270

His Ser Ala Asp Thr Leu Gly Thr Val Glu Lys Leu Ser Val Glu Arg
      275           280           285

Val Arg Val Ala Ala Arg Leu Glu Glu Leu Gly Tyr Ala Val Val Pro
      290           295           300

Ser Glu Ser Asn Phe Val Phe Phe Gly Asp Phe Ser Asp Gln His Ala
      305           310           315           320

```


Ala Trp Gln Ala Phe Leu Asp Arg Gly Val Leu Ile Arg Asp Val Gly
325 330 335

Ile Ala Gly His Leu Arg Thr Thr Ile Gly Val Pro Glu Glu Asn Asp
340 345 350

Ala Phe Leu Asp Ala Ala Ala Glu Ile Ile Lys Leu Asn Leu
355 360 365

<210> 493

<211> 1752

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1729)

<223> RXS02315

<400> 493

cgtttgga aa cgcttgctgc cagcaaagat aggcgtgatt ggtggtttga ggcgcgtgcgt 60

gaatcgtatc cgtacctgga gacgatctag actgttggtgc atg tcc agc acg cca 115
Met Ser Ser Thr Pro
1 5

gct caa gat ctt gcc cgc gcc gtt att gat tcc ctc gca cca cac gtc 163
Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser Leu Ala Pro His Val
10 15 20

act gac gtg gtg tta tgc cca gga tcc agg aac tca ccg ttg tcg ctt 211
Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn Ser Pro Leu Ser Leu
25 30 35

gag ttg ctg gcg cgg cag gat ctg cgt gtc cat gtg cgt atc gac gag 259
Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His Val Arg Ile Asp Glu
40 45 50

cgc agc gcc tca ttt ttg gcg ctg tcc cta gcg cgt acc cag gcc cgg 307
Arg Ser Ala .Ser Phe Leu Ala Leu Ser Leu Ala Arg Thr Gln Ala Arg
55 60 65

ccg gtg gct gtg gtg atg acc tcc ggc acg gct gta gct aac tgc ctg 355
 Pro Val Ala Val Val Met Thr Ser Gly Thr Ala Val Ala Asn Cys Leu
 70 75 80 85

cct gct gtt gct gaa gct gcg cat gcc cat atc ccg ttg att gtg ctc 403
Pro Ala Val Ala Glu Ala Ala His Ala His Ile Pro Leu Ile Val Leu
90 95 100

tct gct gac cgt cct gca cat ttg gtg gga acg ggg gcg agc caa acg 451
Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr Gly Ala Ser Gln Thr
105 110 115

att aac cag acc ggt att ttt ggt gat ctt gca ccg acg gtc ggt atc 499
Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala Pro Thr Val Gly Ile
120 125 130

act gag ctg gat cag gta gcg cag att gct gaa agc ctt gct cag ggg 547

Thr	Glu	Leu	Asp	Gln	Val	Ala	Gln	Ile	Ala	Glu	Ser	Leu	Ala	Gln	Gly		
135						140					145						
gct tcc cag att ccg cgt cat ttc aat ctt gca ctt gat gtt cct ttg 595																	
Ala	Ser	Gln	Ile	Pro	Arg	His	Phe	Asn	Leu	Ala	Leu	Asp	Val	Pro	Leu		
150					155					160					165		
gtt gct cct gaa ctg cca gag ctt cat ggt gag gca gtt gga gca tca 643																	
Val	Ala	Pro	Glu	Leu	Pro	Glu	Leu	His	Gly	Glu	Ala	Val	Gly	Ala	Ser		
				170					175					180			
tgg acg cat cgc tgg atc aac cac ggt gag gtg acc gtg gac ctg ggg 691																	
Trp	Thr	His	Arg	Trp	Ile	Asn	His	Gly	Glu	Val	Thr	Val	Asp	Leu	Gly		
			185					190					195				
gag cac acc ctc gtg att gcc ggt gat gaa gca tgg gaa gtg gaa ggg 739																	
Glu	His	Thr	Leu	Val	Ile	Ala	Gly	Asp	Glu	Ala	Trp	Glu	Val	Glu	Gly		
		200					205					210					
ctg gaa gat gtg ccc acc atc gct gaa cct act gca cca aag cct tat 787																	
Leu	Glu	Asp	Val	Pro	Thr	Ile	Ala	Glu	Pro	Thr	Ala	Pro	Lys	Pro	Tyr		
		215				220					225						
aat ccg gtg cac cca ctg gct gct gaa atc ttg ctg aag gag cag gtc 835																	
Asn	Pro	Val	His	Pro	Leu	Ala	Ala	Glu	Ile	Leu	Leu	Lys	Glu	Gln	Val		
230					235					240					245		
tcc gcg gaa ggc tat gtg gta aac acc agg cct gat cat gtg atc gtg 883																	
Ser	Ala	Glu	Gly	Tyr	Val	Val	Asn	Thr	Arg	Pro	Asp	His	Val	Ile	Val		
				250					255					260			
gtg gga cac ccc acg ctg cac cgc gga gtg ttg aag ttg atg tca gat 931																	
Val	Gly	His	Pro	Thr	Leu	His	Arg	Gly	Val	Leu	Lys	Leu	Met	Ser	Asp		
			265					270					275				
cct ggc att aaa tta act gtg ctt tca cgc acc gat atc atc act gat 979																	
Pro	Gly	Ile	Lys	Leu	Thr	Val	Leu	Ser	Arg	Thr	Asp	Ile	Ile	Thr	Asp		
		280					285					290					
ccc ggc cgc cat gcc gat cag gtg ggc agc aca gtg aaa gtc acc ggc																	
1027																	
Pro	Gly	Arg	His	Ala	Asp	Gln	Val	Gly	Ser	Thr	Val	Lys	Val	Thr	Gly		
		295				300					305						
acc cag gaa aag cag tgg cta aag atc tgt tcg gca gca tca gaa ctt																	
1075																	
Thr	Gln	Glu	Lys	Gln	Trp	Leu	Lys	Ile	Cys	Ser	Ala	Ala	Ser	Glu	Leu		
310					315					320					325		
gcg gcc gat ggt gtg cgt gac gtc ctg gac aac caa gaa ttc ggt ttc																	
1123																	
Ala	Ala	Asp	Gly	Val	Arg	Asp	Val	Leu	Asp	Asn	Gln	Glu	Phe	Gly	Phe		
				330					335					340			
acc ggc ctc cat gtt gcc gca gcc gtg gcg gat acc tta ggc acc ggc																	
1171																	
Thr	Gly	Leu	His	Val	Ala	Ala	Ala	Val	Ala	Asp	Thr	Leu	Gly	Thr	Gly		
			345					350					355				
gat act ctc ttt gct gca gca tcc aac tca atc cgt gac ctc tcc ctg																	
1219																	

Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile Arg Asp Leu Ser Leu
 360 365 370
 gtg ggt atg cct ttt gat ggc gtg gat acc ttc tcc cca cga ggt gtc
 1267
 Val Gly M t Pro Phe Asp Gly Val Asp Thr Phe Ser Pro Arg Gly Val
 375 380 385
 gca ggc att gat ggt tct gtt gct caa gca atc ggc act tca ctt gct
 1315
 Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile Gly Thr Ser Leu Ala
 390 395 400 405
 gtg cag tcc cgc cac ccc gat gaa atc cgc gcg cca cgc act gtg gcc
 1363
 Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala Pro Arg Thr Val Ala
 410 415 420
 ctt ctg ggc gat ctg tcg ttc ctt cac gat att ggc gga ctg ctc atc
 1411
 Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile Gly Gly Leu Leu Ile
 425 430 435
 ggc cct gat gaa cca cgc cca gaa aac ctc acc atc gtg gtc tcc aac
 1459
 Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr Ile Val Val Ser Asn
 440 445 450
 gac aac ggt ggc gga atc ttc gaa ctc cta gaa acc ggc gca gat ggt
 1507
 Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu Thr Gly Ala Asp Gly
 455 460 465
 ctc cgc ccc aac ttc gag cgt gct ttc ggt acc cca cac gac gcg tcc
 1555
 Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr Pro His Asp Ala Ser
 470 475 480 485
 atc gcg gat ctc tgc gca ggc tac ggc att gaa cac caa gtg gta gac
 1603
 Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu His Gln Val Val Asp
 490 495 500
 aac ctc caa gac ctc atc atc gcg cta gtt gat acc acc gaa gta tcc
 1651
 Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp Thr Thr Glu Val Ser
 505 510 515
 gga ttc acc att att gaa gct tcg acc gtc cga gat acc cgc cgt gca
 1699
 Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg Asp Thr Arg Arg Ala
 520 525 530
 caa cag caa gct ctc atg gac acg gtg cac taaatggagt ggtaccaagt
 1749
 Gln Gln Gln Ala Leu Met Asp Thr Val His
 535 540
 gcg
 1752

<210> 494

<211> 543

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 494

```

Met Ser Ser Thr Pro Ala Gln Asp Leu Ala Arg Ala Val Ile Asp Ser
 1          5          10          15

Leu Ala Pro His Val Thr Asp Val Val Leu Cys Pro Gly Ser Arg Asn
          20          25          30

Ser Pro Leu Ser Leu Glu Leu Leu Ala Arg Gln Asp Leu Arg Val His
          35          40          45

Val Arg Ile Asp Glu Arg Ser Ala Ser Phe Leu Ala Leu Ser Leu Ala
          50          55          60

Arg Thr Gln Ala Arg Pro Val Ala Val Val Met Thr Ser Gly Thr Ala
          65          70          75          80

Val Ala Asn Cys Leu Pro Ala Val Ala Glu Ala Ala His Ala His Ile
          85          90          95

Pro Leu Ile Val Leu Ser Ala Asp Arg Pro Ala His Leu Val Gly Thr
          100          105          110

Gly Ala Ser Gln Thr Ile Asn Gln Thr Gly Ile Phe Gly Asp Leu Ala
          115          120          125

Pro Thr Val Gly Ile Thr Glu Leu Asp Gln Val Ala Gln Ile Ala Glu
          130          135          140

Ser Leu Ala Gln Gly Ala Ser Gln Ile Pro Arg His Phe Asn Leu Ala
          145          150          155          160

Leu Asp Val Pro Leu Val Ala Pro Glu Leu Pro Glu Leu His Gly Glu
          165          170          175

Ala Val Gly Ala Ser Trp Thr His Arg Trp Ile Asn His Gly Glu Val
          180          185          190

Thr Val Asp Leu Gly Glu His Thr Leu Val Ile Ala Gly Asp Glu Ala
          195          200          205

Trp Glu Val Glu Gly Leu Glu Asp Val Pro Thr Ile Ala Glu Pro Thr
          210          215          220

Ala Pro Lys Pro Tyr Asn Pro Val His Pro Leu Ala Ala Glu Ile Leu
          225          230          235          240

Leu Lys Glu Gln Val Ser Ala Glu Gly Tyr Val Val Asn Thr Arg Pro
          245          250          255

Asp His Val Ile Val Val Gly His Pro Thr Leu His Arg Gly Val Leu
          260          265          270

Lys Leu Met Ser Asp Pro Gly Ile Lys Leu Thr Val Leu Ser Arg Thr
          275          280          285

```

Asp Ile Ile Thr Asp Pro Gly Arg His Ala Asp Gln Val Gly Ser Thr
290 295 300

Val Lys Val Thr Gly Thr Gln Glu Lys Gln Trp Leu Lys Ile Cys Ser
305 310 315 320

Ala Ala Ser Glu Leu Ala Ala Asp Gly Val Arg Asp Val Leu Asp Asn
325 330 335

Gln Glu Phe Gly Phe Thr Gly Leu His Val Ala Ala Ala Val Ala Asp
340 345 350

Thr Leu Gly Thr Gly Asp Thr Leu Phe Ala Ala Ala Ser Asn Ser Ile
355 360 365

Arg Asp Leu Ser Leu Val Gly Met Pro Phe Asp Gly Val Asp Thr Phe
370 375 380

Ser Pro Arg Gly Val Ala Gly Ile Asp Gly Ser Val Ala Gln Ala Ile
385 390 395 400

Gly Thr Ser Leu Ala Val Gln Ser Arg His Pro Asp Glu Ile Arg Ala
405 410 415

Pro Arg Thr Val Ala Leu Leu Gly Asp Leu Ser Phe Leu His Asp Ile
420 425 430

Gly Gly Leu Leu Ile Gly Pro Asp Glu Pro Arg Pro Glu Asn Leu Thr
435 440 445

Ile Val Val Ser Asn Asp Asn Gly Gly Gly Ile Phe Glu Leu Leu Glu
450 455 460

Thr Gly Ala Asp Gly Leu Arg Pro Asn Phe Glu Arg Ala Phe Gly Thr
465 470 475 480

Pro His Asp Ala Ser Ile Ala Asp Leu Cys Ala Gly Tyr Gly Ile Glu
485 490 495

His Gln Val Val Asp Asn Leu Gln Asp Leu Ile Ile Ala Leu Val Asp
500 505 510

Thr Thr Glu Val Ser Gly Phe Thr Ile Ile Glu Ala Ser Thr Val Arg
515 520 525

Asp Thr Arg Arg Ala Gln Gln Gln Ala Leu Met Asp Thr Val His
530 535 540

<210> 495

<211> 1434

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) .. (1411)

<223> RXS02550

<400> 495

gatcttaggc agccgtggga ttacaccctt ttagagctag aacagtaaaa attcacccaa 60

tagctttcaa	ctacgcacac	aaagtggcaa	cattgagcgg	gtg	act	aca	gac	aag	115
				Val	Thr	Thr	Asp	Lys	
				1				5	
cgc	aaa	acc	tct	aag	acc	acc	gac	acc	163
Arg	Lys	Thr	Ser	Lys	Thr	Thr	Asp	Thr	
				10				15	
gat	cag	gca	gcg	cgt	ccc	act	cgg	cga	211
Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	
				25				30	
cag	tcg	gag	aag	atg	aag	gac	gtg	ctg	259
Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	
				40				45	
gcc	gcy	gag	gcy	gaa	cgc	atg	gag	ctt	307
Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	
				55				60	
ctc	aac	acg	gga	aat	cca	gcc	gtg	ttc	355
Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	
								80	
att	atg	cgt	gac	atg	atc	gcc	aac	ctt	403
Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	
								90	
acc	tcc	aaa	ggc	att	att	ccg	gcc	cgg	451
Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	
								110	
gaa	gtt	gtg	ccc	gga	ttc	ccc	cac	ttc	499
Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	
								125	
ggc	aac	ggt	gtc	tca	gaa	cta	atc	acc	547
Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	
								140	
aac	gac	ggc	gat	gaa	gtt	ctt	atc	ccc	595
Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	
								155	
act	gcc	gca	acc	tcc	ctg	gct	ggt	ggt	643
Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	
								170	
gat	gag	gaa	gat	gac	tgg	aac	cca	tcc	691
Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	
								185	
atc	tca	gag	aaa	acc	aaa	gct	att	gtg	739
Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	
								200	
acg	gga	gct	gtc	tac	ccg	cgc	cgg	gtg	787
Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	
								215	

gca cgc gag cat gac ctg ctg att ttg gcc gat gaa atc tac gac cgc 835
 Ala Arg Glu His Asp Leu Leu Ile Leu Ala Asp Glu Ile Tyr Asp Arg
 230 235 240 245

att ctc tac gat gat gcc gag cac atc agc ctg gca acc ctt gca cca 883
 Ile Leu Tyr Asp Asp Ala Glu His Ile Ser Leu Ala Thr Leu Ala Pro
 250 255 260

gat ctc ctt tgc atc aca tac aac ggt cta tcc aag gca tac cgc gtc 931
 Asp Leu Leu Cys Ile Thr Tyr Asn Gly Leu Ser Lys Ala Tyr Arg Val
 265 270 275

gca gga tac cga gct ggc tgg atg gta ttg act gga cca aag caa tac 979
 Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr Gly Pro Lys Gln Tyr
 280 285 290

gca cgt gga ttt att gag ggc ctc gaa ctc ctc gca ggc act cga ctc
 1027
 Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu Ala Gly Thr Arg Leu
 295 300 305

tgc cca aat gtc cca gct cag cac gct att cag gta gct ctg ggt gga
 1075
 Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln Val Ala Leu Gly Gly
 310 315 320 325

cgc cag tcc atc tac gac ctc act ggc gaa cac ggc cga ctc ctg gaa
 1123
 Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His Gly Arg Leu Leu Glu
 330 335 340

cag cgc aac atg gca tgg acg aaa ctc aac gaa atc cca ggt gtc agc
 1171
 Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu Ile Pro Gly Val Ser
 345 350 355

tgt gtg aaa cca atg gga gct cta tac gcg ttc ccc aag ctc gac ccc
 1219
 Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe Pro Lys Leu Asp Pro
 360 365 370

aac gtg tac gaa atc cac gac gac acc caa ctc atg ctg gat ctt ctc
 1267
 Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu Met Leu Asp Leu Leu
 375 380 385

cgt gcc gag aaa atc ctc atg gtt cag ggc act ggc ttc aac tgg cca
 1315
 Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr Gly Phe Asn Trp Pro
 390 395 400 405

cat cac gat cac ttc cga gtg gtc acc ctg cca tgg gca tcc cag ttg
 1363
 His His Asp His Phe Arg Val Val Thr Leu Pro Trp Ala Ser Gln Leu
 410 415 420

gaa aac gca att gag cgc ctg ggt aac ttc ctg tcc act tac aag cag
 1411
 Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu Ser Thr Tyr Lys Gln
 425 430 435

tagtagttgt taggattcac cac
1434

<210> 496

<211> 437

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

Val	Thr	Thr	Asp	Lys	Arg	Lys	Thr	Ser	Lys	Thr	Thr	Asp	Thr	Ala	Asn
1				5					10					15	
Lys	Ala	Val	Gly	Ala	Asp	Gln	Ala	Ala	Arg	Pro	Thr	Arg	Arg	Thr	Thr
			20					25					30		
Arg	Arg	Ile	Phe	Asp	Gln	Ser	Glu	Lys	Met	Lys	Asp	Val	Leu	Tyr	Glu
		35					40					45			
Ile	Arg	Gly	Pro	Val	Ala	Ala	Glu	Ala	Glu	Arg	Met	Glu	Leu	Asp	Gly
	50					55					60				
His	Asn	Ile	Leu	Lys	Leu	Asn	Thr	Gly	Asn	Pro	Ala	Val	Phe	Gly	Phe
65					70					75					80
Asp	Ala	Pro	Asp	Val	Ile	Met	Arg	Asp	Met	Ile	Ala	Asn	Leu	Pro	Thr
			85						90					95	
Ser	Gln	Gly	Tyr	Ser	Thr	Ser	Lys	Gly	Ile	Ile	Pro	Ala	Arg	Arg	Ala
			100					105					110		
Val	Val	Thr	Arg	Tyr	Glu	Val	Val	Pro	Gly	Phe	Pro	His	Phe	Asp	Val
		115					120					125			
Asp	Asp	Val	Phe	Leu	Gly	Asn	Gly	Val	Ser	Glu	Leu	Ile	Thr	Met	Thr
	130					135					140				
Thr	Gln	Ala	Leu	Leu	Asn	Asp	Gly	Asp	Glu	Val	Leu	Ile	Pro	Ala	Pro
145					150					155					160
Asp	Tyr	Pro	Leu	Trp	Thr	Ala	Ala	Thr	Ser	Leu	Ala	Gly	Gly	Lys	Pro
			165						170					175	
Val	His	Tyr	Leu	Cys	Asp	Glu	Glu	Asp	Asp	Trp	Asn	Pro	Ser	Ile	Glu
			180					185				190			
Asp	Ile	Lys	Ser	Lys	Ile	Ser	Glu	Lys	Thr	Lys	Ala	Ile	Val	Val	Ile
		195					200					205			
Asn	Pro	Asn	Asn	Pro	Thr	Gly	Ala	Val	Tyr	Pro	Arg	Arg	Val	Leu	Glu
	210					215					220				
Gln	Ile	Val	Glu	Ile	Ala	Arg	Glu	His	Asp	Leu	Leu	Ile	Leu	Ala	Asp
225					230					235					240
Glu	Ile	Tyr	Asp	Arg	Ile	Leu	Tyr	Asp	Asp	Ala	Glu	His	Ile	Ser	Leu
			245						250					255	
Ala	Thr	Leu	Ala	Pro	Asp	Leu	Leu	Cys	Ile	Thr	Tyr	Asn	Gly	Leu	Ser
		260						265					270		

Lys Ala Tyr Arg Val Ala Gly Tyr Arg Ala Gly Trp Met Val Leu Thr
 275 280 285
 Gly Pro Lys Gln Tyr Ala Arg Gly Phe Ile Glu Gly Leu Glu Leu Leu
 290 295 300
 Ala Gly Thr Arg Leu Cys Pro Asn Val Pro Ala Gln His Ala Ile Gln
 305 310 315 320
 Val Ala Leu Gly Gly Arg Gln Ser Ile Tyr Asp Leu Thr Gly Glu His
 325 330 335
 Gly Arg Leu Leu Glu Gln Arg Asn Met Ala Trp Thr Lys Leu Asn Glu
 340 345 350
 Ile Pro Gly Val Ser Cys Val Lys Pro Met Gly Ala Leu Tyr Ala Phe
 355 360 365
 Pro Lys Leu Asp Pro Asn Val Tyr Glu Ile His Asp Asp Thr Gln Leu
 370 375 380
 Met Leu Asp Leu Leu Arg Ala Glu Lys Ile Leu Met Val Gln Gly Thr
 385 390 395 400
 Gly Phe Asn Trp Pro His His Asp His Phe Arg Val Val Thr Leu Pro
 405 410 415
 Trp Ala Ser Gln Leu Glu Asn Ala Ile Glu Arg Leu Gly Asn Phe Leu
 420 425 430
 Ser Thr Tyr Lys Gln
 435

<210> 497

<211> 1080

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1057)

<223> RXS02319

<400> 497

atgtgggtga gataaccgac cgtgatgtcg ccctagcaaa agtcacgcgac gcccacgcca 60

agaccttggc catttcggca gaggcttaag gttaaagatt atg agc aac tac agc 115
 Met Ser Asn Tyr Ser
 1 5

acc gac aac cct ttt gat ccc acc caa tgg gcc acc gtt cca ggt ttt 163
 Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala Thr Val Pro Gly Phe
 10 15 20

gaa gaa ttc acc gac atc acc tac cac cgc cac gtg ggc acc acc cgc 211
 Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His Val Gly Thr Thr Arg
 25 30 35

gcc gat ggc atc gtg cgc atc gcc ttc gac cgc ccc gaa gtt cgc aat 259
 Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg Pro Glu Val Arg Asn

40	45	50	
gct ttc cgc ccc cac acc gtc gac gag ctt tac caa gcc ctc gac cac Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr Gln Ala Leu Asp His 55 60 65			307
gcg cgc cgg acc cca gat gtt gga acc atc ctg ctc acc ggc aac ggc Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu Leu Thr Gly Asn Gly 70 75 80 85			355
ccc agc gaa aaa gac ggt ggc tgg gcg ttc tgc tcc ggc ggc gac caa Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys Ser Gly Gly Asp Gln 90 95 100			403
cgc atc cgc ggg cgc tcc ggc tac caa tac gcc acc gaa cac gcg cgc Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala Thr Glu His Ala Arg 105 110 115			451
gac gat gcc acc gct gat gtc ttc acg gta gat att gcc cgc acc aaa Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp Ile Ala Arg Thr Lys 120 125 130			499
gtt gaa ggc gga cgc ctc cac att ttg gaa gtc caa cgc ctc atc cgc Val Glu Gly Gly Arg Leu His Ile Leu Glu Val Gln Arg Leu Ile Arg 135 140 145			547
acc atg cct aaa gtt gtc atc gca gta gtc aac ggc tgg gca gcc ggc Thr Met Pro Lys Val Val Ile Ala Val Val Asn Gly Trp Ala Ala Gly 150 155 160 165			595
ggt ggg cac tcc ctc cat gtc gtt tgc gac ctc acc atc gct tcc cgc Gly Gly His Ser Leu His Val Val Cys Asp Leu Thr Ile Ala Ser Arg 170 175 180			643
caa gaa gca cgc ttc aag caa acc gac gct gac gtg gga tcc ttc gac Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp Val Gly Ser Phe Asp 185 190 195			691
gct ggc tac ggc tcc gcc tac cta gcg aaa atg gtc gga cag aaa aac Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met Val Gly Gln Lys Asn 200 205 210			739
gcc cgc gaa atc ttc ttc ctc gga cgc acc tac gac gcc gaa cgc atg Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr Asp Ala Glu Arg Met 215 220 225			787
caa caa atg ggc gca gtc aac atc gtg gcc gac cac ggc gac cta gaa Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp His Gly Asp Leu Glu 230 235 240 245			835
aaa gaa gcc atc caa gca gcc cgc gaa atc aac acc aaa tcc ccc acc Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn Thr Lys Ser Pro Thr 250 255 260			883
ggg caa cgc atg ctg aaa ttc gcc ttc aat ctc acc gac gat ggc ctc Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu Thr Asp Asp Gly Leu 265 270 275			931
atg gga caa caa gtc ttc gcc ggc gaa gcc acc cgc ctg gcc tac atg Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr Arg Leu Ala Tyr Met 280 285 290			979

acg gat gaa gcc gta gag ggt aag gaa gca ttc cta gaa aag cgc gaa
1027

Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe Leu Glu Lys Arg Glu
295 300 305

ccc aac tgg aat gaa ttc cct tac tac tac tagtgagttc atgggggtcct
1077

Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
310 315

aaa
1080

<210> 498

<211> 319

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

Met Ser Asn Tyr Ser Thr Asp Asn Pro Phe Asp Pro Thr Gln Trp Ala
1 5 10 15

Thr Val Pro Gly Phe Glu Glu Phe Thr Asp Ile Thr Tyr His Arg His
20 25 30

Val Gly Thr Thr Arg Ala Asp Gly Ile Val Arg Ile Ala Phe Asp Arg
35 40 45

Pro Glu Val Arg Asn Ala Phe Arg Pro His Thr Val Asp Glu Leu Tyr
50 55 60

Gln Ala Leu Asp His Ala Arg Arg Thr Pro Asp Val Gly Thr Ile Leu
65 70 75 80

Leu Thr Gly Asn Gly Pro Ser Glu Lys Asp Gly Gly Trp Ala Phe Cys
85 90 95

Ser Gly Gly Asp Gln Arg Ile Arg Gly Arg Ser Gly Tyr Gln Tyr Ala
100 105 110

Thr Glu His Ala Arg Asp Asp Ala Thr Ala Asp Val Phe Thr Val Asp
115 120 125

Ile Ala Arg Thr Lys Val Glu Gly Gly Arg Leu His Ile Leu Glu Val
130 135 140

Gln Arg Leu Ile Arg Thr Met Pro Lys Val Val Ile Ala Val Val Asn
145 150 155 160

Gly Trp Ala Ala Gly Gly Gly His Ser Leu His Val Val Cys Asp Leu
165 170 175

Thr Ile Ala Ser Arg Gln Glu Ala Arg Phe Lys Gln Thr Asp Ala Asp
180 185 190

Val Gly Ser Phe Asp Ala Gly Tyr Gly Ser Ala Tyr Leu Ala Lys Met
195 200 205

Val Gly Gln Lys Asn Ala Arg Glu Ile Phe Phe Leu Gly Arg Thr Tyr

210 215 220
 Asp Ala Glu Arg Met Gln Gln Met Gly Ala Val Asn Ile Val Ala Asp
 225 230 235 240
 His Gly Asp Leu Glu Lys Glu Ala Ile Gln Ala Ala Arg Glu Ile Asn
 245 250 255
 Thr Lys Ser Pro Thr Gly Gln Arg Met Leu Lys Phe Ala Phe Asn Leu
 260 265 270
 Thr Asp Asp Gly Leu Met Gly Gln Gln Val Phe Ala Gly Glu Ala Thr
 275 280 285
 Arg Leu Ala Tyr Met Thr Asp Glu Ala Val Glu Gly Lys Glu Ala Phe
 290 295 300
 Leu Glu Lys Arg Glu Pro Asn Trp Asn Glu Phe Pro Tyr Tyr Tyr
 305 310 315

 <210> 499
 <211> 384
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(361)
 <223> RXS02908

 <400> 499
 gccaacgagg gttggtttac cacctctgat tcagggtgaac tccacgacgg gattctcacc 60

 gtgactggtc gcgtggatac ccgtcattga ttccggtgga ttg aag ttg cac cca 115
 Leu Lys Leu His Pro
 1 5

 gag gta ctg gaa cgt gcc atc gca gat att aaa ggt gtc acc gcg gcg 163
 Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys Gly Val Thr Ala Ala
 10 15 20

 tgt gtt gtg ggt att ccc gat ccc cga tta ggc caa gca att gtg gcc 211
 Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly Gln Ala Ile Val Ala
 25 30 35

 gcg tac tcc gga tcg atc agt ccg tct gaa gtt att gaa ggc ctc gac 259
 Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val Ile Glu Gly Leu Asp
 40 45 50

 gat cta cct cgt tgg cag ctt ccc aaa cgg ctg aag cat ctg gaa tct 307
 Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu Lys His Leu Glu Ser
 55 60 65

 ttg ccc agc att ggt cct gga aaa gct gat cga cgt gct atc gcg aag 355
 Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg Arg Ala Ile Ala Lys
 70 75 80 85

 ctg ttt tagtcttcat tcttgctggc tgc 384
 Leu Phe

<210> 500

<211> 87

<212> PRT

<213> Corynebacterium glutamicum

<400> 500

Leu Lys Leu His Pro Glu Val Leu Glu Arg Ala Ile Ala Asp Ile Lys
 1 5 10 15

Gly Val Thr Ala Ala Cys Val Val Gly Ile Pro Asp Pro Arg Leu Gly
 20 25 30

Gln Ala Ile Val Ala Ala Tyr Ser Gly Ser Ile Ser Pro Ser Glu Val
 35 40 45

Ile Glu Gly Leu Asp Asp Leu Pro Arg Trp Gln Leu Pro Lys Arg Leu
 50 55 60

Lys His Leu Glu Ser Leu Pro Ser Ile Gly Pro Gly Lys Ala Asp Arg
 65 70 75 80

Arg Ala Ile Ala Lys Leu Phe
 85

<210> 501

<211> 775

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(775)

<223> RXS03003

<400> 501

tcgatgatct gggctcccca ggtggtgcgg ctaagcttgg accacaagat tttgatcacc 60

caatgatcgc tgcgctgccg cctcaggcat aatctaacgc atg acc tct cgc acc 115
 Met Thr Ser Arg Thr
 1 5

ccg ctt gtt tct gtt ctt cct gat ttt ccg tgg gat tcg ctc gct tcc 163
 Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp Asp Ser Leu Ala Ser
 10 15 20

gca aaa gcc aaa gct gcg tct cac ccg gat ggg atc gtg aat ctt tct 211
 Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly Ile Val Asn Leu Ser
 25 30 35

gtt ggc act ccg gtt gat ccg gtc gcg ccc agc att cag atc gcg ttg 259
 Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser Ile Gln Ile Ala Leu
 40 45 50

gca gaa gca gcg ggg ttt tcg ggt tac cct caa acc atc ggc acc ccg 307
 Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln Thr Ile Gly Thr Pro
 55 60 65

gaa ctc cgc gca gcc atc agg ggc gcg ctt gag cgg cgc tac aac atg 355

Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu Arg Arg Tyr Asn Met
 70 75 80 85
 aca aag ctt gtc gac gcc tcc ctc ctc ccc gtc gtg ggt acc aag gag 403
 Thr Lys Leu Val Asp Ala Ser Leu Leu Pro Val Val Gly Thr Lys Glu
 90 95 100
 gca att gcc ctt ctt cca ttc gcg ttg ggt att tcc ggc acc gtt gtc 451
 Ala Ile Ala Leu Leu Pro Phe Ala Leu Gly Ile Ser Gly Thr Val Val
 105 110 115
 atc cca gag att gcg tac cca acc tac gaa gtc gct gtc gtg gcc gca 499
 Ile Pro Glu Ile Ala Tyr Pro Thr Tyr Glu Val Ala Val Val Ala Ala
 120 125 130
 gga tgc acc gtg ttg cgt tct gat tcg ctg ttt aag ctc ggc ccg cag 547
 Gly Cys Thr Val Leu Arg Ser Asp Ser Leu Phe Lys Leu Gly Pro Gln
 135 140 145
 atc ccg tcg atg atg ttt atc aac tca cca tcc aac ccc aca ggc aag 595
 Ile Pro Ser Met Met Phe Ile Asn Ser Pro Ser Asn Pro Thr Gly Lys
 150 155 160 165
 gtt ctg ggc atc cca cac ttg cgc aag gtt gtg aag tgg gcg cag gaa 643
 Val Leu Gly Ile Pro His Leu Arg Lys Val Val Lys Trp Ala Gln Glu
 170 175 180
 aac aac gtg atc ctc gca gct gat gaa tgc tac ttg ggt ctt ggc tgg 691
 Asn Asn Val Ile Leu Ala Ala Asp Glu Cys Tyr Leu Gly Leu Gly Trp
 185 190 195
 gac gat gaa aac cca ccg atc tca att ttg gat cca cgt gtc tgc gat 739
 Asp Asp Glu Asn Pro Pro Ile Ser Ile Leu Asp Pro Arg Val Cys Asp
 200 205 210
 ggc gac cac acc aac ttg atc gcc att cac tcg ctg 775
 Gly Asp His Thr Asn Leu Ile Ala Ile His Ser Leu
 215 220 225
 <210> 502
 <211> 225
 <212> PRT
 <213> Corynebacterium glutamicum
 <400> 502
 Met Thr Ser Arg Thr Pro Leu Val Ser Val Leu Pro Asp Phe Pro Trp
 1 5 10 15
 Asp Ser Leu Ala Ser Ala Lys Ala Lys Ala Ala Ser His Pro Asp Gly
 20 25 30
 Ile Val Asn Leu Ser Val Gly Thr Pro Val Asp Pro Val Ala Pro Ser
 35 40 45
 Ile Gln Ile Ala Leu Ala Glu Ala Ala Gly Phe Ser Gly Tyr Pro Gln
 50 55 60
 Thr Ile Gly Thr Pro Glu Leu Arg Ala Ala Ile Arg Gly Ala Leu Glu
 65 70 75 80

Arg	Arg	Tyr	Asn	Met	Thr	Lys	Leu	Val	Asp	Ala	Ser	Leu	Leu	Pro	Val	
				85					90					95		
Val	Gly	Thr	Lys	Glu	Ala	Ile	Ala	Leu	Leu	Pro	Phe	Ala	Leu	Gly	Ile	
				100					105					110		
Ser	Gly	Thr	Val	Val	Ile	Pro	Glu	Ile	Ala	Tyr	Pro	Thr	Tyr	Glu	Val	
				115					120					125		
Ala	Val	Val	Ala	Ala	Gly	Cys	Thr	Val	Leu	Arg	Ser	Asp	Ser	Leu	Phe	
				130					135					140		
Lys	Leu	Gly	Pro	Gln	Ile	Pro	Ser	Met	Met	Phe	Ile	Asn	Ser	Pro	Ser	
				145					150					155		
Asn	Pro	Thr	Gly	Lys	Val	Leu	Gly	Ile	Pro	His	Leu	Arg	Lys	Val	Val	
				165					170					175		
Lys	Trp	Ala	Gln	Glu	Asn	Asn	Val	Ile	Leu	Ala	Ala	Asp	Glu	Cys	Tyr	
				180					185					190		
Leu	Gly	Leu	Gly	Trp	Asp	Asp	Glu	Asn	Pro	Pro	Ile	Ser	Ile	Leu	Asp	
				195					200					205		
Pro	Arg	Val	Cys	Asp	Gly	Asp	His	Thr	Asn	Leu	Ile	Ala	Ile	His	Ser	
				210					215					220		
Leu																
225																

```
<210> 503
<211> 390
<212> DNA
<213> Corynebacterium glutamicum.
```

```
<220>  
<221> CDS  
<222> (101)..(367)  
<223> RXS03026
```

<400> 503
gttggcggcg cagtatcgtg aggtgcggga cctcgagcgg ggaatcccaa actagcatcc 60

cgaactagcc cccaacaac aattagaaat ggaacctaaa atg cct gga aaa att 115
Met Pro Gly Lys Ile
1 5

ctc ctt ctc aac ggc cca aac ctg aac atg ctg ggc aaa cgc gag cct 163
Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu Gly Lys Arg Glu Pro
10 15 20

gac att tac gga cac gac acc ttg gaa gac gtc gtc gcg ctg gca acc 211
Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val Val Ala Leu Ala Thr
25 30 35

gct gag gct gcg aaa cac ggc ctt gag gtt gag gcg ctg cag agc aat 259
Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu Ala Leu Gln Ser Asn
40 45 50

cac caa ggt gag cta atc gat gcg ctg cac aac gct cgc ggg acc cac 307

His Gln Gly Glu Leu Ile Asp Ala Leu His Asn Ala Arg Gly Thr His
 55 60 65
 atc ggt tgc gtg att aac ccc ggc ggc ctg act aca ctt cgg tgg cgc 355
 Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr Thr Leu Arg Trp Arg
 70 75 80 85
 ttt tgg atg ctg tgaagggcgtc tgagcttcct acc 390
 Phe Trp Met Leu

<210> 504
 <211> 89
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 504
 Met Pro Gly Lys Ile Leu Leu Leu Asn Gly Pro Asn Leu Asn Met Leu
 1 5 10 15
 Gly Lys Arg Glu Pro Asp Ile Tyr Gly His Asp Thr Leu Glu Asp Val
 20 25 30
 Val Ala Leu Ala Thr Ala Glu Ala Ala Lys His Gly Leu Glu Val Glu
 35 40 45
 Ala Leu Gln Ser Asn His Gln Gly Glu Leu Ile Asp Ala Leu His Asn
 50 55 60
 Ala Arg Gly Thr His Ile Gly Cys Val Ile Asn Pro Gly Gly Leu Thr
 65 70 75 80
 Thr Leu Arg Trp Arg Phe Trp Met Leu
 85

<210> 505
 <211> 621
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(598)
 <223> RXS03074

<400> 505
 tttgtgggca atctgggtttt ttcgtaattg tgtgggatga atctcttaaa aattcacatt 60
 tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
 Met Thr Gln Ser Ala
 1 5
 cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
 Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
 10 15 20
 gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
 Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
 25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
 Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
 40 45 50

 ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
 Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
 55 60 65

 gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
 Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
 70 75 80 85

 gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
 Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
 90 95 100

 att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
 Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
 105 110 115

 ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
 Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
 120 125 130

 gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
 Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
 135 140 145

 gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
 Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
 150 155 160 165

 cag taatttggtt tgacgacgca gta 621
 Gln

<210> 506

<211> 166

<212> PRT

<213> Corynebacterium glutamicum

<400> 506

Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
 1 5 10 15

 Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
 20 25 30

 Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
 35 40 45

 Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
 50 55 60

 Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
 65 70 75 80

 Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
 85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
 100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
 115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
 130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
 145 150 155 160

Glu Ala Pro Ile Lys Gln
 165

<210> 507
 <211> 3075
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(3052)
 <223> RXC01434

<400> 507
 ggtttcctgc gcaccgtgat gattgggtgcg gcgctgtcgc cggccatcgc ttcggcggttc 60

aacactgccca acacgctgcc caacctgata actggaaatc gtg ttg ggt gcg gtg 115
 Val Leu Gly Ala Val
 1 5

ctg aca tcg ctg gtt att ccg gtc ctt acc cgc gcg gaa aaa gaa gac 163
 Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg Ala Glu Lys Glu Asp
 10 15 20

gcc gac ggc ggt tcc ggg ttc ttc agg cgg ctg ctc acc ctg tcg gtg 211
 Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu Leu Thr Leu Ser Val
 25 30 35

acg ctg ctg ggt ggt gtc acc atc ctg tcg att atc ggc gcg ccg ctg 259
 Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile Ile Gly Ala Pro Leu
 40 45 50

ctg aca cgg atg atg ctg tcc tct gag gga caa gtc aac gtg gtc atg 307
 Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln Val Asn Val Val Met
 55 60 65

tcc acg gcc ttt gcg tat tgg ctg ctg cca cag att ttc ttc tac ggc 355
 Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln Ile Phe Phe Tyr Gly
 70 75 80 85

ctg ttt gcc ctg ttc atg gct gtg ttg aac acc cgt gaa gtg ttc aaa 403
 Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr Arg Glu Val Phe Lys
 90 95 100

ccc ggc gcg tgg gca cct gtt gtc aac aat gtg atc acc ttg acc gtg 451
 Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val Ile Thr Leu Thr Val
 105 110 115

ctg ggc gtg tac atg gtg ctg cct gcg cgt ttg cac ccg cat gag cag	499
Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu His Pro His Glu Gln	
120 125 130	
gtg ggc att ttt gat ccg cag atc att ttc ctc ggc gtg ggc acc acc	547
Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu Gly Val Gly Thr Thr	
135 140 145	
ctt ggt gtg gtt gca cag tgt cta atc atg att ccg tac ctg cgt cgc	595
Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile Pro Tyr Leu Arg Arg	
150 155 160 165	
gcg ggc att gat atg cgc cct ctg tgg ggt atc gat gcg cgt ttg aag	643
Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile Asp Ala Arg Leu Lys	
170 175 180	
caa ttc ggt ggc atg gcg atg gcg atc atc gtg tac gtg gca atc tcc	691
Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val Tyr Val Ala Ile Ser	
185 190 195	
cag ttc ggt tac atc atc acc act cgc att gcg tcg att gca gac gat	739
Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala Ser Ile Ala Asp Asp	
200 205 210	
gct gcg ccg ttt att tat cag cag cac tgg atg ttg ctg caa gtt cct	787
Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met Leu Leu Gln Val Pro	
215 220 225	
tat ggc atc atc ggc gtc acc ttg ctc acc gcg att atg ccg cga ctg	835
Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala Ile Met Pro Arg Leu	
230 235 240 245	
tcc cgc aac gcg gca gac ggc gat gat agg gca gta gtc tct gac ctt	883
Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala Val Val Ser Asp Leu	
250 255 260	
cag ttg ggt tcc aag cta acc ttc atc gca ctg atc ccc atc gtg gtg	931
Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu Ile Pro Ile Val Val	
265 270 275	
ttc ttc acc gcc ttc ggt gtc cct att gcc aat ggc ctt ttt gcc tac	979
Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn Gly Leu Phe Ala Tyr	
280 285 290	
ggc caa ttc gat gcc aac gcc gcc aac atc ctt ggt tgg act ctg agc	
1027	
Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu Gly Trp Thr Leu Ser	
295 300 305	
ttc tct gct ttc acg ctg att cct tac gct ttg gtg ctg cta cat ctg	
1075	
Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu Val Leu Leu His Leu	
310 315 320 325	
cgt gtg ttt tat gcg cgt gaa gag gtc tgg acc cca acc ttc atc atc	
1123	
Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr Pro Thr Phe Ile Ile	
330 335 340	

gcc ggc atc acc gcc acc aag gtc gtg ctt tcc ctg ttg gca ccg ctg
 1171
 Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser Leu Leu Ala Pro Leu
 345 350 355

ctg tcg agc tcc ccg gag cgt gtg gtg gtg ctt ctt ggt gcg gcc aac
 1219
 Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu Leu Gly Ala Ala Asn
 360 365 370

ggt ttc agt ttc atc acc ggc gcg gtc atc ggc gcg tat ctg ttg cgc
 1267
 Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly Ala Tyr Leu Leu Arg
 375 380 385

aac aaa ctc ggc ctg ttg ggt atg cgc tct ttg gct aaa acc tcc ctg
 1315
 Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu Ala Lys Thr Ser Leu
 390 395 400 405

tgg gcg ttg ggc tct gcg gcg gtt ggt gca gca gca gca tgg gcg ttg
 1363
 Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala Ala Ala Trp Ala Leu
 410 415 420

ggg tgg ctg att caa gcc gtc gtg ggc gat ttc ttg ctg ggc act cta
 1411
 Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe Leu Leu Gly Thr Leu
 425 430 435

agc tcc gta ggc tac ttg ttg aac ctg gct gtg ttg ggt gtc ttc ttc
 1459
 Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val Leu Gly Val Phe Phe
 440 445 450

atc ttc gtc acc ggc atc gtg ttg tca cgt tct ggt ttg ccg gag gtc
 1507
 Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser Gly Leu Pro Glu Val
 455 460 465

caa aac ttg ggc cag gca ctg acc cgc atc cca ggt ttg agc cgg ttt
 1555
 Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro Gly Leu Ser Arg Phe
 470 475 480 485

att cgc ccg aat acc aag atc tct ttg gat gtc ggc gaa gtc tcc gag
 1603
 Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val Gly Glu Val Ser Glu
 490 495 500

cag gat ttc tcc acc cag ctg gtc gcg cca agc gag ttc gca gca acc
 1651
 Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser Glu Phe Ala Ala Thr
 505 510 515

cct gtg ccg cca ccg atg tcc gcc ggt att gtc cgc gga cct cgc ctg
 1699
 Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val Arg Gly Pro Arg Leu
 520 525 530

gtt ccc ggc gcc cca gtc ggc gac ggt cgt ttc cgt ctg ctc gcc gat
 1747
 Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe Arg Leu Leu Ala Asp
 535 540 545

cac ggc ggc gtc caa ggc gcg cgt ttc tgg cag gcc cgc gag atc gcc
 1795
 His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln Ala Arg Glu Ile Ala
 550 555 560 565

acc ggc aag gaa gtc gcg ctg atc ttt gtg gat act tcc ggc aac gcc
 1843
 Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp Thr Ser Gly Asn Ala
 570 575 580

cca ttt gcg cca ctg tct tcg gca gcc gca gcg ggc atc gcc tac gag
 1891
 Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala Gly Ile Ala Tyr Glu
 585 590 595

gtg cag cgc cgc acc aag aag ctg gcc agc ttg ggc agc ttg gcg gta
 1939
 Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu Gly Ser Leu Ala Val
 600 605 610

gcc ccc aac atc cac tcc gag gcg tac cgc aac ggt tgc ctc att gtg
 1987
 Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn Gly Cys Leu Ile Val
 615 620 625

gcc gat tgg gtg cct ggc tcc agc ttg agc gcc gtc gcg gaa tcc ggt
 2035
 Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala Val Ala Glu Ser Gly
 630 635 640 645

gcc gat ccc cgc gcc gcc gcg ttc gcg ctc gcg gaa cta act gaa acc
 2083
 Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala Glu Leu Thr Glu Thr
 650 655 660

atc ggc gag gcc cac gag atg ggt atc ccg gcc ggc ttg gac aac aag
 2131
 Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala Gly Leu Asp Asn Lys
 665 670 675

tgc cga att cgt atc aac acc gac ggc cat gcc gtc ctc gcc ttg ccg
 2179
 Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala Val Leu Ala Leu Pro
 680 685 690

gcg att ttg ccc gat gcc tca gag ctc cgc gac gcc aag tcc ctg gcc
 2227
 Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp Ala Lys Ser Leu Ala
 695 700 705

tcg gcc gcc gag atg ctt atc gac gcg acc ctc gct ccc agc gac gtc
 2275
 Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu Ala Pro Ser Asp Val
 710 715 720 725

aag gca atg gtc act gaa gcc cag ggg cta gct aca gaa gac aat ccc
2323
Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala Thr Glu Asp Asn Pro
730 735 740

gat tac gca tca ctt gcc atg gcg atg cgc acc tgc gga ctg ttc acc
2371
Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr Cys Gly Leu Phe Thr
745 750 755

gag gaa cca acc cac ctt gtg gtg aag aag gaa aag aca cca aag cct
2419
Glu Glu Pro Thr His Leu Val Val Lys Lys Glu Lys Thr Pro Lys Pro
760 765 770

gcg aca cgt gat ggt ttc ggt gcc tcc gac tac acc gtc aag ggc atg
2467
Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr Thr Val Lys Gly Met
775 780 785

gca gcc atc gcc gct gtg gtg atc atc ttg gtt tcc ctg gtg gcc gcc
2515
Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val Ser Leu Val Ala Ala
790 795 800 805

ggt acc gcg ttc ctc acc agc ttc ttc ggc agc agc acc aac gaa caa
2563
Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser Ser Thr Asn Glu Gln
810 815 820

tcc ccg ttg gcc tct gtt gaa gcc acc acc tct gca aca cca gaa cct
2611
Ser Pro Leu Ala Ser Val Glu Ala Thr Thr Ser Ala Thr Pro Glu Pro
825 830 835

gtg ggg cca ccg gtc tac ctg gat ctg gat caa gcc cgc acg tgg gat
2659
Val Gly Pro Pro Val Tyr Leu Asp Leu Asp Gln Ala Arg Thr Trp Asp
840 845 850

gac ggt gca gga aca gat gtc acc gac gtc acc gac ggc aac acc tcc
2707
Asp Gly Ala Gly Thr Asp Val Thr Asp Val Thr Asp Gly Asn Thr Ser
855 860 865

acc gca tgg acc tcc acc ggc ggc gac ggc ctc cta gtt gac ctg tcc
2755
Thr Ala Trp Thr Ser Thr Gly Gly Asp Gly Leu Leu Val Asp Leu Ser
870 875 880 885

acg cct gcc cgc ctc gac cgc gtc atc ttg acc acc ggc acc ggc tcc
2803
Thr Pro Ala Arg Leu Asp Arg Val Ile Leu Thr Thr Gly Thr Gly Ser
890 895 900

gac agc aac gtg acc tcg acc gtg aag atc tac gca ttc aac gac gcc
2851
Asp Ser Asn Val Thr Ser Thr Val Lys Ile Tyr Ala Phe Asn Asp Ala
905 910 915

tca cca cac tcc ctg tcg gaa ggc atc gag atc ggc acc gtg gat tat
 2899
 Ser Pro His Ser Leu Ser Glu Gly Ile Glu Ile Gly Thr Val Asp Tyr
 920 925 930

tcc ggc cgc agt ctc agc cac agc atc cgc gat tcc tcc aag ctt ccg
 2947
 Ser Gly Arg Ser Leu Ser His Ser Ile Arg Asp Ser Ser Lys Leu Pro
 935 940 945

ggt cag gtg gaa tcc gtg gtg att ctg gtc gat gag gtt cgt tcc tca
 2995
 Gly Gln Val Glu Ser Val Val Ile Leu Val Asp Glu Val Arg Ser Ser
 950 955 960 965

caa acc tca gac acc aat cca cag atg cag atc gct gaa gta caa ctt
 3043
 Gln Thr Ser Asp Thr Asn Pro Gln Met Gln Ile Ala Glu Val Gln Leu
 970 975 980

gtt ggt tgg taaattacgc gtttgtgatt gac
 3075
 Val Gly Trp

<210> 508

<211> 984

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

Val Leu Gly Ala Val Leu Thr Ser Leu Val Ile Pro Val Leu Thr Arg
 1 5 10 15

Ala Glu Lys Glu Asp Ala Asp Gly Gly Ser Gly Phe Phe Arg Arg Leu
 20 25 30

Leu Thr Leu Ser Val Thr Leu Leu Gly Gly Val Thr Ile Leu Ser Ile
 35 40 45

Ile Gly Ala Pro Leu Leu Thr Arg Met Met Leu Ser Ser Glu Gly Gln
 50 55 60

Val Asn Val Val Met Ser Thr Ala Phe Ala Tyr Trp Leu Leu Pro Gln
 65 70 75 80

Ile Phe Phe Tyr Gly Leu Phe Ala Leu Phe Met Ala Val Leu Asn Thr
 85 90 95

Arg Glu Val Phe Lys Pro Gly Ala Trp Ala Pro Val Val Asn Asn Val
 100 105 110

Ile Thr Leu Thr Val Leu Gly Val Tyr Met Val Leu Pro Ala Arg Leu
 115 120 125

His Pro His Glu Gln Val Gly Ile Phe Asp Pro Gln Ile Ile Phe Leu
 130 135 140

Gly Val Gly Thr Thr Leu Gly Val Val Ala Gln Cys Leu Ile Met Ile
 145 150 155 160

Pro Tyr Leu Arg Arg Ala Gly Ile Asp Met Arg Pro Leu Trp Gly Ile
 165 170 175
 Asp Ala Arg Leu Lys Gln Phe Gly Gly Met Ala Met Ala Ile Ile Val
 180 185 190
 Tyr Val Ala Ile Ser Gln Phe Gly Tyr Ile Ile Thr Thr Arg Ile Ala
 195 200 205
 Ser Ile Ala Asp Asp Ala Ala Pro Phe Ile Tyr Gln Gln His Trp Met
 210 215 220
 Leu Leu Gln Val Pro Tyr Gly Ile Ile Gly Val Thr Leu Leu Thr Ala
 225 230 235 240
 Ile Met Pro Arg Leu Ser Arg Asn Ala Ala Asp Gly Asp Asp Arg Ala
 245 250 255
 Val Val Ser Asp Leu Gln Leu Gly Ser Lys Leu Thr Phe Ile Ala Leu
 260 265 270
 Ile Pro Ile Val Val Phe Phe Thr Ala Phe Gly Val Pro Ile Ala Asn
 275 280 285
 Gly Leu Phe Ala Tyr Gly Gln Phe Asp Ala Asn Ala Ala Asn Ile Leu
 290 295 300
 Gly Trp Thr Leu Ser Phe Ser Ala Phe Thr Leu Ile Pro Tyr Ala Leu
 305 310 315 320
 Val Leu Leu His Leu Arg Val Phe Tyr Ala Arg Glu Glu Val Trp Thr
 325 330 335
 Pro Thr Phe Ile Ile Ala Gly Ile Thr Ala Thr Lys Val Val Leu Ser
 340 345 350
 Leu Leu Ala Pro Leu Leu Ser Ser Ser Pro Glu Arg Val Val Val Leu
 355 360 365
 Leu Gly Ala Ala Asn Gly Phe Ser Phe Ile Thr Gly Ala Val Ile Gly
 370 375 380
 Ala Tyr Leu Leu Arg Asn Lys Leu Gly Leu Leu Gly Met Arg Ser Leu
 385 390 395 400
 Ala Lys Thr Ser Leu Trp Ala Leu Gly Ser Ala Ala Val Gly Ala Ala
 405 410 415
 Ala Ala Trp Ala Leu Gly Trp Leu Ile Gln Ala Val Val Gly Asp Phe
 420 425 430
 Leu Leu Gly Thr Leu Ser Ser Val Gly Tyr Leu Leu Asn Leu Ala Val
 435 440 445
 Leu Gly Val Phe Phe Ile Phe Val Thr Gly Ile Val Leu Ser Arg Ser
 450 455 460
 Gly Leu Pro Glu Val Gln Asn Leu Gly Gln Ala Leu Thr Arg Ile Pro
 465 470 475 480

Gly Leu Ser Arg Phe Ile Arg Pro Asn Thr Lys Ile Ser Leu Asp Val
 485 490 495
 Gly Glu Val Ser Glu Gln Asp Phe Ser Thr Gln Leu Val Ala Pro Ser
 500 505 510
 Glu Phe Ala Ala Thr Pro Val Pro Pro Pro Met Ser Ala Gly Ile Val
 515 520 525
 Arg Gly Pro Arg Leu Val Pro Gly Ala Pro Val Gly Asp Gly Arg Phe
 530 535 540
 Arg Leu Leu Ala Asp His Gly Gly Val Gln Gly Ala Arg Phe Trp Gln
 545 550 555 560
 Ala Arg Glu Ile Ala Thr Gly Lys Glu Val Ala Leu Ile Phe Val Asp
 565 570 575
 Thr Ser Gly Asn Ala Pro Phe Ala Pro Leu Ser Ser Ala Ala Ala Ala
 580 585 590
 Gly Ile Ala Tyr Glu Val Gln Arg Arg Thr Lys Lys Leu Ala Ser Leu
 595 600 605
 Gly Ser Leu Ala Val Ala Pro Asn Ile His Ser Glu Ala Tyr Arg Asn
 610 615 620
 Gly Cys Leu Ile Val Ala Asp Trp Val Pro Gly Ser Ser Leu Ser Ala
 625 630 635 640
 Val Ala Glu Ser Gly Ala Asp Pro Arg Ala Ala Ala Phe Ala Leu Ala
 645 650 655
 Glu Leu Thr Glu Thr Ile Gly Glu Ala His Glu Met Gly Ile Pro Ala
 660 665 670
 Gly Leu Asp Asn Lys Cys Arg Ile Arg Ile Asn Thr Asp Gly His Ala
 675 680 685
 Val Leu Ala Leu Pro Ala Ile Leu Pro Asp Ala Ser Glu Leu Arg Asp
 690 695 700
 Ala Lys Ser Leu Ala Ser Ala Ala Glu Met Leu Ile Asp Ala Thr Leu
 705 710 715 720
 Ala Pro Ser Asp Val Lys Ala Met Val Thr Glu Ala Gln Gly Leu Ala
 725 730 735
 Thr Glu Asp Asn Pro Asp Tyr Ala Ser Leu Ala Met Ala Met Arg Thr
 740 745 750
 Cys Gly Leu Phe Thr Glu Glu Pro Thr His Leu Val Val Lys Lys Glu
 755 760 765
 Lys Thr Pro Lys Pro Ala Thr Arg Asp Gly Phe Gly Ala Ser Asp Tyr
 770 775 780
 Thr Val Lys Gly Met Ala Ala Ile Ala Ala Val Val Ile Ile Leu Val
 785 790 795 800
 Ser Leu Val Ala Ala Gly Thr Ala Phe Leu Thr Ser Phe Phe Gly Ser

805								810				815			
Ser	Thr	Asn	Glu	Gln	Ser	Pro	Leu	Ala	Ser	Val	Glu	Ala	Thr	Thr	Ser
820								825				830			
Ala	Thr	Pro	Glu	Pro	Val	Gly	Pro	Pro	Val	Tyr	Leu	Asp	Leu	Asp	Gln
835								840				845			
Ala	Arg	Thr	Trp	Asp	Asp	Gly	Ala	Gly	Thr	Asp	Val	Thr	Asp	Val	Thr
850								855				860			
Asp	Gly	Asn	Thr	Ser	Thr	Ala	Trp	Thr	Ser	Thr	Gly	Gly	Asp	Gly	Leu
865								870				875			
Leu	Val	Asp	Leu	Ser	Thr	Pro	Ala	Arg	Leu	Asp	Arg	Val	Ile	Leu	Thr
885								890				895			
Thr	Gly	Thr	Gly	Ser	Asp	Ser	Asn	Val	Thr	Ser	Thr	Val	Lys	Ile	Tyr
900								905				910			
Ala	Phe	Asn	Asp	Ala	Ser	Pro	His	Ser	Leu	Ser	Glu	Gly	Ile	Glu	Ile
915								920				925			
Gly	Thr	Val	Asp	Tyr	Ser	Gly	Arg	Ser	Leu	Ser	His	Ser	Ile	Arg	Asp
930								935				940			
Ser	Ser	Lys	Leu	Pro	Gly	Gln	Val	Glu	Ser	Val	Val	Ile	Leu	Val	Asp
945								950				955			
Glu	Val	Arg	Ser	Ser	Gln	Thr	Ser	Asp	Thr	Asn	Pro	Gln	Met	Gln	Ile
965								970				975			
Ala	Glu	Val	Gln	Leu	Val	Gly	Trp								
980															

<210> 509
 <211> 930
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(907)
 <223> RXC02080

<400> 509
 cgtaaattcg aagcgagctt ctaattctag caagcttggt gatggagtat cctgccaaaa 60
 tttgtcctgt tgcttattgt gcaggaattc ggaggcggac atg tca atc gag tgg 115
 Met Ser Ile Glu Trp
 1 5
 tta caa att gtt gaa tta gga gcg atc ttt ggt gca ggt ttc ctc gca 163
 Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly Ala Gly Phe Leu Ala
 10 15 20
 gga agc atc aat gta att gtc gga gca gga aca tta gtg tcg ttt cct 211
 Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr Leu Val Ser Phe Pro
 25 30 35

att ctc gtg ttc ctg ggc ctt cca ccg ttg act gcc acc atc gcc aac	259
Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr Ala Thr Ile Ala Asn	
40 45 50	
acc atc ggc atc gtt cct gga agt att tcg ggt gtg gtt gct tat aga	307
Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly Val Val Ala Tyr Arg	
55 60 65	
cgt gaa cta cac gcc cat gta aaa acc atc aga ttt ctg ctg cca gca	355
Arg Glu Leu His Ala His Val Lys Thr Ile Arg Phe Leu Leu Pro Ala	
70 75 80 85	
tca atc ctc gga ggg atc acc ggc gcc tcg ctc ttg ctg cat ttc tcc	403
Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu Leu Leu His Phe Ser	
90 95 100	
gca gat gtt ttt aca gca gta att ccc tgg ctg att gga ttc ggc acg	451
Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu Ile Gly Phe Gly Thr	
105 110 115	
ctg ttg gtt atc gca ggt cca tca att aag aag cat gtt ggc gct cat	499
Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys His Val Gly Ala His	
120 125 130	
act tca ggt ggc atc tct gct ggg ttt agg caa ttg cct ttc ccg agc	547
Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln Leu Pro Phe Pro Ser	
135 140 145	
cga acc acc ttc atc gtc tca gta tgt ggt gcc ctg ttg ctg ggc atg	595
Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala Leu Leu Leu Gly Met	
150 155 160 165	
tat gga ggg tac ttc agc gca gct caa ggc att ctt ctc atc gca ttg	643
Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile Leu Leu Ile Ala Leu	
170 175 180	
ctt ggc atc aca tca acg ctg cag atg cag gaa ctc aac gcc atc aaa	691
Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu Leu Asn Ala Ile Lys	
185 190 195	
aac ctc aca gtg gcg gca gtt aat ctc atc gca gcc agt gtt ttt ata	739
Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala Ala Ser Val Phe Ile	
200 205 210	
atc atc tcc cct gag ttg atc tcc tgg ccg acc gtt gcc tta atc gcg	787
Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr Val Ala Leu Ile Ala	
215 220 225	
ctt ggc tca gct tta ggt gga tac atc ggc gga cgg tac gcc cgc cga	835
Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly Arg Tyr Ala Arg Arg	
230 235 240 245	
ctt cgc ccc agt gtt ttt aga gca ttt gtg gtc atc gtc gga atc acc	883
Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val Ile Val Gly Ile Thr	
250 255 260	
acg gtc atc gtt atg acg atc ggt taatgcagca gactagtaac ccc	930
Thr Val Ile Val Met Thr Ile Gly	
265	

<210> 510

<211> 269

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 510

```

Met Ser Ile Glu Trp Leu Gln Ile Val Glu Leu Gly Ala Ile Phe Gly
 1           5           10           15

Ala Gly Phe Leu Ala Gly Ser Ile Asn Val Ile Val Gly Ala Gly Thr
      20           25           30

Leu Val Ser Phe Pro Ile Leu Val Phe Leu Gly Leu Pro Pro Leu Thr
      35           40           45

Ala Thr Ile Ala Asn Thr Ile Gly Ile Val Pro Gly Ser Ile Ser Gly
      50           55           60

Val Val Ala Tyr Arg Arg Glu Leu His Ala His Val Lys Thr Ile Arg
      65           70           75           80

Phe Leu Leu Pro Ala Ser Ile Leu Gly Gly Ile Thr Gly Ala Ser Leu
      85           90           95

Leu Leu His Phe Ser Ala Asp Val Phe Thr Ala Val Ile Pro Trp Leu
      100          105          110

Ile Gly Phe Gly Thr Leu Leu Val Ile Ala Gly Pro Ser Ile Lys Lys
      115          120          125

His Val Gly Ala His Thr Ser Gly Gly Ile Ser Ala Gly Phe Arg Gln
      130          135          140

Leu Pro Phe Pro Ser Arg Thr Thr Phe Ile Val Ser Val Cys Gly Ala
      145          150          155          160

Leu Leu Leu Gly Met Tyr Gly Gly Tyr Phe Ser Ala Ala Gln Gly Ile
      165          170          175

Leu Leu Ile Ala Leu Leu Gly Ile Thr Ser Thr Leu Gln Met Gln Glu
      180          185          190

Leu Asn Ala Ile Lys Asn Leu Thr Val Ala Ala Val Asn Leu Ile Ala
      195          200          205

Ala Ser Val Phe Ile Ile Ile Ser Pro Glu Leu Ile Ser Trp Pro Thr
      210          215          220

Val Ala Leu Ile Ala Leu Gly Ser Ala Leu Gly Gly Tyr Ile Gly Gly
      225          230          235          240

Arg Tyr Ala Arg Arg Leu Arg Pro Ser Val Phe Arg Ala Phe Val Val
      245          250          255

Ile Val Gly Ile Thr Thr Val Ile Val Met Thr Ile Gly
      260          265

```

<210> 511

<211> 669

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(646)

<223> RXC02789

<400> 511

```

ttcttccgta cggctatgct taaaagctaa atttgtcttt gtgccttgca acacattaat 60

ttcttaacac taaacaatgg aaaggtaagc gggtttttct atg aag gtt tcc gcc 115
                                         Met Lys Val Ser Ala
                                         1 5

gat aca ccc ggt cac gat gat cca ggc cca ggc cgg cgc ctt ggc tta 163
Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly Arg Arg Leu Gly Leu
                        10 15 20

gat gtc ggc acc gtg cgc atc gga gtg gca gcc tct gac cgc gat gcc 211
Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala Ser Asp Arg Asp Ala
                        25 30 35

aag ctt gcc atg cct gtg gaa acc gtt ccg cgg gaa act gga ttc aaa 259
Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg Glu Thr Gly Phe Lys
                        40 45 50

ggg cca gac ctg gcc gat att gat cgg ttg gtc gcc atc gtt gag gaa 307
Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val Ala Ile Val Glu Glu
                        55 60 65

tac aac gcc gtg gaa gtc att gtt ggt cta ccc aca gat ctg cag gga 355
Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro Thr Asp Leu Gln Gly
                        70 75 80 85

aat ggc tcc gcc agt gtg aag cat gca aag gaa att gct ttc cgc gtc 403
Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu Ile Ala Phe Arg Val
                        90 95 100

cgt cgg cgc ctc acc aat gct gga aag aac att ccg gta cgg ctt ggc 451
Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile Pro Val Arg Leu Gly
                        105 110 115

gac gaa cgc ctc acc acc gtc gtg gcc acc caa gcc ttg cgg gcc tca 499
Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln Ala Leu Arg Ala Ser
                        120 125 130

gga gtc agc gaa aaa gcg gga cgt aaa gtt att gat caa gct gcc gca 547
Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile Asp Gln Ala Ala Ala
                        135 140 145

gta gaa atc ctt caa acc tgg ttg gat gct cgc acc cga gcc ctt gaa 595
Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg Thr Arg Ala Leu Glu
                        150 155 160 165

cca caa tcc aca gac acc caa gat ttc gac gag aag gga aat ttc cca 643
Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu Lys Gly Asn Phe Pro
                        170 175 180

gga tgaaccaaat ccgaaaccgc cgg 669
Gly

```

<210> 512
 <211> 182
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 512

```

Met Lys Val Ser Ala Asp Thr Pro Gly His Asp Asp Pro Gly Pro Gly
 1             5             10             15

Arg Arg Leu Gly Leu Asp Val Gly Thr Val Arg Ile Gly Val Ala Ala
 20             25             30

Ser Asp Arg Asp Ala Lys Leu Ala Met Pro Val Glu Thr Val Pro Arg
 35             40             45

Glu Thr Gly Phe Lys Gly Pro Asp Leu Ala Asp Ile Asp Arg Leu Val
 50             55             60

Ala Ile Val Glu Glu Tyr Asn Ala Val Glu Val Ile Val Gly Leu Pro
 65             70             75             80

Thr Asp Leu Gln Gly Asn Gly Ser Ala Ser Val Lys His Ala Lys Glu
 85             90             95

Ile Ala Phe Arg Val Arg Arg Arg Leu Thr Asn Ala Gly Lys Asn Ile
100            105            110

Pro Val Arg Leu Gly Asp Glu Arg Leu Thr Thr Val Val Ala Thr Gln
115            120            125

Ala Leu Arg Ala Ser Gly Val Ser Glu Lys Ala Gly Arg Lys Val Ile
130            135            140

Asp Gln Ala Ala Ala Val Glu Ile Leu Gln Thr Trp Leu Asp Ala Arg
145            150            155            160

Thr Arg Ala Leu Glu Pro Gln Ser Thr Asp Thr Gln Asp Phe Asp Glu
165            170            175

Lys Gly Asn Phe Pro Gly
180

```

<210> 513
 <211> 903
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(880)
 <223> RXC02295

<400> 513

```

ttcccatgct aatccgcgaa aatggcactt caacagccat atactttaaa caacacaaat 60

gatgcaagac tgataccggg atgtgatagg agcgcaccac atg ggg ttg gaa tta 115
Met Gly Leu Glu Leu
1             5

```

gca gct agc ggg tgg ggc atc ctc atc gca ggc gcc gcc gta gcc gga Ala Ala Ser Gly Trp Gly Ile Leu Ile Ala Gly Ala Ala Val Ala Gly	163
10 15 20	
tgg atc gac gca gta atc ggc ggt ggc gga ctc gtc ctc atc ccg ctg Trp Ile Asp Ala Val Ile Gly Gly Gly Gly Leu Val Leu Ile Pro Leu	211
25 30 35	
atc ctc gcg gtc atg ccg caa ctc gca cct gtg aca gcg ctg gcc tcc Ile Leu Ala Val Met Pro Gln Leu Ala Pro Val Thr Ala Leu Ala Ser	259
40 45 50	
aac aaa ctg gca gcc gtc acc ggc acg gca tcg gcg gca ttc acc ctg Asn Lys Leu Ala Ala Val Thr Gly Thr Ala Ser Ala Ala Phe Thr Leu	307
55 60 65	
gtc agg cgc gtc aaa ccc gac aaa aaa ctg ctt gcg ctc tac gtt ctg Val Arg Arg Val Lys Pro Asp Lys Lys Leu Leu Ala Leu Tyr Val Leu	355
70 75 80 85	
gtg gca gct gtg tgc tcc ggt gca ggc gcc ctg gct gcg agt ctc att Val Ala Ala Val Cys Ser Gly Ala Gly Ala Leu Ala Ala Ser Leu Ile	403
90 95 100	
gac aaa caa atc atg cga ccg ctg atc atc gtg ttg atg ctg gtc gtt Asp Lys Gln Ile Met Arg Pro Leu Ile Ile Val Leu Met Leu Val Val	451
105 110 115	
ggc ctg atc gtg gtg ttc aaa cca aac ttc gga acc ggc gaa agc aaa Gly Leu Ile Val Val Phe Lys Pro Asn Phe Gly Thr Gly Glu Ser Lys	499
120 125 130	
gcc ctg ccc acc gga tgg aaa cgc tgg gcc gcc atc gtt gca gtc gga Ala Leu Pro Thr Gly Trp Lys Arg Trp Ala Ala Ile Val Ala Val Gly	547
135 140 145	
ctc atc gca gcc tac gac ggc atc ttc gga ccc gga acc ggc atg ttc Leu Ile Ala Ala Tyr Asp Gly Ile Phe Gly Pro Gly Thr Gly Met Phe	595
150 155 160 165	
ctc atc atg gcg ttc acc gca ctg ctc tcc caa aat ttc ctg tcc tcc Leu Ile Met Ala Phe Thr Ala Leu Leu Ser Gln Asn Phe Leu Ser Ser	643
170 175 180	
gca gcc atg gcg aag gtc gta aac acc gca aca aac ctg ggt gcg cta Ala Ala Met Ala Lys Val Val Asn Thr Ala Thr Asn Leu Gly Ala Leu	691
185 190 195	
att gta ttc atc atc ggc ggc cac atg tgg tgg acc cta gga ctc gtg Ile Val Phe Ile Ile Gly Gly His Met Trp Trp Thr Leu Gly Leu Val	739
200 205 210	
ctg gca gtc gcc aat gtc gca ggc gca caa ctc ggt gcc cga acg gtg Leu Ala Val Ala Asn Val Ala Gly Ala Gln Leu Gly Ala Arg Thr Val	787
215 220 225	
ctt ggt ggc ggt acc agg cta att aga tac gca cta cta acc ctg gtt Leu Gly Gly Gly Thr Arg Leu Ile Arg Tyr Ala Leu Leu Thr Leu Val	835
230 235 240 245	

gtc gtc atg agc gtc tac ctc acc tgg caa caa atc caa gga atg 880
Val Val Met Ser Val Tyr Leu Thr Trp Gln Gln Ile Gln Gly Met
250 255 260

tagataagtc ggggcaaact cta 903

```
<210> 514
<211> 260
<212> PRT
<213> Corynebacterium glutamicum
```

<400> 514																
Met	Gly	Leu	Glu	Leu	Ala	Ala	Ser	Gly	Trp	Gly	Ile	Leu	Ile	Ala	Gly	
1				5					10					15		
Ala	Ala	Val	Ala	Gly	Trp	Ile	Asp	Ala	Val	Ile	Gly	Gly	Gly	Gly	Leu	
			20					25					30			
Val	Leu	Ile	Pro	Leu	Ile	Leu	Ala	Val	Met	Pro	Gln	Leu	Ala	Pro	Val	
		35					40					45				
Thr	Ala	Leu	Ala	Ser	Asn	Lys	Leu	Ala	Ala	Val	Thr	Gly	Thr	Ala	Ser	
	50					55					60					
Ala	Ala	Phe	Thr	Leu	Val	Arg	Arg	Val	Lys	Pro	Asp	Lys	Lys	Leu	Leu	
65					70					75					80	
Ala	Leu	Tyr	Val	Leu	Val	Ala	Ala	Val	Cys	Ser	Gly	Ala	Gly	Ala	Leu	
				85					90					95		
Ala	Ala	Ser	Leu	Ile	Asp	Lys	Gln	Ile	Met	Arg	Pro	Leu	Ile	Ile	Val	
			100					105					110			
Leu	Met	Leu	Val	Val	Gly	Leu	Ile	Val	Val	Phe	Lys	Pro	Asn	Phe	Gly	
		115					120					125				
Thr	Gly	Glu	Ser	Lys	Ala	Leu	Pro	Thr	Gly	Trp	Lys	Arg	Trp	Ala	Ala	
	130					135					140					
Ile	Val	Ala	Val	Gly	Leu	Ile	Ala	Ala	Tyr	Asp	Gly	Ile	Phe	Gly	Pro	
145					150					155					160	
Gly	Thr	Gly	Met	Phe	Leu	Ile	Met	Ala	Phe	Thr	Ala	Leu	Leu	Ser	Gln	
				165					170					175		
Asn	Phe	Leu	Ser	Ser	Ala	Ala	Met	Ala	Lys	Val	Val	Asn	Thr	Ala	Thr	
		180						185					190			
Asn	Leu	Gly	Ala	Leu	Ile	Val	Phe	Ile	Ile	Gly	Gly	His	Met	Trp	Trp	
		195					200					205				
Thr	Leu	Gly	Leu	Val	Leu	Ala	Val	Ala	Asn	Val	Ala	Gly	Ala	Gln	Leu	
	210					215					220					
Gly	Ala	Arg	Thr	Val	Leu	Gly	Gly	Gly	Thr	Arg	Leu	Ile	Arg	Tyr	Ala	
225					230					235					240	
Leu	Leu	Thr	Leu	Val	Val	Val	Met	Ser	Val	Tyr	Leu	Thr	Trp	Gln	Gln	
				245					250					255		

Ile Gln Gly Met
260

<210> 515
<211> 1132
<212> DNA
<213> *Corynebacterium glutamicum*

<220>
<221> CDS
<222> (101) .. (1132)
<223> RXN03063

<400> 515
tgtctacaac ttcgccctca tggacatatt aacttcgttg cctcggagag aatactcatc 60

acctagacaa cagtttgtat ctcacctcac aggaggaacc gtg gaa gat ctc tca 115
Val Glu Asp Leu Ser
1 5

tac cgc atc ccg cag tcg cgc acc gtg gcc gag cag gtg cca ggg ccg 163
Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu Gln Val Pro Gly Pro
10 15 20

aag tcg aaa gcg ctg gat gag cgt cga caa gca gca gta gca cga gca 211
Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala Ala Val Ala Arg Ala
25 30 35

ctt gca ccg ggt ctg cct gga tac gtg gtg gac gca gac ggt ggc atc 259
Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp Ala Asp Gly Gly Ile
40 45 50

ttg gct gac gcg gac ggc aac cgt ttc atc gac ctg gcc tcc ggc atc 307
Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp Leu Ala Ser Gly Ile
55 60 65

gcc gtg acc acg gtc ggc gga tcc aac gcg gcc gtc gcg aaa gcc gtc 355
Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala Val Ala Lys Ala Val
70 75 80 85

ggc gcc gca gct gcc cgc ttc acc cac acc tgc ttc atg gtc tca cct 403
Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys Phe Met Val Ser Pro
90 95 100

tat gaa act tac gtg gcc atg gcg gag aga ctc aac gcc ttg act cca 451
Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu Asn Ala Leu Thr Pro
105 110 115

ggc gat cac gac aag aag agc gcg ctg ttt aac tct ggc gcc gaa gcc 499
Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn Ser Gly Ala Glu Ala
120 125 130

gtg gaa aac gcc gtc aag gtg gca cgc gcc tac acc ggc aag ggc gcg 547
Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr Thr Gly Lys Gly Ala
135 140 145

gtc gtg gtg ttc gac aac gcg tac cac gga cgg acc aac ctc acc atg 595
Val Val Val Phe Asp Asn Ala Tyr His Gly Arg Thr Asn Leu Thr Met
150 155 160 165

```

gcg atg acc gcg aag aac cgc cca tac aag tcc gga ttc gga cca cta 643
Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser Gly Phe Gly Pro Leu
170 175 180

gcc gca gac gtc tac cgt gca cca atg tct tac cca ctg cgc gac gga 691
Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr Pro Leu Arg Asp Gly
185 190 195

ctg tcc ggc ccg gaa gcc gca gag cgc gcg atc tcc gtg atc gaa tcc 739
Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile Ser Val Ile Glu Ser
200 205 210

cag gtc gga gcc gaa aac ctc gcc tgc gtg gtc att gaa ccg atc cag 787
Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val Ile Glu Pro Ile Gln
215 220 225

ggc gaa ggc gga ttc atc gtc ccc gca cca gga ttc ctc gca gcc att 835
Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly Phe Leu Ala Ala Ile
230 235 240 245

tcc acc tgg tgc cgc gag aac gac gtg gtg ttc atc gcc gat gaa atc 883
Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe Ile Ala Asp Glu Ile
250 255 260

caa tct ggc ttc ctg cgc acc ggc gac tgg ttc gcc agc gac gca gaa 931
Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe Ala Ser Asp Ala Glu
265 270 275

ggg gtg atc ccc gac gtc atc acc acc gca aaa ggc atc gcc ggc ggc 979
Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys Gly Ile Ala Gly Gly
280 285 290

atg cca cta tcc gca gtg acc ggc cgc gca gaa atc atg gac gca ccc
1027
Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu Ile Met Asp Ala Pro
295 300 305

ggc ccc ggc gcg ctc ggc gga acc tac ggc gga aac ccc gtt gct tgc
1075
Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly Asn Pro Val Ala Cys
310 315 320 325

gcc gcg gca ctt gca gcc att gaa gtg atg gaa caa gcc gac ctt aag
1123
Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu Gln Ala Asp Leu Lys
330 335 340

acc cgc gcg
1132
Thr Arg Ala

```

<210> 516

<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

```

Val Glu Asp Leu Ser Tyr Arg Ile Pro Gln Ser Arg Thr Val Ala Glu
1 5 10 15

```

Gln Val Pro Gly Pro Lys Ser Lys Ala Leu Asp Glu Arg Arg Gln Ala
 20 25 30
 Ala Val Ala Arg Ala Leu Ala Pro Gly Leu Pro Gly Tyr Val Val Asp
 35 40 45
 Ala Asp Gly Gly Ile Leu Ala Asp Ala Asp Gly Asn Arg Phe Ile Asp
 50 55 60
 Leu Ala Ser Gly Ile Ala Val Thr Thr Val Gly Gly Ser Asn Ala Ala
 65 70 75 80
 Val Ala Lys Ala Val Gly Ala Ala Ala Ala Arg Phe Thr His Thr Cys
 85 90 95
 Phe Met Val Ser Pro Tyr Glu Thr Tyr Val Ala Met Ala Glu Arg Leu
 100 105 110
 Asn Ala Leu Thr Pro Gly Asp His Asp Lys Lys Ser Ala Leu Phe Asn
 115 120 125
 Ser Gly Ala Glu Ala Val Glu Asn Ala Val Lys Val Ala Arg Ala Tyr
 130 135 140
 Thr Gly Lys Gly Ala Val Val Val Phe Asp Asn Ala Tyr His Gly Arg
 145 150 155 160
 Thr Asn Leu Thr Met Ala Met Thr Ala Lys Asn Arg Pro Tyr Lys Ser
 165 170 175
 Gly Phe Gly Pro Leu Ala Ala Asp Val Tyr Arg Ala Pro Met Ser Tyr
 180 185 190
 Pro Leu Arg Asp Gly Leu Ser Gly Pro Glu Ala Ala Glu Arg Ala Ile
 195 200 205
 Ser Val Ile Glu Ser Gln Val Gly Ala Glu Asn Leu Ala Cys Val Val
 210 215 220
 Ile Glu Pro Ile Gln Gly Glu Gly Gly Phe Ile Val Pro Ala Pro Gly
 225 230 235 240
 Phe Leu Ala Ala Ile Ser Thr Trp Cys Arg Glu Asn Asp Val Val Phe
 245 250 255
 Ile Ala Asp Glu Ile Gln Ser Gly Phe Leu Arg Thr Gly Asp Trp Phe
 260 265 270
 Ala Ser Asp Ala Glu Gly Val Ile Pro Asp Val Ile Thr Thr Ala Lys
 275 280 285
 Gly Ile Ala Gly Gly Met Pro Leu Ser Ala Val Thr Gly Arg Ala Glu
 290 295 300
 Ile Met Asp Ala Pro Gly Pro Gly Ala Leu Gly Gly Thr Tyr Gly Gly
 305 310 315 320
 Asn Pro Val Ala Cys Ala Ala Ala Leu Ala Ala Ile Glu Val Met Glu
 325 330 335

Gln Ala Asp Leu Lys Thr Arg Ala
340

<210> 517
<211> 1491
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1468)
<223> RXN02970

<400> 517
aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60

ttattttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc	643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr	
170 175 180	
acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc	691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser	
185 190 195	
tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag	739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys	
200 205 210	
cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg	787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala	
215 220 225	
atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca	835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro	
230 235 240 245	
gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc	883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile	
250 255 260	
ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa	931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys	
265 270 275	
ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc	979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile	
280 285 290	
acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc	
1027	
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile	
295 300 305	
gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc	
1075	
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser	
310 315 320 325	
ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag	
1123	
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys	
330 335 340	
gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct	
1171	
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala	
345 350 355	
cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa	
1219	
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu	
360 365 370	
gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca	
1267	
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala	
375 380 385	

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa
1315

Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac
1363

Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
410 415 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg
1411

Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
425 430 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg
1459

Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
440 445 450

gcg ttg ttc taagttttct agataacaag gcc
1491

Ala Leu Phe
455

<210> 518

<211> 456

<212> PRT

<213> Corynebacterium glutamicum

<400> 518

Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
1 5 10 15

Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr

145		150		155		160
His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg	165		170		175	
Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro	180		185		190	
Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Cys	195		200		205	
Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala	210		215		220	
Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly	225		230		235	240
Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys		245		250		255
Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe	260		265		270	
Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe	275		280		285	
Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala	290		295		300	
Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly	305		310		315	320
Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala		325		330		335
Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile		340		345		350
Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu	355		360		365	
Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile	370		375		380	
Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala	385		390		395	400
Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser		405		410		415
Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu		420		425		430
Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu	435		440		445	
Leu Thr Phe Ala Gly Ala Leu Phe	450		455			

<210> 519

<211> 1330
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1330)
 <223> FRXA01009

<400> 519
 aaccgacaaa acagccgttc acgtgctaaa gcagctcggc ttgatctagg gtgaggtgag 60
 ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
 Leu Ala Leu Lys Gly
 1 5
 tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
 Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
 10 15 20
 aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
 Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
 25 30 35
 cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
 His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
 40 45 50
 gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
 Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
 55 60 65
 atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
 Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70 75 80 85
 tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
 Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
 90 95 100
 ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451
 Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
 105 110 115
 tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
 Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
 120 125 130
 gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
 Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
 135 140 145
 cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
 Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
 150 155 160 165
 tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
 Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
 170 175 180
 acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691

Thr	Asp	Pro	Asp	Ile	Tyr	His	Phe	Trp	Ala	Pro	Phe	Leu	His	His	Ser		
			185					190					195				
tca	ttc	ttt	gcc	acc	acc	caa	gaa	gaa	gaa	tgc	gaa	cgc	gca	ctc	aag	739	
Ser	Phe	Phe	Ala	Thr	Thr	Gln	Glu	Glu	Glu	Cys	Glu	Arg	Ala	Leu	Lys		
		200					205					210					
cac	ttg	gaa	gat	gtc	atc	gcg	ttt	gaa	ggg	gct	ggc	atg	atc	gca	gcg	787	
His	Leu	Glu	Asp	Val	Ile	Ala	Phe	Glu	Gly	Ala	Gly	Met	Ile	Ala	Ala		
	215					220					225						
atc	gtc	ctg	gag	cca	gtg	gtg	gga	tca	tca	gga	atc	atc	ctg	cca	cca	835	
Ile	Val	Leu	Glu	Pro	Val	Val	Gly	Ser	Ser	Gly	Ile	Ile	Leu	Pro	Pro		
230					235					240					245		
gca	ggg	tac	tta	aat	ggc	gtg	cgc	gaa	ctt	tgc	aac	aag	cac	ggc	atc	883	
Ala	Gly	Tyr	Leu	Asn	Gly	Val	Arg	Glu	Leu	Cys	Asn	Lys	His	Gly	Ile		
				250				255						260			
ctc	ttc	atc	gcc	gac	gaa	gtc	atg	gtc	gga	ttc	gga	cgc	acc	gga	aaa	931	
Leu	Phe	Ile	Ala	Asp	Glu	Val	Met	Val	Gly	Phe	Gly	Arg	Thr	Gly	Lys		
			265					270					275				
ctg	ttt	gct	tac	gag	cat	gct	ggc	gac	gat	ttc	cag	cca	gac	atg	atc	979	
Leu	Phe	Ala	Tyr	Glu	His	Ala	Gly	Asp	Asp	Phe	Gln	Pro	Asp	Met	Ile		
		280					285					290					
acc	ttc	gcc	aag	ggg	gtt	aac	gca	ggg	tac	gcc	cca	ctc	ggg	ggc	atc		
1027																	
Thr	Phe	Ala	Lys	Gly	Val	Asn	Ala	Gly	Tyr	Ala	Pro	Leu	Gly	Gly	Ile		
	295					300					305						
gtg	atg	acc	caa	tca	atc	cgc	gat	acc	ttc	gga	tca	gag	gca	tac	tcc		
1075																	
Val	Met	Thr	Gln	Ser	Ile	Arg	Asp	Thr	Phe	Gly	Ser	Glu	Ala	Tyr	Ser		
310					315					320					325		
ggc	gga	ctc	acc	tac	tcc	gga	cac	cca	ctt	gca	gta	gca	ccc	gcc	aag		
1123																	
Gly	Gly	Leu	Thr	Tyr	Ser	Gly	His	Pro	Leu	Ala	Val	Ala	Pro	Ala	Lys		
				330				335					340				
gca	gcg	ctg	gag	att	tac	gcg	gaa	gga	gag	atc	att	cca	cgc	gta	gct		
1171																	
Ala	Ala	Leu	Glu	Ile	Tyr	Ala	Glu	Gly	Glu	Ile	Ile	Pro	Arg	Val	Ala		
			345				350					355					
cga	ctt	ggc	gct	gaa	ctg	atc	gaa	cct	cgc	ctt	cgt	gaa	cta	gcg	gaa		
1219																	
Arg	Leu	Gly	Ala	Glu	Leu	Ile	Glu	Pro	Arg	Leu	Arg	Glu	Leu	Ala	Glu		
		360					365					370					
gaa	aac	gta	gcg	atc	gct	gac	gtg	cgg	ggc	atc	gga	ttc	ttc	tgg	gca		
1267																	
Glu	Asn	Val	Ala	Ile	Ala	Asp	Val	Arg	Gly	Ile	Gly	Phe	Phe	Trp	Ala		
	375					380					385						
gtg	gag	ttc	aat	gca	gac	gcc	act	gcc	atg	gct	gcc	ggg	gct	gca	gaa		
1315																	
Val	Glu	Phe	Asn	Ala	Asp	Ala	Thr	Ala	Met	Ala	Ala	Gly	Ala	Ala	Glu		
390					395					400					405		

ttc aag gaa cgc ggc
 1330
 Phe Lys Glu Arg Gly
 410

<210> 520
 <211> 410
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 520
 Leu Ala Leu Lys Gly Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe
 1 5 10 15
 Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
 20 25 30
 Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
 35 40 45
 Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
 50 55 60
 Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
 65 70 75 80
 His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
 85 90 95
 Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
 100 105 110
 Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
 115 120 125
 Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
 130 135 140
 Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
 145 150 155 160
 His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
 165 170 175
 Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
 180 185 190
 Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
 195 200 205
 Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
 210 215 220
 Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
 225 230 235 240
 Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
 245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
 260 265 270
 Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
 275 280 285
 Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
 290 295 300
 Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
 305 310 315 320
 Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
 325 330 335
 Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
 340 345 350
 Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
 355 360 365
 Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
 370 375 380
 Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
 385 390 395 400
 Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
 405 410

<210> 521
 <211> 1998
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1975)
 <223> RXA01551

<400> 521
 cactacgtag gcgtacccca ccatcaccgc gtcgaaaagc gccctctctt aacccccgca 60
 agggggtaac ttttacgcgc acgcgtgcaa cgcgctagtt ttg aag gca gtc ccc 115
 Leu Lys Ala Val Pro
 1 5
 acg ggc gcc cga gca cgg gct gag atc gcg ctg att gct gcg cga gca 163
 Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu Ile Ala Ala Arg Ala
 10 15 20
 ccg ttt gaa cct gtc cgg tta gca ccg gcg aag gaa gag agg aat ggt 211
 Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys Glu Glu Arg Asn Gly
 25 30 35
 gca atg acg cct acc caa aat gag atc cac ccg aaa cat agc tac tcc 259
 Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro Lys His Ser Tyr Ser
 40 45 50
 ccc atc cgc aag gac ggt ctc gag gtc ccg gag acc gaa atc cgc ctc 307

Pro	Ile	Arg	Lys	Asp	Gly	Leu	Glu	Val	Pro	Glu	Thr	Glu	Ile	Arg	Leu	
55						60					65					
gat	gac	tcg	cca	agc	ggc	ccc	aac	gaa	ccc	ttc	cgc	atc	tac	cgc	acc	355
Asp	Asp	Ser	Pro	Ser	Gly	Pro	Asn	Glu	Pro	Phe	Arg	Ile	Tyr	Arg	Thr	
70					75				80						85	
cgt	ggc	cca	gaa	acc	aac	ccc	aag	cag	gga	ctt	ccg	cgg	ctg	cgc	gag	403
Arg	Gly	Pro	Glu	Thr	Asn	Pro	Lys	Gln	Gly	Leu	Pro	Arg	Leu	Arg	Glu	
				90					95						100	
tca	tgg	atc	acc	gcc	cgc	ggc	gac	gtt	gcc	acc	tat	cag	ggg	cgc	gag	451
Ser	Trp	Ile	Thr	Ala	Arg	Gly	Asp	Val	Ala	Thr	Tyr	Gln	Gly	Arg	Glu	
			105					110					115			
cgt	ttg	ctt	atc	gac	gac	ggc	cgc	tcg	gca	atg	cgt	cga	ggt	caa	gct	499
Arg	Leu	Leu	Ile	Asp	Asp	Gly	Arg	Ser	Ala	Met	Arg	Arg	Gly	Gln	Ala	
			120				125					130				
tcg	gct	gag	tgg	aaa	ggc	caa	aaa	cca	gct	cct	ttg	aag	gcg	cta	cct	547
Ser	Ala	Glu	Trp	Lys	Gly	Gln	Lys	Pro	Ala	Pro	Leu	Lys	Ala	Leu	Pro	
	135					140					145					
ggc	aaa	aga	gtc	acc	caa	atg	gcc	tat	gca	cgt	gct	ggc	gtg	att	act	595
Gly	Lys	Arg	Val	Thr	Gln	Met	Ala	Tyr	Ala	Arg	Ala	Gly	Val	Ile	Thr	
150					155					160					165	
cgt	gaa	atg	gag	ttt	gta	gcg	ctg	cgc	gaa	cac	gtt	gat	gcg	gag	ttt	643
Arg	Glu	Met	Glu	Phe	Val	Ala	Leu	Arg	Glu	His	Val	Asp	Ala	Glu	Phe	
				170					175					180		
gtg	cgc	tct	gag	gtg	gcg	cgc	ggt	cgg	gcc	att	att	ccc	aac	aac	gtc	691
Val	Arg	Ser	Glu	Val	Ala	Arg	Gly	Arg	Ala	Ile	Ile	Pro	Asn	Asn	Val	
			185					190					195			
aac	cac	ccc	gaa	tct	gaa	ccg	atg	att	att	ggt	cgc	aaa	ttt	ttg	acc	739
Asn	His	Pro	Glu	Ser	Glu	Pro	Met	Ile	Ile	Gly	Arg	Lys	Phe	Leu	Thr	
		200					205					210				
aaa	atc	aac	gcc	aat	att	ggc	aat	tct	gcg	gtc	acc	tct	tca	atc	gag	787
Lys	Ile	Asn	Ala	Asn	Ile	Gly	Asn	Ser	Ala	Val	Thr	Ser	Ser	Ile	Glu	
	215					220					225					
gaa	gag	gtg	tcc	aag	ctg	cag	tgg	gcc	acg	cgc	tgg	ggt	gcc	gat	acc	835
Glu	Glu	Val	Ser	Lys	Leu	Gln	Trp	Ala	Thr	Arg	Trp	Gly	Ala	Asp	Thr	
230					235					240				245		
gtg	atg	gat	cta	tcc	acc	ggc	gat	gat	att	cac	acc	acc	cgc	gaa	tgg	883
Val	Met	Asp	Leu	Ser	Thr	Gly	Asp	Asp	Ile	His	Thr	Thr	Arg	Glu	Trp	
				250					255					260		
att	atc	cgc	aac	tcc	ccc	gtt	cct	atc	ggc	acc	gtc	ccg	atc	tac	caa	931
Ile	Ile	Arg	Asn	Ser	Pro	Val	Pro	Ile	Gly	Thr	Val	Pro	Ile	Tyr	Gln	
			265					270					275			
gcg	ctg	gaa	aaa	gta	aat	ggc	gtg	gcc	gca	gac	ctt	aac	tgg	gaa	gta	979
Ala	Leu	Glu	Lys	Val	Asn	Gly	Val	Ala	Ala	Asp	Leu	Asn	Trp	Glu	Val	
		280					285					290				
ttc	cgc	gat	acc	atc	att	gag	cag	tgt	gaa	caa	ggc	gtg	gac	tat	atg	
1027																

Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln Gly Val Asp Tyr Met
 295 300 305
 acc atc cac gcc ggc gtc ctg ctg gct tat atc cca ctg act acc cgt
 1075
 Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile Pro Leu Thr Thr Arg
 310 315 320 325
 cgt gtc acc ggc att gtc tcc cgc ggc gga tcc att atg gcc ggt tgg
 1123
 Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser Ile Met Ala Gly Trp
 330 335 340
 tgt ctg gcg cat cac cgc gaa tca ttc ctc tac gag cat ttc gac gag
 1171
 Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr Glu His Phe Asp Glu
 345 350 355
 ctg tgc gaa atc ttt gca caa tat gac gtc gca ttc tcc ctc ggt gat
 1219
 Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala Phe Ser Leu Gly Asp
 360 365 370
 ggc cta cgc ccc gga tcg ctt gcc gat gcc aac gac gcc gcg caa ttc
 1267
 Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn Asp Ala Ala Gln Phe
 375 380 385
 gcc gag ctg aaa acc att ggt gag ctc acc caa cgc gcc tgg gaa tac
 1315
 Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln Arg Ala Trp Glu Tyr
 390 395 400 405
 gat gta caa gta atg gtc gaa gga cct gga cac gtg cca cta aac atg
 1363
 Asp Val Gln Val Met Val Glu Gly Pro Gly His Val Pro Leu Asn Met
 410 415 420
 atc cag gaa aac aac gag ctg gaa caa aag tgg gca gcg gac gca cct
 1411
 Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp Ala Ala Asp Ala Pro
 425 430 435
 ttt tac act ctt gga cca cta gtt acc gac atc gct cca ggt tat gac
 1459
 Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile Ala Pro Gly Tyr Asp
 440 445 450
 cac atc act tct gcc att ggt gca gct cac atc gcc atg ggt ggc acc
 1507
 His Ile Thr Ser Ala Ile Gly Ala Ala His Ile Ala Met Gly Gly Thr
 455 460 465
 gcc atg ctg tgt tat gtc acc ccg aaa gaa cac ctt ggc ctg ccc aac
 1555
 Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His Leu Gly Leu Pro Asn
 470 475 480 485
 cgt gac gac gtc aaa acc ggc gta atc acc tac aag ctc gct gcc cac
 1603
 Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr Lys Leu Ala Ala His

490 495 500
 gca gca gat gtg gcc aag ggt cat ccc ggc gcg cgt gcc tgg gac gac
 1651
 Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala Arg Ala Trp Asp Asp
 505 510 515
 gcc atg agt aaa gcg cgt ttt gaa ttc cgt tgg aat gat cag ttt gcg
 1699
 Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp Asn Asp Gln Phe Ala
 520 525 530
 ctc tcc ctc gac ccc gac act gca atc gct tat cac gac gaa acc ctg
 1747
 Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr His Asp Glu Thr Leu
 535 540 545
 ccg gca gag cct gcg aaa acc gca cac ttc tgt tca atg tgt ggc ccg
 1795
 Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys Ser Met Cys Gly Pro
 550 555 560 565
 aag ttc tgc tcc atg cga att agc cag gac att cgc gat atg ttt ggc
 1843
 Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile Arg Asp Met Phe Gly
 570 575 580
 gat caa atc gcg gaa ttg ggg atg cct ggg gtt ggg gat tct tct agt
 1891
 Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val Gly Asp Ser Ser Ser
 585 590 595
 gct gtt gct tct agt ggg gca cgg gag ggg atg gct gag aaa tcc cgg
 1939
 Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met Ala Glu Lys Ser Arg
 600 605 610
 gaa ttt att gct ggt ggt gcg gag gtt tat cgg cgt tagacagagc
 1985
 Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg Arg
 615 620 625
 gatcccagat agc
 1998

<210> 522

<211> 625

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 522

Leu Lys Ala Val Pro Thr Gly Ala Arg Ala Arg Ala Glu Ile Ala Leu
 1 5 10 15

Ile Ala Ala Arg Ala Pro Phe Glu Pro Val Arg Leu Ala Pro Ala Lys
 20 25 30

Glu Glu Arg Asn Gly Ala Met Thr Pro Thr Gln Asn Glu Ile His Pro
 35 40 45

Lys His Ser Tyr Ser Pro Ile Arg Lys Asp Gly Leu Glu Val Pro Glu
 50 55 60
 Thr Glu Ile Arg Leu Asp Asp Ser Pro Ser Gly Pro Asn Glu Pro Phe
 65 70 75 80
 Arg Ile Tyr Arg Thr Arg Gly Pro Glu Thr Asn Pro Lys Gln Gly Leu
 85 90 95
 Pro Arg Leu Arg Glu Ser Trp Ile Thr Ala Arg Gly Asp Val Ala Thr
 100 105 110
 Tyr Gln Gly Arg Glu Arg Leu Leu Ile Asp Asp Gly Arg Ser Ala Met
 115 120 125
 Arg Arg Gly Gln Ala Ser Ala Glu Trp Lys Gly Gln Lys Pro Ala Pro
 130 135 140
 Leu Lys Ala Leu Pro Gly Lys Arg Val Thr Gln Met Ala Tyr Ala Arg
 145 150 155 160
 Ala Gly Val Ile Thr Arg Glu Met Glu Phe Val Ala Leu Arg Glu His
 165 170 175
 Val Asp Ala Glu Phe Val Arg Ser Glu Val Ala Arg Gly Arg Ala Ile
 180 185 190
 Ile Pro Asn Asn Val Asn His Pro Glu Ser Glu Pro Met Ile Ile Gly
 195 200 205
 Arg Lys Phe Leu Thr Lys Ile Asn Ala Asn Ile Gly Asn Ser Ala Val
 210 215 220
 Thr Ser Ser Ile Glu Glu Glu Val Ser Lys Leu Gln Trp Ala Thr Arg
 225 230 235 240
 Trp Gly Ala Asp Thr Val Met Asp Leu Ser Thr Gly Asp Asp Ile His
 245 250 255
 Thr Thr Arg Glu Trp Ile Ile Arg Asn Ser Pro Val Pro Ile Gly Thr
 260 265 270
 Val Pro Ile Tyr Gln Ala Leu Glu Lys Val Asn Gly Val Ala Ala Asp
 275 280 285
 Leu Asn Trp Glu Val Phe Arg Asp Thr Ile Ile Glu Gln Cys Glu Gln
 290 295 300
 Gly Val Asp Tyr Met Thr Ile His Ala Gly Val Leu Leu Ala Tyr Ile
 305 310 315 320
 Pro Leu Thr Thr Arg Arg Val Thr Gly Ile Val Ser Arg Gly Gly Ser
 325 330 335
 Ile Met Ala Gly Trp Cys Leu Ala His His Arg Glu Ser Phe Leu Tyr
 340 345 350
 Glu His Phe Asp Glu Leu Cys Glu Ile Phe Ala Gln Tyr Asp Val Ala
 355 360 365
 Phe Ser Leu Gly Asp Gly Leu Arg Pro Gly Ser Leu Ala Asp Ala Asn

370	375	380
Asp Ala Ala Gln Phe Ala Glu Leu Lys Thr Ile Gly Glu Leu Thr Gln 385 390 395 400		
Arg Ala Trp Glu Tyr Asp Val Gln Val Met Val Glu Gly Pro Gly His 405 410 415		
Val Pro Leu Asn Met Ile Gln Glu Asn Asn Glu Leu Glu Gln Lys Trp 420 425 430		
Ala Ala Asp Ala Pro Phe Tyr Thr Leu Gly Pro Leu Val Thr Asp Ile 435 440 445		
Ala Pro Gly Tyr Asp His Ile Thr Ser Ala Ile Gly Ala Ala His Ile 450 455 460		
Ala Met Gly Gly Thr Ala Met Leu Cys Tyr Val Thr Pro Lys Glu His 465 470 475 480		
Leu Gly Leu Pro Asn Arg Asp Asp Val Lys Thr Gly Val Ile Thr Tyr 485 490 495		
Lys Leu Ala Ala His Ala Ala Asp Val Ala Lys Gly His Pro Gly Ala 500 505 510		
Arg Ala Trp Asp Asp Ala Met Ser Lys Ala Arg Phe Glu Phe Arg Trp 515 520 525		
Asn Asp Gln Phe Ala Leu Ser Leu Asp Pro Asp Thr Ala Ile Ala Tyr 530 535 540		
His Asp Glu Thr Leu Pro Ala Glu Pro Ala Lys Thr Ala His Phe Cys 545 550 555 560		
Ser Met Cys Gly Pro Lys Phe Cys Ser Met Arg Ile Ser Gln Asp Ile 565 570 575		
Arg Asp Met Phe Gly Asp Gln Ile Ala Glu Leu Gly Met Pro Gly Val 580 585 590		
Gly Asp Ser Ser Ser Ala Val Ala Ser Ser Gly Ala Arg Glu Gly Met 595 600 605		
Ala Glu Lys Ser Arg Glu Phe Ile Ala Gly Gly Ala Glu Val Tyr Arg 610 615 620		
Arg 625		

<210> 523
 <211> 1013
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(990)
 <223> RXA01019

<400> 523

act ttg gcg cac tca ctt tca ttc ccg gat tcg ctt cgc gac ggg cca	48
Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro	
1 5 10 15	
acc gtt gga gac ctc ggg gaa ttt gaa gtg att cgg gta atc acg gag	96
Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu	
20 25 30	
caa gct gga tca tct ctc aac ggc gat gac gca gct gtg ctt cgg cat	144
Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His	
35 40 45	
gca tca ccc aat tcc agg gct gtt gtc acc acc gac atg ttg gtt gcg	192
Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala	
50 55 60	
ggg agg cat ttc caa ttg gat tgg tcc acc ccg gaa caa ata ggg cag	240
Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln	
65 70 75 80	
aag gcg att gtg cag aac ttt gct gat att gag gcg atg ggt gca cgt	288
Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg	
85 90 95	
cca gta gcc gca ttg ttg gcg att tcc gcc ccc aca cac acc ccc gtg	336
Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val	
100 105 110	
gag ttt gtc cga ggc tta gcc cgt ggc atg aat caa cgc ttg gag gag	384
Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu	
115 120 125	
tac tcc gcg gaa ctt gtt ggc gga gac atc acc agc ggg gac tcc ttg	432
Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu	
130 135 140	
gtt att gct gta act gca att ggt caa ctg ggt gga tcc ttg cca gag	480
Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu	
145 150 155 160	
ctg acg ttg gga cgt gcc cga cca gga cag acc ctg gtg gcc cac gga	528
Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly	
165 170 175	
aag atc ggt tac tcc gca gca ggc ctt gct cta ctg cag cac ttt ggt	576
Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly	
180 185 190	
cca gac aac gtt cca gag cac ctt cgc ccc ttg gtg gat gca cac tgc	624
Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys	
195 200 205	
gca cca gtt ctc acc cca ggc cga ggc atg gtg gca cgc gct gct gga	672
Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly	
210 215 220	
gcg acc gcc atg act gat aac tcg gac gga ctg att gtg gat ctt aac	720
Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn	
225 230 235 240	

caa atg gcc atg aag tct ggt gtg cgc atc gat gtg gat tcc tgt agc 768
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255

atc agc ccc gat gaa ctc ctt agc gaa gcc gct tcc gta ctc gga aca 816
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270

gac gcc tgg cga tgg atc tta agc ggc ggg gaa gac cac acc ctg ctc 864
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285

tct acg acg ttt ggc gat gcc ccc tct gga ttc cgc acc atc ggc caa 912
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300

gtc acc aaa aca cgc cac gaa gac ctc gtc acc gta gat aag aaa acc 960
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320

ccc gca ttt tcc gat gga tgg aga agc ttc taatgaccaa caccctatgg
 1010
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

aat
 1013

<210> 524

<211> 330

<212> PRT

<213> Corynebacterium glutamicum

<400> 524

Thr Leu Ala His Ser Leu Ser Phe Pro Asp Ser Leu Arg Asp Gly Pro
 1 5 10 15

Thr Val Gly Asp Leu Gly Glu Phe Glu Val Ile Arg Val Ile Thr Glu
 20 25 30

Gln Ala Gly Ser Ser Leu Asn Gly Asp Asp Ala Ala Val Leu Arg His
 35 40 45

Ala Ser Pro Asn Ser Arg Ala Val Val Thr Thr Asp Met Leu Val Ala
 50 55 60

Gly Arg His Phe Gln Leu Asp Trp Ser Thr Pro Glu Gln Ile Gly Gln
 65 70 75 80

Lys Ala Ile Val Gln Asn Phe Ala Asp Ile Glu Ala Met Gly Ala Arg
 85 90 95

Pro Val Ala Ala Leu Leu Ala Ile Ser Ala Pro Thr His Thr Pro Val
 100 105 110

Glu Phe Val Arg Gly Leu Ala Arg Gly Met Asn Gln Arg Leu Glu Glu
 115 120 125

Tyr Ser Ala Glu Leu Val Gly Gly Asp Ile Thr Ser Gly Asp Ser Leu
 130 135 140

Val Ile Ala Val Thr Ala Ile Gly Gln Leu Gly Gly Ser Leu Pro Glu
 145 150 155 160
 Leu Thr Leu Gly Arg Ala Arg Pro Gly Gln Thr Leu Val Ala His Gly
 165 170 175
 Lys Ile Gly Tyr Ser Ala Ala Gly Leu Ala Leu Leu Gln His Phe Gly
 180 185 190
 Pro Asp Asn Val Pro Glu His Leu Arg Pro Leu Val Asp Ala His Cys
 195 200 205
 Ala Pro Val Leu Thr Pro Gly Arg Gly Met Val Ala Arg Ala Ala Gly
 210 215 220
 Ala Thr Ala Met Thr Asp Asn Ser Asp Gly Leu Ile Val Asp Leu Asn
 225 230 235 240
 Gln Met Ala Met Lys Ser Gly Val Arg Ile Asp Val Asp Ser Cys Ser
 245 250 255
 Ile Ser Pro Asp Glu Leu Leu Ser Glu Ala Ala Ser Val Leu Gly Thr
 260 265 270
 Asp Ala Trp Arg Trp Ile Leu Ser Gly Gly Glu Asp His Thr Leu Leu
 275 280 285
 Ser Thr Thr Phe Gly Asp Ala Pro Ser Gly Phe Arg Thr Ile Gly Gln
 290 295 300
 Val Thr Lys Thr Arg His Glu Asp Leu Val Thr Val Asp Lys Lys Thr
 305 310 315 320
 Pro Ala Phe Ser Asp Gly Trp Arg Ser Phe
 325 330

<210> 525
 <211> 706
 <212> DNA
 <213> *Corynebacterium glutamicum*

<220>
 <221> CDS
 <222> (101)..(706)
 <223> RXA01352

<400> 525
 gtgcccaatg cattgggctg agattgcgcg ctgttgctgc gcgggaccgt tcgaacctgt 60
 ctggttaaca ccagcgaagg aagcgaggat tgattgtccc gtg ttt gaa aat cgt 115
 Val Phe Glu Asn Arg
 1 5
 ttt gac ctg cgt tgt tat gtt gtg act ggt gcg ggc tcg gtg gat gag 163
 Phe Asp Leu Arg Cys Tyr Val Val Thr Gly Ala Gly Ser Val Asp Glu
 10 15 20
 gtt gtg cac act gcg tct gct gcg gct cgt ggt ggc gcg ggt gtg gtg 211
 Val Val His Thr Ala Ser Ala Ala Ala Arg Gly Gly Ala Gly Val Val

25	30	35	
cag gtg cgt tca aag cct att tcg cca gaa gcg atg agg gag ttg gca			259
Gln Val Arg Ser Lys Pro Ile Ser Pro Glu Ala Met Arg Glu Leu Ala			
40	45	50	
tca aag gtt gcg ctt gag gtt gcg cgg tgc agc cca aca acg agg gtg			307
Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser Pro Thr Thr Arg Val			
55	60	65	
ctt atc gac gac cac ctc cac gtt gct tct tcc tta atg cgc gaa gga			355
Leu Ile Asp Asp His Leu His Val Ala Ser Ser Leu Met Arg Glu Gly			
70	75	80	85
ctc ccg att cac ggt gtg cat ctt ggg cag gat gat atg tcg gtg ctt			403
Leu Pro Ile His Gly Val His Leu Gly Gln Asp Asp Met Ser Val Leu			
90	95	100	
gag gct cgt gag ttg ttg ggg cct gag gcg atc att ggg ttg act act			451
Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile Ile Gly Leu Thr Thr			
105	110	115	
gga acc cta gaa ctt gtg gcg gcg gcg aat gag ctg tcc gat gtg ttg			499
Gly Thr Leu Glu Leu Val Ala Ala Asn Glu Leu Ser Asp Val Leu			
120	125	130	
gat tac atc ggt gct ggg ccg ttt cgg aag act ccc acc aag gat tca			547
Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr Pro Thr Lys Asp Ser			
135	140	145	
ggt cgg cca ccg att ggc ctt gcg ggt tat ccc cct ttg gtg gaa ttg			595
Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro Pro Leu Val Glu Leu			
150	155	160	165
tcc aag gtg ccg atc gtt gcg att ggt gat gtc acc cct gcc gat gtg			643
Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val Thr Pro Ala Asp Val			
170	175	180	
cgc gct ctc agc gca acc ggt gtg gct ggc gtt gcc atg gtg cgg gct			691
Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val Ala Met Val Arg Ala			
185	190	195	
ttt tct gaa tct gat			706
Phe Ser Glu Ser Asp			
200			

<210> 526

<211> 202

<212> PRT

<213> Corynebacterium glutamicum

<400> 526

Val	Phe	Glu	Asn	Arg	Phe	Asp	Leu	Arg	Cys	Tyr	Val	Val	Thr	Gly	Ala
1				5					10					15	

Gly	Ser	Val	Asp	Glu	Val	Val	His	Thr	Ala	Ser	Ala	Ala	Ala	Arg	Gly
			20					25					30		

Gly	Ala	Gly	Val	Val	Gln	Val	Arg	Ser	Lys	Pro	Ile	Ser	Pro	Glu	Ala
		35					40					45			

Met Arg Glu Leu Ala Ser Lys Val Ala Leu Glu Val Ala Arg Cys Ser
 50 55 60

Pro Thr Thr Arg Val Leu Ile Asp Asp His Leu His Val Ala Ser Ser
 65 70 75 80

Leu Met Arg Glu Gly Leu Pro Ile His Gly Val His Leu Gly Gln Asp
 85 90 95

Asp Met Ser Val Leu Glu Ala Arg Glu Leu Leu Gly Pro Glu Ala Ile
 100 105 110

Ile Gly Leu Thr Thr Gly Thr Leu Glu Leu Val Ala Ala Ala Asn Glu
 115 120 125

Leu Ser Asp Val Leu Asp Tyr Ile Gly Ala Gly Pro Phe Arg Lys Thr
 130 135 140

Pro Thr Lys Asp Ser Gly Arg Pro Pro Ile Gly Leu Ala Gly Tyr Pro
 145 150 155 160

Pro Leu Val Glu Leu Ser Lys Val Pro Ile Val Ala Ile Gly Asp Val
 165 170 175

Thr Pro Ala Asp Val Arg Ala Leu Ser Ala Thr Gly Val Ala Gly Val
 180 185 190

Ala Met Val Arg Ala Phe Ser Glu Ser Asp
 195 200

<210> 527

<211> 944

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(921)

<223> RXA01381

<400> 527

tcc gca ggc gtt gga acc atc acg gtc atc gat gac gac acc gtc gac	48
Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp	
1 5 10 15	
att tcc aac att cac cgc caa atc ctc ttc ggc gca agc gat gtc ggt	96
Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly	
20 25 30	
cga ccc aag gtc gag gtt gcc gcc gag cgc ctc aaa gaa ctc caa cca	144
Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro	
35 40 45	
gac atc acc gtc aac gcg ttg cac gaa cgg atc act cca gaa aac gcc	192
Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala	
50 55 60	
tgc gag ctg ctc aat tcc gtg gac ctc gtc tta gac ggc tcc gat tct	240
Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser	

65	70	75	80	
ttc tcc aca aaa tac tta gtg tct gat gcc gcc gaa atc acc gga act	288			
Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr				
85	90	95		
ccc ctc atc tgg gca acg gta ctg cgc ttt cac ggc gaa ctg gca ctc	336			
Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu				
100	105	110		
ttc aac tct ggc ccc gac cac cgc gga gtc ggc ctg cgc gac gtc ttc	384			
Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe				
115	120	125		
ccc gaa caa ccc tcc gcc gat ttc gtc cct gac tgc gcc acc gct ggt	432			
Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly				
130	135	140		
gtt ctt ggc gcc acc aca gcc acc atc ggc gca ctc atg gcc act cac	480			
Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His				
145	150	155		
gcc atc gga ttt ctc aca gaa atc ggc gac gtc caa cca ggc aca atc	528			
Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile				
165	170	175		
ctc tcc tac gac gca ttc ccc gcc gcc acg cgc agc ttc cgc gtc tcc	576			
Leu Ser Tyr Asp Ala Phe Pro Ala Thr Arg Ser Phe Arg Val Ser				
180	185	190		
gcc gac ccg gcg cgc cca ctg gtc acc cgc ctc cgc gcc tcc tac gag	624			
Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu				
195	200	205		
gca gcg cgc acc gat aca act tcg ctt atc gac gcc acc ctc aac ggc	672			
Ala Ala Arg Thr Asp Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly				
210	215	220		
tcc ctc acc gcc ctc gat atc cga gag cca cat gaa gtt ctg ctc aaa	720			
Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys				
225	230	235		
gac ctc ccc gag ggc gca acg tca ctg aag ctc ccc tta agc cag atc	768			
Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile				
245	250	255		
acc tcg gac agc gac att tta gag gca ctg tct gga atc gac ggc gac	816			
Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp				
260	265	270		
att ttg gtc tac tgc gct tcg gga atc cgc agt tcc gac ttc atc gac	864			
Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp				
275	280	285		
aac tac tcc cac ctc ggc cac aaa ttt gtg aat ctt ccc ggt ggg gtc	912			
Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val				
290	295	300		
aac gcg ctg tagctgtcaa tttaagaggc cag	944			
Asn Ala Leu				
305				

<210> 528

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

Ser Ala Gly Val Gly Thr Ile Thr Val Ile Asp Asp Asp Thr Val Asp
 1 5 10 15

Ile Ser Asn Ile His Arg Gln Ile Leu Phe Gly Ala Ser Asp Val Gly
 20 25 30

Arg Pro Lys Val Glu Val Ala Ala Glu Arg Leu Lys Glu Leu Gln Pro
 35 40 45

Asp Ile Thr Val Asn Ala Leu His Glu Arg Ile Thr Pro Glu Asn Ala
 50 55 60

Cys Glu Leu Leu Asn Ser Val Asp Leu Val Leu Asp Gly Ser Asp Ser
 65 70 75 80

Phe Ser Thr Lys Tyr Leu Val Ser Asp Ala Ala Glu Ile Thr Gly Thr
 85 90 95

Pro Leu Ile Trp Ala Thr Val Leu Arg Phe His Gly Glu Leu Ala Leu
 100 105 110

Phe Asn Ser Gly Pro Asp His Arg Gly Val Gly Leu Arg Asp Val Phe
 115 120 125

Pro Glu Gln Pro Ser Ala Asp Phe Val Pro Asp Cys Ala Thr Ala Gly
 130 135 140

Val Leu Gly Ala Thr Thr Ala Thr Ile Gly Ala Leu Met Ala Thr His
 145 150 155 160

Ala Ile Gly Phe Leu Thr Glu Ile Gly Asp Val Gln Pro Gly Thr Ile
 165 170 175

Leu Ser Tyr Asp Ala Phe Pro Ala Ala Thr Arg Ser Phe Arg Val Ser
 180 185 190

Ala Asp Pro Ala Arg Pro Leu Val Thr Arg Leu Arg Ala Ser Tyr Glu
 195 200 205

Ala Ala Arg Thr Asp Thr Thr Ser Leu Ile Asp Ala Thr Leu Asn Gly
 210 215 220

Ser Leu Thr Ala Leu Asp Ile Arg Glu Pro His Glu Val Leu Leu Lys
 225 230 235 240

Asp Leu Pro Glu Gly Ala Thr Ser Leu Lys Leu Pro Leu Ser Gln Ile
 245 250 255

Thr Ser Asp Ser Asp Ile Leu Glu Ala Leu Ser Gly Ile Asp Gly Asp
 260 265 270

Ile Leu Val Tyr Cys Ala Ser Gly Ile Arg Ser Ser Asp Phe Ile Asp
 275 280 285

Asn Tyr Ser His Leu Gly His Lys Phe Val Asn Leu Pro Gly Gly Val
 290 295 300

Asn Ala Leu
 305

<210> 529
 <211> 259
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(259)
 <223> RXA01360

<400> 529
 gtggcaatca acgccgcggt cgtaccaga tcccagtggt cacgcgcat ttgtgacaac 60

gattccgtag aagttctcac cgcaattcag ggaggttaaa atg ctg cat att gct 115
 Met Leu His Ile Ala
 1 5

gat aaa act ttc gat tcc cac ctc atc atg ggc acc ggc gga gcc acc 163
 Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly Thr Gly Gly Ala Thr
 10 15 20

tct cag gcg ttg ctg gag gaa tcc ctt gtc gcc agt gga act caa ttg 211
 Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala Ser Gly Thr Gln Leu
 25 30 35

acc acc gtg gcg atg cgt cga cac caa gca acc acc tct agc gga gaa 259
 Thr Thr Val Ala Met Arg Arg His Gln Ala Thr Thr Ser Ser Gly Glu
 40 45 50

<210> 530
 <211> 53
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 530
 Met Leu His Ile Ala Asp Lys Thr Phe Asp Ser His Leu Ile Met Gly
 1 5 10 15

Thr Gly Gly Ala Thr Ser Gln Ala Leu Leu Glu Glu Ser Leu Val Ala
 20 25 30

Ser Gly Thr Gln Leu Thr Thr Val Ala Met Arg Arg His Gln Ala Thr
 35 40 45

Thr Ser Ser Gly Glu
 50

<210> 531
 <211> 629
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(606)

<223> RXA01361

<400> 531

gcc gac gct gtg atc tct att gat ggc cac gat ccg tgt ttg acc gtg	48
Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val	
1 5 10 15	
acg atg aat tcg ggg gtg agg gtt gcg tcg aaa agc gtt gtt gtt ttg	96
Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu	
20 25 30	
gcg gcg ggc ctg ggc gcc gca agc att ccc ggc tgg ttt gag ggc gcg	144
Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala	
35 40 45	
aac cca ttg cag ttg agg ccg gtg tac ggc gat att gtg cgc gtg cgc	192
Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg	
50 55 60	
gtg ccg gag cga ctg cag ccg atg gtc acc aag gtg gtg cgc ggg ttt	240
Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe	
65 70 75 80	
gtg gaa gat cgt cag att tat atc att ccg cgt acc gat ggc acc ctc	288
Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu	
85 90 95	
gcg atc ggc gcg aca agc cgt gag gat cac ccg caa cct cga acg ggc	336
Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly	
100 105 110	
gca gtg cat gat ttg cta cgc gat gct atc cgt ttg att ccg ggc att	384
Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile	
115 120 125	
gaa gaa acc gaa ttt atc gaa gtc acc tgc ggc gcc cgc ccc ggc acc	432
Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr	
130 135 140	
ccg gat gac ctg ccg tac ctg gga tgg gtt gga tcc aat gtg att gcg	480
Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala	
145 150 155 160	
tcc aca gga tat ttc cgc cat gga att ttg ctg tca gcc ctt ggt gca	528
Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala	
165 170 175	
cgc gct gcc gtt gat atg gca acc aac cag cca ctg ttc ccc act ctt	576
Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu	
180 185 190	
gat gtg tgc gat ccg ttt cgc cac caa att taaggatttt tcacaagtga	626
Asp Val Cys Asp Pro Phe Arg His Gln Ile	
195 200	
tta	629

<210> 532
 <211> 202
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 532
 Ala Asp Ala Val Ile Ser Ile Asp Gly His Asp Pro Cys Leu Thr Val
 1 5 10 15
 Thr Met Asn Ser Gly Val Arg Val Ala Ser Lys Ser Val Val Val Leu
 20 25 30
 Ala Ala Gly Leu Gly Ala Ala Ser Ile Pro Gly Trp Phe Glu Gly Ala
 35 40 45
 Asn Pro Leu Gln Leu Arg Pro Val Tyr Gly Asp Ile Val Arg Val Arg
 50 55 60
 Val Pro Glu Arg Leu Gln Pro Met Val Thr Lys Val Val Arg Gly Phe
 65 70 75 80
 Val Glu Asp Arg Gln Ile Tyr Ile Ile Pro Arg Thr Asp Gly Thr Leu
 85 90 95
 Ala Ile Gly Ala Thr Ser Arg Glu Asp His Pro Gln Pro Arg Thr Gly
 100 105 110
 Ala Val His Asp Leu Leu Arg Asp Ala Ile Arg Leu Ile Pro Gly Ile
 115 120 125
 Glu Glu Thr Glu Phe Ile Glu Val Thr Cys Gly Ala Arg Pro Gly Thr
 130 135 140
 Pro Asp Asp Leu Pro Tyr Leu Gly Trp Val Gly Ser Asn Val Ile Ala
 145 150 155 160
 Ser Thr Gly Tyr Phe Arg His Gly Ile Leu Leu Ser Ala Leu Gly Ala
 165 170 175
 Arg Ala Ala Val Asp Met Ala Thr Asn Gln Pro Leu Phe Pro Thr Leu
 180 185 190
 Asp Val Cys Asp Pro Phe Arg His Gln Ile
 195 200

<210> 533
 <211> 927
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(904)
 <223> RXA01208

<400> 533
 tactaggcac ggggtgccaa ccggatggaa aaattccgga ggctgagaaa acaccggttg 60
 aacctgctct agctcgctact agcgaaggga tggccttaac gtg gct aac tcg ttt 115

																Val Ala Asn Ser Phe	
																1	5
ttg	gat	tct	tta	act	ctt	gtt	cga	caa	aac	act	ccc	ctt	gtt	cag	tgt	163	
Leu	Asp	Ser	Leu	Thr	Leu	Val	Arg	Gln	Asn	Thr	Pro	Leu	Val	Gln	Cys		
				10							15					20	
ttg	acc	aac	tct	gtg	gtc	atg	caa	ttc	acg	gcc	aat	gtg	ttg	ctt	gcc	211	
Leu	Thr	Asn	Ser	Val	Val	Met	Gln	Phe	Thr	Ala	Asn	Val	Leu	Leu	Ala		
				25							30					35	
gcg	ggt	gcg	acc	cct	gcg	atg	gtg	gat	act	cca	gct	gaa	tcg	gca	gaa	259	
Ala	Gly	Ala	Thr	Pro	Ala	Met	Val	Asp	Thr	Pro	Ala	Glu	Ser	Ala	Glu		
				40							45					50	
ttc	gcc	gct	gtg	gcc	aat	gga	gtg	ctc	atc	aat	gcg	gga	act	cct	tct	307	
Phe	Ala	Ala	Val	Ala	Asn	Gly	Val	Leu	Ile	Asn	Ala	Gly	Thr	Pro	Ser		
				55							60					65	
gcg	gag	caa	tac	caa	ggc	atg	acc	aag	gcc	att	gag	ggt	gca	cga	aaa	355	
Ala	Glu	Gln	Tyr	Gln	Gly	Met	Thr	Lys	Ala	Ile	Glu	Gly	Ala	Arg	Lys		
				70							75					80	85
gct	ggc	aca	cca	tgg	gtg	tta	gac	cca	gtt	gct	gtg	ggt	ggg	ttg	tcg	403	
Ala	Gly	Thr	Pro	Trp	Val	Leu	Asp	Pro	Val	Ala	Val	Gly	Gly	Leu	Ser		
				90							95					100	
gag	agg	acc	aag	tat	gcg	gag	gga	atc	gtc	gat	aag	cag	cct	gcc	gca	451	
Glu	Arg	Thr	Lys	Tyr	Ala	Glu	Gly	Ile	Val	Asp	Lys	Gln	Pro	Ala	Ala		
				105							110					115	
att	cgt	gga	aac	gcc	tca	gag	gtc	gtg	gcg	ctt	gcg	ggg	ctc	ggt	gcc	499	
Ile	Arg	Gly	Asn	Ala	Ser	Glu	Val	Val	Ala	Leu	Ala	Gly	Leu	Gly	Ala		
				120							125					130	
ggt	ggg	cgc	ggc	gta	gac	gcg	acc	gat	tcc	gtg	gaa	gtg	gcg	ttg	gag	547	
Gly	Gly	Arg	Gly	Val	Asp	Ala	Thr	Asp	Ser	Val	Glu	Val	Ala	Leu	Glu		
				135							140					145	
gcg	gcg	caa	ttg	ttg	gcc	aag	cgc	act	ggt	ggc	gtc	gtg	gct	gtc	tct	595	
Ala	Ala	Gln	Leu	Leu	Ala	Lys	Arg	Thr	Gly	Gly	Val	Val	Ala	Val	Ser		
				150							155					160	165
ggt	gcg	gag	gac	ttg	att	gtg	tct	gcg	gat	cgg	gtg	acg	tgg	ttg	cgt	643	
Gly	Ala	Glu	Asp	Leu	Ile	Val	Ser	Ala	Asp	Arg	Val	Thr	Trp	Leu	Arg		
				170							175					180	
tcg	ggg	gat	ccg	atg	ttg	cag	ctg	gtg	att	ggc	act	gga	tgc	tct	ttg	691	
Ser	Gly	Asp	Pro	Met	Leu	Gln	Leu	Val	Ile	Gly	Thr	Gly	Cys	Ser	Leu		
				185							190					195	
ggc	gcg	ctg	aca	gct	gca	tat	cta	ggc	gcc	acg	gtt	gac	tca	gat	att	739	
Gly	Ala	Leu	Thr	Ala	Ala	Tyr	Leu	Gly	Ala	Thr	Val	Asp	Ser	Asp	Ile		
				200							205					210	
tcc	gcg	cac	gat	gct	gtg	ttg	gct	gcg	cat	gcc	cat	gtg	ggt	gct	gct	787	
Ser	Ala	His	Asp	Ala	Val	Leu	Ala	Ala	His	Ala	His	Val	Gly	Ala	Ala		
				215							220					225	
ggc	cag	att	gca	gca	cag	aag	gca	tcg	gcg	cca	ggc	agc	ttt	gcg	gtg	835	
Gly	Gln	Ile	Ala	Ala	Gln	Lys	Ala	Ser	Ala	Pro	Gly	Ser	Phe	Ala	Val		

230 235 240 245
 gcg ttt att gat gcg ctt tat gac gtg gat gcc cag gct gtg gcc tcg 883
 Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala Gln Ala Val Ala Ser
 250 255 260

 ttg gtt gat gtg cga gag gcc tgaaaagtac gtgactgatt ttt 927
 Leu Val Asp Val Arg Glu Ala
 265

 <210> 534
 <211> 268
 <212> PRT
 <213> *Corynebacterium glutamicum*

 <400> 534
 Val Ala Asn Ser Phe Leu Asp Ser Leu Thr Leu Val Arg Gln Asn Thr
 1 5 10 15
 Pro Leu Val Gln Cys Leu Thr Asn Ser Val Val Met Gln Phe Thr Ala
 20 25 30
 Asn Val Leu Leu Ala Ala Gly Ala Thr Pro Ala Met Val Asp Thr Pro
 35 40 45
 Ala Glu Ser Ala Glu Phe Ala Ala Val Ala Asn Gly Val Leu Ile Asn
 50 55 60
 Ala Gly Thr Pro Ser Ala Glu Gln Tyr Gln Gly Met Thr Lys Ala Ile
 65 70 75 80
 Glu Gly Ala Arg Lys Ala Gly Thr Pro Trp Val Leu Asp Pro Val Ala
 85 90 95
 Val Gly Gly Leu Ser Glu Arg Thr Lys Tyr Ala Glu Gly Ile Val Asp
 100 105 110
 Lys Gln Pro Ala Ala Ile Arg Gly Asn Ala Ser Glu Val Val Ala Leu
 115 120 125
 Ala Gly Leu Gly Ala Gly Gly Arg Gly Val Asp Ala Thr Asp Ser Val
 130 135 140
 Glu Val Ala Leu Glu Ala Ala Gln Leu Leu Ala Lys Arg Thr Gly Gly
 145 150 155 160
 Val Val Ala Val Ser Gly Ala Glu Asp Leu Ile Val Ser Ala Asp Arg
 165 170 175
 Val Thr Trp Leu Arg Ser Gly Asp Pro Met Leu Gln Leu Val Ile Gly
 180 185 190
 Thr Gly Cys Ser Leu Gly Ala Leu Thr Ala Ala Tyr Leu Gly Ala Thr
 195 200 205
 Val Asp Ser Asp Ile Ser Ala His Asp Ala Val Leu Ala Ala His Ala
 210 215 220
 His Val Gly Ala Ala Gly Gln Ile Ala Ala Gln Lys Ala Ser Ala Pro
 225 230 235 240

Gly Ser Phe Ala Val Ala Phe Ile Asp Ala Leu Tyr Asp Val Asp Ala
245 250 255

Gln Ala Val Ala Ser Leu Val Asp Val Arg Glu Ala
260 265

<210> 535

<211> 1023

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101) . . (1000)

<223> RXA00838

<400> 535

tcgtctaata gtgctgccaa tccaccggcc attgatgact cctttgtaga gaaggggtag 60

tgcttacaaa tcttatctgt gctcaggcaa gatagcaggt atg aaa att gcg atc 115
Met Lys Ile Ala Ile
1 5

gtt ggc gct ggt gca gtt ggt gga tat ttc gga gcg ttg tta caa gaa 163
Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly Ala Leu Leu Gln Glu
10 15 20

tct ggt gca gat atc acg atg gtt gca cgt gga cga aca tta gaa gcc 211
Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly Arg Thr Leu Glu Ala
25 30 35

ttg aag tct aaa gga ctc cac atc aac gat gca aga ggc gaa cgc tac 259
Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala Arg Gly Glu Arg Tyr
40 45 50

gta cca att cct gca gtt gcg agc gtg caa gaa cta aaa gat gca gat 307
Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu Leu Lys Asp Ala Asp
55 60 65

gta gtg atg att gct act aaa gca tta tcg cgg tct tta gat ctc gct 355
Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg Ser Leu Asp Leu Ala
70 75 80 85

gaa ctt ttg ggt ggg ata cct gcg aat tcg gtg gtc gcg att act cag 403
Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val Val Ala Ile Thr Gln
90 95 100

aat tcg att gaa tct gct gat cta gca gcg aag agt atc ggt gct gat 451
Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys Ser Ile Gly Ala Asp
105 110 115

cgt gtg tgg cct ggt gtg gtt cgt ggg ttc ttt gtt cat gag ggg cca 499
 Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe Val His Glu Gly Pro
 120 125 130

gcc tca gtg tca tac aag gga ggc cca ctg tcc tac acg ttt ggt gat 547
Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser Tyr Thr Phe Gly Asp
135 140 145

tct ggt gaa ctt tct agg caa ttc gca agc act ctt gaa cag gcc ggt 595
 Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr Leu Glu Gln Ala Gly
 150 155 160 165

 att gac gga gtt ctg cat ccc gat att ttg gtg gat gtg tgg gag aaa 643
 Ile Asp Gly Val Leu His Pro Asp Ile Leu Val Asp Val Trp Glu Lys
 170 175 180

 gcc atg ttc gta gag gtt ttc ggc ggg ttg ggg gct ttc gtc gaa aag 691
 Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly Ala Phe Val Glu Lys
 185 190 195

 caa tta ggt acc ttg cgt acg cat ttt agg gct tcc ctg gaa gcc ttg 739
 Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala Ser Leu Glu Ala Leu
 200 205 210

 atg gaa gag gtg gct gag gtg gct cgc gcg gca ggt gtt gcg ttg ccg 787
 Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala Gly Val Ala Leu Pro
 215 220 225

 agc gat gcg gtg gag cgc acc atg aat ttt gcg gat cgg atg cct gag 835
 Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala Asp Arg Met Pro Glu
 230 235 240 245

 aat tcg acg agt tcg atg cag cgt gat ttg gcc gcg gga gtg gct agt 883
 Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala Ala Gly Val Ala Ser
 250 255 260

 gag ctt gag gct cag aca ggt gca att gtg cgg gca gcg cac aaa gtg 931
 Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg Ala Ala His Lys Val
 265 270 275

 ggt gtg aaa act ccg ctt cat gac ctt att tat gct ggt ctt aag ctg 979
 Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr Ala Gly Leu Lys Leu
 280 285 290

 aaa gaa gag gaa aat tca ctt tagggataga atcaagatcc atg
 1023
 Lys Glu Glu Glu Asn Ser Leu
 295 300

<210> 536

<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 536

Met Lys Ile Ala Ile Val Gly Ala Gly Ala Val Gly Gly Tyr Phe Gly
 1 5 10 15

Ala Leu Leu Gln Glu Ser Gly Ala Asp Ile Thr Met Val Ala Arg Gly
 20 25 30

Arg Thr Leu Glu Ala Leu Lys Ser Lys Gly Leu His Ile Asn Asp Ala
 35 40 45

Arg Gly Glu Arg Tyr Val Pro Ile Pro Ala Val Ala Ser Val Gln Glu
 50 55 60

Leu Lys Asp Ala Asp Val Val Met Ile Ala Thr Lys Ala Leu Ser Arg

65	70	75	80
Ser Leu Asp Leu Ala Glu Leu Leu Gly Gly Ile Pro Ala Asn Ser Val	85	90	95
Val Ala Ile Thr Gln Asn Ser Ile Glu Ser Ala Asp Leu Ala Ala Lys	100	105	110
Ser Ile Gly Ala Asp Arg Val Trp Pro Gly Val Val Arg Gly Phe Phe	115	120	125
Val His Glu Gly Pro Ala Ser Val Ser Tyr Lys Gly Gly Pro Leu Ser	130	135	140
Tyr Thr Phe Gly Asp Ser Gly Glu Leu Ser Arg Gln Phe Ala Ser Thr	145	150	155
Leu Glu Gln Ala Gly Ile Asp Gly Val Leu His Pro Asp Ile Leu Val	165	170	175
Asp Val Trp Glu Lys Ala Met Phe Val Glu Val Phe Gly Gly Leu Gly	180	185	190
Ala Phe Val Glu Lys Gln Leu Gly Thr Leu Arg Thr His Phe Arg Ala	195	200	205
Ser Leu Glu Ala Leu Met Glu Glu Val Ala Glu Val Ala Arg Ala Ala	210	215	220
Gly Val Ala Leu Pro Ser Asp Ala Val Glu Arg Thr Met Asn Phe Ala	225	230	235
Asp Arg Met Pro Glu Asn Ser Thr Ser Ser Met Gln Arg Asp Leu Ala	245	250	255
Ala Gly Val Ala Ser Glu Leu Glu Ala Gln Thr Gly Ala Ile Val Arg	260	265	270
Ala Ala His Lys Val Gly Val Lys Thr Pro Leu His Asp Leu Ile Tyr	275	280	285
Ala Gly Leu Lys Leu Lys Glu Glu Glu Asn Ser Leu	290	295	300

<210> 537

<211> 693

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(670)

<223> RXA02400

<400> 537

aggtgcccc aacgttgcc tttgactgca aattttccga aagaatccat aaactacttc 60

tttaagtcgc cagattaaag tcgtcaatga aaggacatac atg tct att tcc cgc 115

Met Ser Ile Ser Arg

1

5

```

acc gtc ttc ggc atc gca gcc acc gca gcc ctg tct gca gct ctc gtt 163
Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu Ser Ala Ala Leu Val
          10                      15                      20

gcg tgt tct cca cct cac cag cag gat tcc cca gtc cag cgc acc aat 211
Ala Cys Ser Pro Pro His Gln Gln Asp Ser Pro Val Gln Arg Thr Asn
          25                      30                      35

gag atc ttg act act tct cag aac cca act tct gcg agc agc acc tca 259
Glu Ile Leu Thr Thr Ser Gln Asn Pro Thr Ser Ala Ser Ser Thr Ser
          40                      45                      50

acc tct tcc gca acg act act tcc tca gct cct gtg gaa gag gac gta 307
Thr Ser Ser Ala Thr Thr Thr Ser Ser Ala Pro Val Glu Glu Asp Val
          55                      60                      65

gag atc gtt gtt tca cca gca gcg ttg gtg gac ggt gag cag gtt acc 355
Glu Ile Val Val Ser Pro Ala Ala Leu Val Asp Gly Glu Gln Val Thr
          70                      75                      80                      85

ttc gaa atc tct gga ctt gat cca gag ggc ggc tac tac gca gcg atc 403
Phe Glu Ile Ser Gly Leu Asp Pro Glu Gly Gly Tyr Tyr Ala Ala Ile
          90                      95                      100

tgc gat tcc gta gcg aac cct ggt aac cca gtt cct tct tgc acc ggc 451
Cys Asp Ser Val Ala Asn Pro Gly Asn Pro Val Pro Ser Cys Thr Gly
          105                      110                      115

gaa atg gct gat ttc acg tcc cag gca tgg ttg agc aac tcc cag ccc 499
Glu Met Ala Asp Phe Thr Ser Gln Ala Trp Leu Ser Asn Ser Gln Pro
          120                      125                      130

ggc gcg act gta gag atc gca gaa gac ggc acc gca act gtg gag ctt 547
Gly Ala Thr Val Glu Ile Ala Glu Asp Gly Thr Ala Thr Val Glu Leu
          135                      140                      145

gaa gct acc gca acc ggc act ggc ttg gac tgc acc act cag gct tgt 595
Glu Ala Thr Ala Thr Gly Thr Gly Leu Asp Cys Thr Thr Gln Ala Cys
          150                      155                      160                      165

gta gcg aag gtc ttc ggc gat cat acc gaa ggt ttc cgc gat gtt gct 643
Val Ala Lys Val Phe Gly Asp His Thr Glu Gly Phe Arg Asp Val Ala
          170                      175                      180

gaa gtc cca gtt act ttc gca gcc gct taagttttct taaaacgcac 690
Glu Val Pro Val Thr Phe Ala Ala Ala
          185                      190

tca 693

```

<210> 538

<211> 190

<212> PRT

<213> Corynebacterium glutamicum

<400> 538

```

Met Ser Ile Ser Arg Thr Val Phe Gly Ile Ala Ala Thr Ala Ala Leu
  1             5             10             15

```



```
<210> 539
<211> 1528
<212> DNA
<213> Corynebacterium glutamicum
```

```
<220>
<221> CDS
<222> (101)..(1528)
<223> RXN01209
```

```

<400> 539
cagattgcag cacagaaggc atcggcgcca ggcagctttg cgggtggcgtt tattgatgcg 60

ctttatgacg tggatgcccc ggctgtggcc tcgttggttg atg tgc gag agg cct 115
                                         Met Cys Glu Arg Pro
                                         1                               5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
                        10                               15                               20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
                        25                               30                               35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg 259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val

```

40	45	50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct Glu Asp Val Arg Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala 55 60 65			307
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu 70 75 80 85			355
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa Leu Gly Leu His Leu His Ile Gly Gln Asp Thr Pro Tyr Thr Gln 90 95 100			403
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu 105 110 115			451
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly 120 125 130			499
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala 135 140 145			547
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu 150 155 160 165			595
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly 170 175 180			643
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp 185 190 195			691
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala 200 205 210			739
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu 215 220 225			787
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn 230 235 240 245			835
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr 250 255 260			883
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly 265 270 275			931
ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His 280 285 290			979

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528
 Ala Ala Gly Glu Ser Val Glu
 470 475

<210> 540

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 540

```

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
  1              5              10              15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
      20              25              30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
      35              40              45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
      50              55              60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
      65              70              75              80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
      85              90              95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
      100              105              110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
      115              120              125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
      130              135              140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
      145              150              155              160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
      165              170              175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
      180              185              190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
      195              200              205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
      210              215              220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
      225              230              235              240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
      245              250              255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
      260              265              270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
      275              280              285

```

Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300

Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320

Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335

Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350

Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365

Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380

Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400

Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415

Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430

Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445

Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460

Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

<210> 541

<211> 1528

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1528)

<223> FRXA01209

<400> 541

cagattgcag cacagaaggc atcggcgcca ggcagctttg cgggtggcggtt tattgatgcg 60

ctttatgacg tggatgccca ggctgtggcc tcgttggttg atg tgc gag agg cct 115
 Met Cys Glu Arg Pro
 1 5

gaa aag tac gtg act gat ttt tct ttg tat ctg gtc acc gat ccc gtt 163
 Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu Val Thr Asp Pro Val
 10 15 20

ttg ggt ggc ggg cca aaa aaa gta gct gga att gtt gac agc gca att 211
 Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile Val Asp Ser Ala Ile
 25 30 35

tcc ggc gga gtt tct gtg gtg cag ctg cgc gat aag aac tca ggc gtg	259
Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp Lys Asn Ser Gly Val	
40 45 50	
gaa gat gtt cgt gcg gca gca aag gag ctg aaa gaa ctc tgc gat gct	307
Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys Glu Leu Cys Asp Ala	
55 60 65	
cgc ggg gtg gcg ctt gtt gtc aac gat tac tta gat atc gcc gtt gag	355
Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu Asp Ile Ala Val Glu	
70 75 80 85	
ctg ggt ctt cac ctg cac att ggt caa ggc gat aca cct tat acg caa	403
Leu Gly Leu His Leu His Ile Gly Gln Gly Asp Thr Pro Tyr Thr Gln	
90 95 100	
gca cgg gag ctg ctt cca gct cat ctt gaa ttg ggt ttg agc att gaa	451
Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu Gly Leu Ser Ile Glu	
105 110 115	
aac ctg gat caa ttg cat gct gtg atc gcg cag tgc gcc gag act ggt	499
Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln Cys Ala Glu Thr Gly	
120 125 130	
gtg gca ttg ccc gat gtg att ggc att ggt ccg gtg gcc tct act gcg	547
Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro Val Ala Ser Thr Ala	
135 140 145	
acc aaa cca gat gcg gca ccc gca ttg ggt gtg gag ggc atc gct gag	595
Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val Glu Gly Ile Ala Glu	
150 155 160 165	
atc gcc gct gta gct caa gac cac ggc atc gca tca gta gct att gga	643
Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala Ser Val Ala Ile Gly	
170 175 180	
ggc gtt ggt cta cgc aac gcg gcc gaa ctc gct gct acg ccc atc gac	691
Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala Ala Thr Pro Ile Asp	
185 190 195	
ggt ctg tgc gtg gtc tct gaa atc atg acc gcc gcc aat cca gca gct	739
Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala Ala Asn Pro Ala Ala	
200 205 210	
gcg gca act cgc ctg cgg act gct ttt caa cct act ttc tcg cct gaa	787
Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro Thr Phe Ser Pro Glu	
215 220 225	
act caa act gaa ctc tct caa aca gaa ctc caa gga gcc ttc gtg aat	835
Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln Gly Ala Phe Val Asn	
230 235 240 245	
tcg cct tct gcc cca cgt gtg ttg tct att gca ggc act gat ccc aca	883
Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala Gly Thr Asp Pro Thr	
250 255 260	
ggt ggt gca ggt att cag gct gat ctg aag tcc att gca gca ggt ggc	931
Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser Ile Ala Ala Gly Gly	
265 270 275	

ggc tac ggc atg tgc gtt gtg acc tcg ctg gtc gcg caa aac acc cac 979
 Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val Ala Gln Asn Thr His
 280 285 290

ggc gtc aac acg atc cac acc cca ccc ttg acc ttt ttg gaa gaa cag
 1027
 Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr Phe Leu Glu Glu Gln
 295 300 305

ctg gaa gcg gtc ttt tcc gat gtc acc gtc gat gcc atc aag ctc ggc
 1075
 Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp Ala Ile Lys Leu Gly
 310 315 320 325

atg ttg ggc tct gcc gac acc gtc gat ctg gtg gct tca tgg ctt ggt
 1123
 Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val Ala Ser Trp Leu Gly
 330 335 340

tcc cac gag cac ggt ccc gtg gtg ctt gat ccc gtc atg atc gcc acc
 1171
 Ser His Glu His Gly Pro Val Val Leu Asp Pro Val Met Ile Ala Thr
 345 350 355

agc ggt gat cgc cta ctg gat gcg agc gct gaa gaa tcg ctg cgc cgc
 1219
 Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu Glu Ser Leu Arg Arg
 360 365 370

ctg gcc gtg cac gtc gat gtg gtc acc ccg aat atc ccc gaa ctt gcc
 1267
 Leu Ala Val His Val Asp Val Val Thr Pro Asn Ile Pro Glu Leu Ala
 375 380 385

gtg ttg tgc gac agt gct cct gcc atc acc atg gat gag gcc att gct
 1315
 Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met Asp Glu Ala Ile Ala
 390 395 400 405

cag gct cag gga ttt gcg cgg act cat gac acc atc gtc att gtc aag
 1363
 Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr Ile Val Ile Val Lys
 410 415 420

ggt gga cat ctg act ggc gcg ctt gct gat aac gct gtc gtg cgc ccc
 1411
 Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn Ala Val Val Arg Pro
 425 430 435

gac ggc tcg gtg ttc cag gtg gaa aac ctg cgt gtc aac acc acc aac
 1459
 Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg Val Asn Thr Thr Asn
 440 445 450

tcc cat ggc aca ggc tgt tcg ctc tct gcg tca ctt gcc acc aag atc
 1507
 Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser Leu Ala Thr Lys Ile
 455 460 465

gcc gcc ggc gaa agc gtg gaa
 1528

Ala Ala Gly Glu Ser Val Glu
470 475

<210> 542

<211> 476

<212> PRT

<213> Corynebacterium glutamicum

<400> 542

Met Cys Glu Arg Pro Glu Lys Tyr Val Thr Asp Phe Ser Leu Tyr Leu
1 5 10 15

Val Thr Asp Pro Val Leu Gly Gly Gly Pro Lys Lys Val Ala Gly Ile
20 25 30

Val Asp Ser Ala Ile Ser Gly Gly Val Ser Val Val Gln Leu Arg Asp
35 40 45

Lys Asn Ser Gly Val Glu Asp Val Arg Ala Ala Ala Lys Glu Leu Lys
50 55 60

Glu Leu Cys Asp Ala Arg Gly Val Ala Leu Val Val Asn Asp Tyr Leu
65 70 75 80

Asp Ile Ala Val Glu Leu Gly Leu His Leu His Ile Gly Gln Gly Asp
85 90 95

Thr Pro Tyr Thr Gln Ala Arg Glu Leu Leu Pro Ala His Leu Glu Leu
100 105 110

Gly Leu Ser Ile Glu Asn Leu Asp Gln Leu His Ala Val Ile Ala Gln
115 120 125

Cys Ala Glu Thr Gly Val Ala Leu Pro Asp Val Ile Gly Ile Gly Pro
130 135 140

Val Ala Ser Thr Ala Thr Lys Pro Asp Ala Ala Pro Ala Leu Gly Val
145 150 155 160

Glu Gly Ile Ala Glu Ile Ala Ala Val Ala Gln Asp His Gly Ile Ala
165 170 175

Ser Val Ala Ile Gly Gly Val Gly Leu Arg Asn Ala Ala Glu Leu Ala
180 185 190

Ala Thr Pro Ile Asp Gly Leu Cys Val Val Ser Glu Ile Met Thr Ala
195 200 205

Ala Asn Pro Ala Ala Ala Ala Thr Arg Leu Arg Thr Ala Phe Gln Pro
210 215 220

Thr Phe Ser Pro Glu Thr Gln Thr Glu Leu Ser Gln Thr Glu Leu Gln
225 230 235 240

Gly Ala Phe Val Asn Ser Pro Ser Ala Pro Arg Val Leu Ser Ile Ala
245 250 255

Gly Thr Asp Pro Thr Gly Gly Ala Gly Ile Gln Ala Asp Leu Lys Ser
260 265 270

Ile Ala Ala Gly Gly Gly Tyr Gly Met Cys Val Val Thr Ser Leu Val
 275 280 285
 Ala Gln Asn Thr His Gly Val Asn Thr Ile His Thr Pro Pro Leu Thr
 290 295 300
 Phe Leu Glu Glu Gln Leu Glu Ala Val Phe Ser Asp Val Thr Val Asp
 305 310 315 320
 Ala Ile Lys Leu Gly Met Leu Gly Ser Ala Asp Thr Val Asp Leu Val
 325 330 335
 Ala Ser Trp Leu Gly Ser His Glu His Gly Pro Val Val Leu Asp Pro
 340 345 350
 Val Met Ile Ala Thr Ser Gly Asp Arg Leu Leu Asp Ala Ser Ala Glu
 355 360 365
 Glu Ser Leu Arg Arg Leu Ala Val His Val Asp Val Val Thr Pro Asn
 370 375 380
 Ile Pro Glu Leu Ala Val Leu Cys Asp Ser Ala Pro Ala Ile Thr Met
 385 390 395 400
 Asp Glu Ala Ile Ala Gln Ala Gln Gly Phe Ala Arg Thr His Asp Thr
 405 410 415
 Ile Val Ile Val Lys Gly Gly His Leu Thr Gly Ala Leu Ala Asp Asn
 420 425 430
 Ala Val Val Arg Pro Asp Gly Ser Val Phe Gln Val Glu Asn Leu Arg
 435 440 445
 Val Asn Thr Thr Asn Ser His Gly Thr Gly Cys Ser Leu Ser Ala Ser
 450 455 460
 Leu Ala Thr Lys Ile Ala Ala Gly Glu Ser Val Glu
 465 470 475

 <210> 543
 <211> 723
 <212> DNA
 <213> *Corynebacterium glutamicum*

 <220>
 <221> CDS
 <222> (101)..(700)
 <223> RXN01413

 <400> 543
 ttggccctat tggaagaagt aaattccaca ccttcacttt ccaatacttc ttttggtgag 60

 cgggtttcct cagcgtttta ccatctgaaa ccatctgaga ttg acc cat ctg ttc 115
 Leu Thr His Leu Phe
 1 5

 tta gaa ctc gat gag cgt tta gta ctg ggt gtt cag caa gat ggt tac 163
 Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val Gln Gln Asp Gly Tyr
 10 15 20

```

caa tgg act gag cat ttg ttc cgg ctg cca ctg caa cat ctc cgt aac 211
Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu Gln His Leu Arg Asn
      25                      30                      35

tcg ccc aat gac ctg cag gga ttg aag ata cga tgg tgt gaa ctt tat 259
Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg Trp Cys Glu Leu Tyr
      40                      45                      50

tcc aca acg ggg aaa gat caa ggg gta gaa ctt ctg cct caa gca acc 307
Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu Pro Gln Ala Thr
      55                      60                      65

gtc gtt acc cca aat aac ttc gag gct tcc acc ctc tcc ggc ctt gag 355
Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr Leu Ser Gly Leu Glu
      70                      75                      80                      85

aag ctt gag acc gtc gag gac ctc aag gag gct gcc cgc ctc att tat 403
Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala Ala Arg Leu Ile Tyr
      90                      95                      100

gag caa ggc ccc cag tac gta gtc gtc aag ggt ggc atg gac ttc ccc 451
Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly Gly Met Asp Phe Pro
      105                      110                      115

ggc gag aac gcc gtg gat gtg ctt ttc gac gga tcc tcc tac cac gtc 499
Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly Ser Ser Tyr His Val
      120                      125                      130

ttc tct gag cca aag att ggt gaa gag cgc gtt tcc ggc gca gtc tgc 547
Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val Ser Gly Ala Val Cys
      135                      140                      145

acc ttc gca gct gtt atc acc gca gag cta gca aag ggt gct gag gtt 595
Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Ala Glu Val
      150                      155                      160                      165

gta gac cca gtg gca acc gca aag cgt gtg gtc acc cgt gcg gtt caa 643
Val Asp Pro Val Ala Thr Ala Lys Arg Val Val Thr Arg Ala Val Gln
      170                      175                      180

gat gct gtt gca tcc aac gca cct ttt acc tcc gta tgg ctt gct gag 691
Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu
      185                      190                      195

gac aac aag tagagtttta aaataccgat caa 723
Asp Asn Lys
      200

```

<210> 544

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 544

```

Leu Thr His Leu Phe Leu Glu Leu Asp Glu Arg Leu Val Leu Gly Val
  1                      5                      10                      15

```

```

Gln Gln Asp Gly Tyr Gln Trp Thr Glu His Leu Phe Arg Leu Pro Leu
      20                      25                      30

```

Gln His Leu Arg Asn Ser Pro Asn Asp Leu Gln Gly Leu Lys Ile Arg
 35 40 45
 Trp Cys Glu Leu Tyr Ser Thr Thr Gly Lys Asp Gln Gly Val Glu Leu
 50 55 60
 Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu Ala Ser Thr
 65 70 75 80
 Leu Ser Gly Leu Glu Lys Leu Glu Thr Val Glu Asp Leu Lys Glu Ala
 85 90 95
 Ala Arg Leu Ile Tyr Glu Gln Gly Pro Gln Tyr Val Val Val Lys Gly
 100 105 110
 Gly Met Asp Phe Pro Gly Glu Asn Ala Val Asp Val Leu Phe Asp Gly
 115 120 125
 Ser Ser Tyr His Val Phe Ser Glu Pro Lys Ile Gly Glu Glu Arg Val
 130 135 140
 Ser Gly Ala Val Cys Thr Phe Ala Ala Val Ile Thr Ala Glu Leu Ala
 145 150 155 160
 Lys Gly Ala Glu Val Val Asp Pro Val Ala Thr Ala Lys Arg Val Val
 165 170 175
 Thr Arg Ala Val Gln Asp Ala Val Ala Ser Asn Ala Pro Phe Thr Ser
 180 185 190
 Val Trp Leu Ala Glu Asp Asn Lys
 195 200

<210> 545

<211> 795

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(772);

<223> RXN01617

<400> 545

tcagaagcta ccggcggcgc cggcatccag gttgatttga agaccttcca gcatttaaga 60

tgtttatggc attgggtcca tcacatgctt ggggtggcctt ttg atc cta aag aca 115
 Leu Ile Leu Lys Thr
 1 5

act gga atc acc gtt ttg tcc cgg ttt gat gcg cag gtt atc gct aat 163
 Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala Gln Val Ile Ala Asn
 10 15 20

cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg aag atc 211
 Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val Lys Ile
 25 30 35

ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc gct ttg 259
 Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr Ala Leu

40	45	50	
gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg atc tgc			307
Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu Ile Cys			
55	60	65	
aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc ctt cgc			355
Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala Leu Arg			
70	75	80	85
gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac ttc gag			403
Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn Phe Glu			
	90	95	100
gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac gac ctg			451
Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp Asp Leu			
	105	110	115
aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac gtc gtt			499
Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr Val Val			
	120	125	130
gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac gta ctt			547
Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp Val Leu			
	135	140	145
ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc ggc gac			595
Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile Gly Asp			
150	155	160	165
gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc acc gca			643
Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile Thr Ala			
	170	175	180
gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc gct aag			691
Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr Ala Lys			
	185	190	195
cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac gca ccg			739
Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn Ala Pro			
	200	205	210
ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt aaacaagctc			792
Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
215	220		
cct			795
<210> 546			
<211> 224			
<212> PRT			
<213> Corynebacterium glutamicum			
<400> 546			
Leu Ile Leu Lys Thr Thr Gly Ile Thr Val Leu Ser Arg Phe Asp Ala			
1	5	10	15
Gln Val Ile Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu			
	20	25	30

Asp Val Val Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr
 35 40 45
 Val Ala Thr Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp
 50 55 60
 Pro Val Leu Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr
 65 70 75 80
 Asp Thr Ala Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr
 85 90 95
 Pro Asn Asn Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu
 100 105 110
 Thr Ile Asp Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly
 115 120 125
 Pro Gln Tyr Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn
 130 135 140
 Ala Val Asp Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu
 145 150 155 160
 Pro Lys Ile Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala
 165 170 175
 Ala Val Ile Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala
 180 185 190
 Val Thr Thr Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val
 195 200 205
 Ala Ser Asn Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys
 210 215 220

<210> 547

<211> 638

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1) .. (615)

<223> FRXA01617

<400> 547

gct aat cag att gag gcc gcc acc gca gcg cac gat ctt gat gtg gtg 48
 Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
 1 5 10 15
 aag atc ggt atg ttg ggt act cct gca acg atc gat act gtg gca acc 96
 Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
 20 25 30
 gct ttg gag gaa aac agc ttc aag cac gtt gtc cta gac ccg gta ctg 144
 Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu

35	40	45	
atc tgc aag ggc cag gag ccc ggc gcg gca ctt gat act gac act gcc			192
Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala			
50	55	60	
ctt cgc gcg aag gtg ctg cca cag gca acc gtg gtt act cca aac aac			240
Leu Arg Ala Lys Val Leu Pro Gln Ala Thr Val Val Thr Pro Asn Asn			
65	70	75	80
ttc gag gcc acc acc ctg tct ggc cta gac aag ctg gag acc atc gac			288
Phe Glu Ala Thr Thr Leu Ser Gly Leu Asp Lys Leu Glu Thr Ile Asp			
85	90	95	
gac ctg aag gaa gca gcc cgc ctc att cat gag caa gga cct cag tac			336
Asp Leu Lys Glu Ala Ala Arg Leu Ile His Glu Gln Gly Pro Gln Tyr			
100	105	110	
gtc gtt gtt aag ggt ggc atc gac ttc cca ggc gac aac gct gtg gac			384
Val Val Val Lys Gly Gly Ile Asp Phe Pro Gly Asp Asn Ala Val Asp			
115	120	125	
gta ctt ttc gac ggc acc gac tac cac gtg ttc tct gaa cca aag atc			432
Val Leu Phe Asp Gly Thr Asp Tyr His Val Phe Ser Glu Pro Lys Ile			
130	135	140	
ggc gac gag cgc gtc tcc ggc gct ggc tgt acc ttc gca gct gtc atc			480
Gly Asp Glu Arg Val Ser Gly Ala Gly Cys Thr Phe Ala Ala Val Ile			
145	150	155	160
acc gca gag ctg gcc aag ggc aac tct gcc gtt gat gca gtg acc acc			528
Thr Ala Glu Leu Ala Lys Gly Asn Ser Ala Val Asp Ala Val Thr Thr			
165	170	175	
gct aag cgc gta gtc acc cgc gca gtg aag gac gct gtc gca tcc aac			576
Ala Lys Arg Val Val Thr Arg Ala Val Lys Asp Ala Val Ala Ser Asn			
180	185	190	
gca ccg ttt acc tct gtg tgg ttg gcg gaa gac aac aag tagaaatctt			625
Ala Pro Phe Thr Ser Val Trp Leu Ala Glu Asp Asn Lys			
195	200	205	
aaacaagctc cct			638

<210> 548

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

Ala Asn Gln Ile Glu Ala Ala Thr Ala Ala His Asp Leu Asp Val Val
1 5 10 15

Lys Ile Gly Met Leu Gly Thr Pro Ala Thr Ile Asp Thr Val Ala Thr
20 25 30

Ala Leu Glu Glu Asn Ser Phe Lys His Val Val Leu Asp Pro Val Leu
35 40 45

Ile Cys Lys Gly Gln Glu Pro Gly Ala Ala Leu Asp Thr Asp Thr Ala

50	55	60
Leu Arg Ala Lys Val 65	Leu Pro Gln Ala Thr 70	Val Val Thr Pro Asn Asn 75 80
Phe Glu Ala Thr Thr 85	Leu Ser Gly Leu Asp 90	Lys Leu Glu Thr Ile Asp 95
Asp Leu Lys Glu Ala 100	Ala Arg Leu Ile His 105	Glu Gln Gly Pro Gln Tyr 110
Val Val Val Lys Gly 115	Gly Ile Asp Phe Pro 120	Gly Asp Asn Ala Val Asp 125
Val Leu Phe Asp Gly 130	Thr Asp Tyr His Val 135	Phe Ser Glu Pro Lys Ile 140
Gly Asp Glu Arg Val 145	Ser Gly Ala Gly Cys 150 155	Thr Phe Ala Ala Val Ile 160
Thr Ala Glu Leu Ala 165	Lys Gly Asn Ser Ala 170	Val Asp Ala Val Thr Thr 175
Ala Lys Arg Val Val 180	Thr Arg Ala Val Lys 185	Asp Ala Val Ala Ser Asn 190
Ala Pro Phe Thr Ser 195	Val Trp Leu Ala Glu 200	Asp Asn Lys 205

<210> 549

<211> 915

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(892)

<223> RXS01807

<400> 549

```

gctcaccgag ctggacacca agctccgcg agtgcaggaa gaacacggcg agctggaaat 60
gcagtggctg gaactcggcg aggaaatcga gggctagttc atg ccg tcg gca ggc 115
                                     Met Pro Ser Ala Gly
                                     1 5
gag gag att tta gag cag cgc gca cag ctg gag ttt gat cag cgc cgc 163
Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu Phe Asp Gln Arg Arg
                                     10 15 20
gcc gat gtg gtg atg atc ggc agc cag gtg gtt tat ggt tcc gtg ggg 211
Ala Asp Val Val Met Ile Gly Ser Gln Val Val Tyr Gly Ser Val Gly
                                     25 30 35
ctc agt gct gcc att ccg gtg atg cac aac gaa ggc ctc cgc gtg gtc 259
Leu Ser Ala Ala Ile Pro Val Met His Asn Glu Gly Leu Arg Val Val
                                     40 45 50
gct gtc ccc acc gtg gtg tta agt tcc atg ccg cgt tat gca agt tct 307
Ala Val Pro Thr Val Val Leu Ser Ser Met Pro Arg Tyr Ala Ser Ser

```

55	60	65	
cac cgc cag ccg atg tcg gac caa tgg ctc gcc gac gcg ctg caa gac			355
His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala Asp Ala Leu Gln Asp			
70	75	80	85
ctg gtg gat ctg ggg att atc gat gag gtt tcc acc att tcc acc ggc			403
Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser Thr Ile Ser Thr Gly			
	90	95	100
tat ttt acc tcc gct tct cag gtg cgt gtg gtc gct gcg tgg ctg cag			451
Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val Ala Ala Trp Leu Gln			
	105	110	115
aaa atc cgc gaa acc cat ccg cat gtg cgc atc gtg gtg gat ccc atc			499
Lys Ile Arg Glu Thr His Pro His Val Arg Ile Val Val Asp Pro Ile			
	120	125	130
atg ggg gac agt gac gtg gga att tat gtc gcc gac gag atc gca acc			547
Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala Asp Glu Ile Ala Thr			
	135	140	145
gcc atc tgc cag gac tta tgc cct ctg gct acc gga atc att ccc aat			595
Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr Gly Ile Ile Pro Asn			
	150	155	160
gct ttc gag ctc tcc cac atg gtt ggc tcc ggc gat ccg cgc tcg ctg			643
Ala Phe Glu Leu Ser His Met Val Gly Ser Gly Asp Pro Arg Ser Leu			
	170	175	180
ctc ggc ccg ttt ggc gag tgg atc atc atc acc agc gcc act gaa act			691
Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr Ser Ala Thr Glu Thr			
	185	190	195
gtg ggc acc acc gtc acc cgc atc gtc acc cgt gac agc gtc cag gaa			739
Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg Asp Ser Val Gln Glu			
	200	205	210
atc gcc tcc gcc acc gtc gat acc acg gcc aaa ggg gca ggc gac gtc			787
Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys Gly Ala Gly Asp Val			
	215	220	225
tac gcc gca gca tta atc gcc gcc ctg cat aaa gat ttt tcg ctt atc			835
Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys Asp Phe Ser Leu Ile			
	230	235	240
gac gcc gcc agc cac gca tcc aac acc gtc tgc gcc ggc ctg cag acc			883
Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys Ala Gly Leu Gln Thr			
	250	255	260
aaa gcg ctt taggtttcgt ccgtctctga cag			915
Lys Ala Leu			

<210> 550

<211> 264

<212> PRT

<213> Corynebacterium glutamicum

<400> 550


```

Met Pro Ser Ala Gly Glu Glu Ile Leu Glu Gln Arg Ala Gln Leu Glu
 1           5           10           15
Phe Asp Gln Arg Arg Ala Asp Val Val Met Ile Gly Ser Gln Val Val
           20           25           30
Tyr Gly Ser Val Gly Leu Ser Ala Ala Ile Pro Val Met His Asn Glu
           35           40           45
Gly Leu Arg Val Val Ala Val Pro Thr Val Val Leu Ser Ser Met Pro
 50           55           60
Arg Tyr Ala Ser Ser His Arg Gln Pro Met Ser Asp Gln Trp Leu Ala
 65           70           75           80
Asp Ala Leu Gln Asp Leu Val Asp Leu Gly Ile Ile Asp Glu Val Ser
           85           90           95
Thr Ile Ser Thr Gly Tyr Phe Thr Ser Ala Ser Gln Val Arg Val Val
           100          105          110
Ala Ala Trp Leu Gln Lys Ile Arg Glu Thr His Pro His Val Arg Ile
           115          120          125
Val Val Asp Pro Ile Met Gly Asp Ser Asp Val Gly Ile Tyr Val Ala
 130          135          140
Asp Glu Ile Ala Thr Ala Ile Cys Gln Asp Leu Cys Pro Leu Ala Thr
 145          150          155          160
Gly Ile Ile Pro Asn Ala Phe Glu Leu Ser His Met Val Gly Ser Gly
           165          170          175
Asp Pro Arg Ser Leu Leu Gly Pro Phe Gly Glu Trp Ile Ile Ile Thr
           180          185          190
Ser Ala Thr Glu Thr Val Gly Thr Thr Val Thr Arg Ile Val Thr Arg
           195          200          205
Asp Ser Val Gln Glu Ile Ala Ser Ala Thr Val Asp Thr Thr Ala Lys
 210          215          220
Gly Ala Gly Asp Val Tyr Ala Ala Ala Leu Ile Ala Ala Leu His Lys
 225          230          235          240
Asp Phe Ser Leu Ile Asp Ala Ala Ser His Ala Ser Asn Thr Val Cys
           245          250          255
Ala Gly Leu Gln Thr Lys Ala Leu
           260

```

<210> 551

<211> 622

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(622)

<223> RXC01021

<400> 551

cgagaggctt ttttggctct aagcctttta gtcgtgcgaa cgaaatctta agcagcctcg 60

gtgccaccga gatcgattgg tcgctgtaag gtatctgatt atg tcc agt tcc gaa 115
 Met Ser Ser Ser Glu
 1 5

agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu
 10 15 20

cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala
 25 30 35

tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala
 40 45 50

gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val
 55 60 65

ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met
 70 75 80 85

aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val
 90 95 100

gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg
 105 110 115

gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag 499
 Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu Arg Ala Ile Ala Gln
 120 125 130

gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta 547
 Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu
 135 140 145

tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag 595
 Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu
 150 155 160 165

ggc act gtt gtc act gtg ttg cgt tct 622
 Gly Thr Val Val Thr Val Leu Arg Ser
 170

<210> 552

<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 552

Met Ser Ser Ser Glu Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro
 1 5 10 15

Ser	Val	Gln	Pro	Glu	Arg	Arg	Ala	Asp	Ser	Thr	Gly	Ala	Pro	Ala	Ala
			20					25					30		
Ala	Ser	Lys	Glu	Ala	Ser	Gln	Gln	Met	Asp	Ala	Ala	Gly	Val	Leu	Glu
		35					40					45			
Trp	Ala	Arg	Thr	Ala	Val	Glu	Gln	Leu	Ser	Glu	Arg	Arg	Ala	Glu	Ile
	50					55					60				
Asn	Ala	Leu	Asn	Val	Phe	Pro	Val	Pro	Asp	Ala	Asp	Thr	Gly	Ser	Asn
	65				70					75					80
Met	Thr	Tyr	Thr	Met	Thr	Ala	Ala	Leu	Asp	Glu	Ala	Leu	Lys	Leu	Gly
				85					90					95	
Glu	Leu	Gly	Asp	Val	Ala	Arg	Ile	Thr	Glu	Ala	Leu	Ala	Val	Gly	Ser
			100					105					110		
Val	Arg	Gly	Ala	Arg	Gly	Asn	Ser	Gly	Val	Val	Leu	Ser	Gln	Val	Leu
		115					120					125			
Arg	Ala	Ile	Ala	Gln	Ala	Ala	Ala	Asp	Gly	Val	Ile	Asp	Gly	His	Thr
	130					135					140				
Ile	Gln	Glu	Ala	Leu	Ser	Ile	Ala	Arg	Ser	Leu	Val	Asp	Arg	Ala	Ile
145					150					155					160
Thr	Asp	Pro	Val	Glu	Gly	Thr	Val	Val	Thr	Val	Leu	Arg	Ser		
				165					170						

<210> 553
<211> 1107
<212> DNA
<213> *Corynebacterium glutamicum*

```
<220>  
<221> CDS  
<222> (101)..(1084)  
<223> RXN02246
```

<400> 553																	
tgccgacgct	ggcgtggatg	ccttcggttg	aggttccgct	gtgtacggcg	ctgaggatcc												60
caacaaggcg atccaggagt tgcgagcact cgcgagtaa atg gat gtt gcg cac																	115
Met Asp Val Ala His																	
1 5																	
gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc																	163
Ala	Leu	Asp	Leu	Ala	His	His	Val	Ser	Asp	Gln	Val	Arg	Gly	Thr	Thr		
10 15 20																	
agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag																	211
Ser	Pro	Asn	Pro	Pro	Val	Gly	Ala	Val	Ile	Leu	Asp	Ala	Asp	Gly	Glu		
25 30 35																	
gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa																	259
Val	Val	Gly	Val	Gly	Ala	Thr	Ala	Pro	Pro	Gly	Gly	Pro	His	Ala	Glu		
40 45 50																	

gtg	gtg	gcg	ctt	gca	gct	gcc	gga	gtg	cgt	gcc	aac	ggg	ggc	acg	gcg	307
Val	Val	Ala	Leu	Ala	Ala	Ala	Gly	Val	Arg	Ala	Asn	Gly	Gly	Thr	Ala	
55						60					65					
gtg	gtc	acc	ctc	gag	ccg	tgc	aac	cat	tac	ggc	cgc	acg	ggg	cca	tgt	355
Val	Val	Thr	Leu	Glu	Pro	Cys	Asn	His	Tyr	Gly	Arg	Thr	Gly	Pro	Cys	
70					75					80					85	
tcc	aag	gcg	ctt	ctc	gac	gcc	ggg	atc	gca	cac	gtg	ttt	tac	gcc	aat	403
Ser	Lys	Ala	Leu	Leu	Asp	Ala	Gly	Ile	Ala	His	Val	Phe	Tyr	Ala	Asn	
				90					95					100		
gcg	gat	ccc	ttc	ccg	tca	gcc	gct	ggg	ggc	ggg	gcc	ttt	ttg	gcg	gag	451
Ala	Asp	Pro	Phe	Pro	Ser	Ala	Ala	Gly	Gly	Gly	Ala	Phe	Leu	Ala	Glu	
			105					110					115			
gcg	ggc	gtc	gat	acg	cat	ttt	tta	gat	gag	cgg	atc	agg	gca	ctg	gag	499
Ala	Gly	Val	Asp	Thr	His	Phe	Leu	Asp	Glu	Arg	Ile	Arg	Ala	Leu	Glu	
		120					125					130				
ccc	tgg	ctg	gtt	gcg	acg	cgt	ctg	ggc	agg	ccc	cat	gtc	acg	ttg	aag	547
Pro	Trp	Leu	Val	Ala	Thr	Arg	Leu	Gly	Arg	Pro	His	Val	Thr	Leu	Lys	
	135					140					145					
ttt	gcg	tcc	acc	gtg	gac	ggg	ttt	gct	ggg	gcc	acc	gat	ggc	acc	agc	595
Phe	Ala	Ser	Thr	Val	Asp	Gly	Phe	Ala	Gly	Ala	Thr	Asp	Gly	Thr	Ser	
150					155					160					165	
cag	tgg	att	acc	ggg	ccg	gat	gcg	cgg	gcg	ttt	gtg	cac	gaa	gat	cga	643
Gln	Trp	Ile	Thr	Gly	Pro	Asp	Ala	Arg	Ala	Phe	Val	His	Glu	Asp	Arg	
				170					175					180		
agt	aaa	aga	gat	gcg	atc	atc	gtg	ggg	acc	ggg	act	gcg	ttg	act	gat	691
Ser	Lys	Arg	Asp	Ala	Ile	Ile	Val	Gly	Thr	Gly	Thr	Ala	Leu	Thr	Asp	
			185					190					195			
aat	ccc	tcc	ttg	acg	gcg	cgg	acc	gat	acg	ggg	ctt	tat	gaa	aat	caa	739
Asn	Pro	Ser	Leu	Thr	Ala	Arg	Thr	Asp	Thr	Gly	Leu	Tyr	Glu	Asn	Gln	
		200					205					210				
ccc	agg	cgc	gtt	gtt	att	ggc	tcc	cgc	gag	gtt	cca	gca	gat	tcc	aac	787
Pro	Arg	Arg	Val	Val	Ile	Gly	Ser	Arg	Glu	Val	Pro	Ala	Asp	Ser	Asn	
	215					220					225					
ttg	gct	cgc	ttg	gga	tat	gag	cag	tac	gcg	gga	ata	cca	gag	gct	tta	835
Leu	Ala	Arg	Leu	Gly	Tyr	Glu	Gln	Tyr	Ala	Gly	Ile	Pro	Glu	Ala	Leu	
230					235					240					245	
tca	gcg	ctg	tgg	gat	aaa	ggg	tgc	cga	gac	att	tta	atc	gaa	ggg	ggc	883
Ser	Ala	Leu	Trp	Asp	Lys	Gly	Cys	Arg	Asp	Ile	Leu	Ile	Glu	Gly	Gly	
				250					255					260		
cca	acg	tta	gct	ggg	gca	gcg	ctg	cgc	tta	ggc	att	gtt	gat	cag	gtg	931
Pro	Thr	Leu	Ala	Gly	Ala	Ala	Leu	Arg	Leu	Gly	Ile	Val	Asp	Gln	Val	
			265					270					275			
cag	gcc	tat	gtt	gcc	ccc	gct	ttg	ttg	ggc	gct	gga	cga	tca	gtg	att	979
Gln	Ala	Tyr	Val	Ala	Pro	Ala	Leu	Leu	Gly	Ala	Gly	Arg	Ser	Val	Ile	
		280					285					290				

aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc
1027

Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr
295 300 305

acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga
1075

Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg
310 315 320 325

aag gaa cac taaatgttca caggtattgt cga
1107

Lys Glu His

<210> 554

<211> 328

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220
 Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240
 Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255
 Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 555
 <211> 1107
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1084)
 <223> FRXA02246

<400> 555
 tgccgacgct ggcgtggatg ccttcgttgc aggttccgct gtgtacggcg ctgaggatcc 60
 caacaaggcg atccaggagt tgcgagcact cgcgcagtaa atg gat gtt gcg cac 115
 Met Asp Val Ala His
 1 5
 gcg tta gat ctg gcc cac cac gtg tca gat caa gtc cga ggc acc acc 163
 Ala Leu Asp Leu Ala His His Val Ser Asp Gln Val Arg Gly Thr Thr
 10 15 20
 agc cct aat ccg cca gtc ggc gct gtc att ttg gac gcc gac ggc gag 211
 Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu Asp Ala Asp Gly Glu
 25 30 35
 gtc gtt ggc gtt ggc gcc acg gca cct cct ggt ggc ccg cac gcc gaa 259
 Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly Gly Pro His Ala Glu
 40 45 50
 gtg gtg gcg ctt gca gct gcc gga gtg cgt gcc aac ggg ggc acg gcg 307
 Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala Asn Gly Gly Thr Ala
 55 60 65
 gtg gtc acc ctc gag ccg tgc aac cat tac ggc cgc acg ggt cca tgt 355
 Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly Arg Thr Gly Pro Cys
 70 75 80 85

tcc aag gcg ctt ctc gac gcc ggg atc gca cac gtg ttt tac gcc aat	403
Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His Val Phe Tyr Ala Asn	
90 95 100	
gcg gat ccc ttc ccg tca gcc gct ggg ggc ggt gcc ttt ttg gcg gag	451
Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly Ala Phe Leu Ala Glu	
105 110 115	
gcg ggc gtc gat acg cat ttt tta gat gag cgg atc agg gca ctg gag	499
Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg Ile Arg Ala Leu Glu	
120 125 130	
ccc tgg ctg gtt gcg acg cgt ctg ggc agg ccc cat gtc acg ttg aag	547
Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro His Val Thr Leu Lys	
135 140 145	
ttt gcg tcc acc gtg gac ggt ttt gct ggt gcc acc gat ggc acc agc	595
Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala Thr Asp Gly Thr Ser	
150 155 160 165	
cag tgg att acc ggg ccg gat gcg cgg gcg ttt gtg cac gaa gat cga	643
Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe Val His Glu Asp Arg	
170 175 180	
agt aaa aga gat gcg atc atc gtg ggt acc ggt act gcg ttg act gat	691
Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly Thr Ala Leu Thr Asp	
185 190 195	
aat ccc tcc ttg acg gcg cgg acc gat acg ggt ctt tat gaa aat caa	739
Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly Leu Tyr Glu Asn Gln	
200 205 210	
ccc agg cgc gtt gtt att ggc tcc cgc gag gtt cca gca gat tcc aac	787
Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val Pro Ala Asp Ser Asn	
215 220 225	
ttg gct cgc ttg gga tat gag cag tac gcg gga ata cca gag gct tta	835
Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly Ile Pro Glu Ala Leu	
230 235 240 245	
tca gcg ctg tgg gat aaa ggg tgc cga gac att tta atc gaa ggt ggc	883
Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile Leu Ile Glu Gly Gly	
250 255 260	
cca acg tta gct ggg gca gcg ctg cgc tta ggc att gtt gat cag gtg	931
Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly Ile Val Asp Gln Val	
265 270 275	
cag gcc tat gtt gcc ccc gct ttg ttg ggc gct gga cga tca gtg att	979
Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala Gly Arg Ser Val Ile	
280 285 290	
aac tgg cca caa gaa acc acg atg gat cag att atg cgt ttt gac acc	1027
Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile Met Arg Phe Asp Thr	
295 300 305	
acg tcc gtg aga cag ttg ggt tca gat gta ttg ata gaa atg atg aga	1075
Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu Ile Glu Met Met Arg	

310

315

320

325

aag gaa cac taaatgttca caggtattgt cga
 1107
 Lys Glu His

<210> 556

<211> 328

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 556

Met Asp Val Ala His Ala Leu Asp Leu Ala His His Val Ser Asp Gln
 1 5 10 15

Val Arg Gly Thr Thr Ser Pro Asn Pro Pro Val Gly Ala Val Ile Leu
 20 25 30

Asp Ala Asp Gly Glu Val Val Gly Val Gly Ala Thr Ala Pro Pro Gly
 35 40 45

Gly Pro His Ala Glu Val Val Ala Leu Ala Ala Ala Gly Val Arg Ala
 50 55 60

Asn Gly Gly Thr Ala Val Val Thr Leu Glu Pro Cys Asn His Tyr Gly
 65 70 75 80

Arg Thr Gly Pro Cys Ser Lys Ala Leu Leu Asp Ala Gly Ile Ala His
 85 90 95

Val Phe Tyr Ala Asn Ala Asp Pro Phe Pro Ser Ala Ala Gly Gly Gly
 100 105 110

Ala Phe Leu Ala Glu Ala Gly Val Asp Thr His Phe Leu Asp Glu Arg
 115 120 125

Ile Arg Ala Leu Glu Pro Trp Leu Val Ala Thr Arg Leu Gly Arg Pro
 130 135 140

His Val Thr Leu Lys Phe Ala Ser Thr Val Asp Gly Phe Ala Gly Ala
 145 150 155 160

Thr Asp Gly Thr Ser Gln Trp Ile Thr Gly Pro Asp Ala Arg Ala Phe
 165 170 175

Val His Glu Asp Arg Ser Lys Arg Asp Ala Ile Ile Val Gly Thr Gly
 180 185 190

Thr Ala Leu Thr Asp Asn Pro Ser Leu Thr Ala Arg Thr Asp Thr Gly
 195 200 205

Leu Tyr Glu Asn Gln Pro Arg Arg Val Val Ile Gly Ser Arg Glu Val
 210 215 220

Pro Ala Asp Ser Asn Leu Ala Arg Leu Gly Tyr Glu Gln Tyr Ala Gly
 225 230 235 240

Ile Pro Glu Ala Leu Ser Ala Leu Trp Asp Lys Gly Cys Arg Asp Ile
 245 250 255

Leu Ile Glu Gly Gly Pro Thr Leu Ala Gly Ala Ala Leu Arg Leu Gly
 260 265 270
 Ile Val Asp Gln Val Gln Ala Tyr Val Ala Pro Ala Leu Leu Gly Ala
 275 280 285
 Gly Arg Ser Val Ile Asn Trp Pro Gln Glu Thr Thr Met Asp Gln Ile
 290 295 300
 Met Arg Phe Asp Thr Thr Ser Val Arg Gln Leu Gly Ser Asp Val Leu
 305 310 315 320
 Ile Glu Met Met Arg Lys Glu His
 325

<210> 557

<211> 756

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(733)

<223> RXA02247

<400> 557

acaagaaacc acgatggatc agattatgcg ttttgacacc acgtccgtga gacagttggg 60

ttcagatgta ttgatagaaa tgatgagaaa ggaacactaa atg ttc aca ggt att 115
 Met Phe Thr Gly Ile
 1 5

gtc gag gag ctt ggc tcc gtt gca ggc gtg gaa cat ctg gga gat tcc 163
 Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu His Leu Gly Asp Ser
 10 15 20

atc cgg atg cag att tcc gcg tcc acc gtt tta gag ggt gtg cat ttg 211
 Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu Glu Gly Val His Leu
 25 30 35

ggg gat tcc att tct gtc aat ggt gtg tgc ttg aca gtg gcg tcc ttt 259
 Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu Thr Val Ala Ser Phe
 40 45 50

ggc gag gga cat ttc act gca gac ctc atg cag gaa acc tta gat cgc 307
 Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln Glu Thr Leu Asp Arg
 55 60 65

agc tcc ctg ggc gca tta tcc acc ggt agc aaa gtc aac ctt gag cgc 355
 Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys Val Asn Leu Glu Arg
 70 75 80 85

gcc atg gca gcc gat ggc cgt ctg ggt gga cac atc atg caa ggc cat 403
 Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His Ile Met Gln Gly His
 90 95 100

gtt gat gcc acc acc tcg ctg atc aag cgc acc agc tca gag aac tgg 451
 Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr Ser Ser Glu Asn Trp
 105 110 115

gat gtt ctg cgt ttt gag ctg cca gct gat ttg gct cgc tat gtg gtg 499
Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu Ala Arg Tyr Val Val
120 125 130

gaa aaa ggc tcc atc gca ctc aat ggc aca tcc ttg act gta tcg tct 547
Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser Leu Thr Val Ser Ser
135 140 145

ttg ggt gat gat tgg ttt gag gtt tcc ctg att ccc acc acc ttg cgc 595
Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile Pro Thr Thr Leu Arg
150 155 160 165

gac acc acc cac ggc gaa ctg gcg gta ggg gat atc gta aac att gag 643
Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp Ile Val Asn Ile Glu
170 175 180

gtt gat gtg atc gct aag tac gtc gaa cgc atg atg acg cgc ggc gtg 691
Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met Met Thr Arg Gly Val
185 190 195

gct gga aac act ccc aat gac tac acc gat ttc acg aga gac 733
Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe Thr Arg Asp
200 205 210

taggttagac aacgtgagtg aac 756

<210> 558

<211> 211

<212> PRT

<213> Corynebacterium glutamicum

<400> 558

Met Phe Thr Gly Ile Val Glu Glu Leu Gly Ser Val Ala Gly Val Glu
1 5 10 15

His Leu Gly Asp Ser Ile Arg Met Gln Ile Ser Ala Ser Thr Val Leu
20 25 30

Glu Gly Val His Leu Gly Asp Ser Ile Ser Val Asn Gly Val Cys Leu
35 40 45

Thr Val Ala Ser Phe Gly Glu Gly His Phe Thr Ala Asp Leu Met Gln
50 55 60

Glu Thr Leu Asp Arg Ser Ser Leu Gly Ala Leu Ser Thr Gly Ser Lys
65 70 75 80

Val Asn Leu Glu Arg Ala Met Ala Ala Asp Gly Arg Leu Gly Gly His
85 90 95

Ile Met Gln Gly His Val Asp Ala Thr Thr Ser Leu Ile Lys Arg Thr
100 105 110

Ser Ser Glu Asn Trp Asp Val Leu Arg Phe Glu Leu Pro Ala Asp Leu
115 120 125

Ala Arg Tyr Val Val Glu Lys Gly Ser Ile Ala Leu Asn Gly Thr Ser
130 135 140

Leu Thr Val Ser Ser Leu Gly Asp Asp Trp Phe Glu Val Ser Leu Ile
 145 150 155 160
 Pro Thr Thr Leu Arg Asp Thr Thr His Gly Glu Leu Ala Val Gly Asp
 165 170 175
 Ile Val Asn Ile Glu Val Asp Val Ile Ala Lys Tyr Val Glu Arg Met
 180 185 190
 Met Thr Arg Gly Val Ala Gly Asn Thr Pro Asn Asp Tyr Thr Asp Phe
 195 200 205
 Thr Arg Asp
 210

<210> 559
 <211> 1389
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1366)
 <223> RXN02248

<400> 559
 gatgtgatcg ctaagtacgt cgaacgcgatg atgacgcgcg gcgtggctgg aaacactccc 60
 aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
 Val Ser Glu His Glu 5
 1
 cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
 Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile 20
 10 15
 gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
 Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn 35
 25 30
 gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
 Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val 50
 40 45
 gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
 Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr 65
 55 60
 gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
 Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn 85
 70 75 80
 cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
 Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr 100
 90 95
 ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
 Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu 115
 105 110

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
 Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
 120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
 Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
 135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
 His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
 150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
 Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
 170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
 Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
 185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739
 Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg Arg Lys Asn Glu Ile
 200 205 210

ttg gtg gag cgc cag gtg gaa act gtg ctg cct acc gat ttc ggc acg 787
 Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro Thr Asp Phe Gly Thr
 215 220 225

ttc aag gct gtt ggt tac cgt tcc atc atc gat ggc acc gag ctt gtt 835
 Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp Gly Thr Glu Leu Val
 230 235 240 245

gcc att gtt gcc ggc gac gtg gca tcc gac ggt ggc gaa aac gtc ctg 883
 Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly Gly Glu Asn Val Leu
 250 255 260

gtt cga gtc cac tct gag tgc ttg act ggt gat gtt ttt gga tcc cgg 931
 Val Arg Val His Ser Glu Cys Leu Thr Gly Asp Val Phe Gly Ser Arg
 265 270 275

cgc tgc gac tgt gga cag cag ctg cac gag tct ttg cgc ctg atc cag 979
 Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser Leu Arg Leu Ile Gln
 280 285 290

gaa gct ggt cgg gga gta gtg gtg tac atg cgt ggg cat gag gga cga
 1027
 Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg Gly His Glu Gly Arg
 295 300 305

ggc att ggt ctg ctc gcc aag cta cgc gcc tac caa ctc cag gat gaa
 1075
 Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr Gln Leu Gln Asp Glu
 310 315 320 325

ggt gcc gac acc gtc gat gcc aac ctc gca ctt ggt ctt cca gcc gat
 1123
 Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu Gly Leu Pro Ala Asp
 330 335 340

gcc cgc gaa ttt ggc acc agc gcc cag att ctc tac gac ttg ggt gtg
 1171

Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu Tyr Asp Leu Gly Val
 345 350 355

cgc tcg ctc aac ttg atc agc aac aac cca gcc aag aag gtg gga ctt
 1219

Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala Lys Lys Val Gly Leu
 360 365 370

gaa ggc cac ggc att tcc att gcc agc cga acc ccc atc cct gtt gct
 1267

Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr Pro Ile Pro Val Ala
 375 380 385

gtt cat gaa gac aat gtt cga tac ctg aaa acc aag cgt gac cgc atg
 1315

Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr Lys Arg Asp Arg Met
 390 395 400 405

gga cat gac ctc cca gat gtc gca ctg tgg gaa caa gag cac cca gaa
 1363

Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu Gln Glu His Pro Glu
 410 415 420

aac taaggagcac aacaatggct aaa

1389

Asn

<210> 560

<211> 422

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
 1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp
 20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
 35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
 50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
 65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
 85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
 100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
 115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
 130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
 145 150 155 160
 Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
 165 170 175
 Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
 180 185 190
 Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
 195 200 205
 Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
 210 215 220
 Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
 225 230 235 240
 Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
 245 250 255
 Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

<210> 561

<211> 1389

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1366)

<223> FRXA02248

<400> 561

```

gatgtgatcg ctaagtacgt cgaacgcatg atgacgcgcg gcgtggctgg aaacactccc 60

aatgactaca ccgatttcac gagagactag gttagacaac gtg agt gaa cat gag 115
Val Ser Glu His Glu
1 5

cag gca cac agc caa tta gat tct gtt gaa gag gcc atc gct gac atc 163
Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu Ala Ile Ala Asp Ile
10 15 20

gct gcg ggt aaa gcc gtc gtg gtg gta gat gat gaa gat cgt gaa aat 211
Ala Ala Gly Lys Ala Val Val Val Val Asp Asp Glu Asp Arg Glu Asn
25 30 35

gaa ggc gac atc atc ttt gcc gcc gaa tta gcc act cca gaa tta gtc 259
Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala Thr Pro Glu Leu Val
40 45 50

gct ttc atg gtg cgt tat tcc tcg gga tac atc tgt gcg cca tta acc 307
Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile Cys Ala Pro Leu Thr
55 60 65

gca aag gat gca gat cgt ctt gat ctg cct ccg atg acc gcg cac aat 355
Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro Met Thr Ala His Asn
70 75 80 85

cag gat gcc cgc ggc acc gct tac acc gtg acc gtt gat gcc aac acc 403
Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr Val Asp Ala Asn Thr
90 95 100

ggc acc aca ggc att tct gca aca gac cgc gcc cac act ttg cgc ttg 451
Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala His Thr Leu Arg Leu
105 110 115

ctt gct gat cca gaa gcc gac cgc acg gat ttc acc cgt ccc gga cac 499
Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe Thr Arg Pro Gly His
120 125 130

gtt gtg cca ctg cgt gct cgt gaa ggt ggc gtc ttg gtg cgc gct gga 547
Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val Leu Val Arg Ala Gly
135 140 145

cac acc gaa gca gct gtc gat ttg gct cgc gct gca ggc ctg cgc cca 595
His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala Ala Gly Leu Arg Pro
150 155 160 165

gca ggt gtt atc tgc gaa gtg gtc agt gaa gag gac ccc acc ggc atg 643
Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu Asp Pro Thr Gly Met
170 175 180

gct cgg gtt cct gag ctg cgc cgc ttc tgc gat gag cac gat ctg aag 691
Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp Glu His Asp Leu Lys
185 190 195

ctg atc tct att gag cag ctc att gag tgg cgt cgc aag aat gaa att 739

```

Leu	Ile	Ser	Ile	Glu	Gln	Leu	Ile	Glu	Trp	Arg	Arg	Lys	Asn	Glu	Ile		
		200					205					210					
ttg	gtg	gag	cgc	cag	gtg	gaa	act	gtg	ctg	cct	acc	gat	ttc	ggc	acg	787	
Leu	Val	Glu	Arg	Gln	Val	Glu	Thr	Val	Leu	Pro	Thr	Asp	Phe	Gly	Thr		
	215					220					225						
ttc	aag	gct	gtt	ggt	tac	cgt	tcc	atc	atc	gat	ggc	acc	gag	ctt	gtt	835	
Phe	Lys	Ala	Val	Gly	Tyr	Arg	Ser	Ile	Ile	Asp	Gly	Thr	Glu	Leu	Val		
230					235					240					245		
gcc	att	gtt	gcc	ggc	gac	gtg	gca	tcc	gac	ggg	ggc	gaa	aac	gtc	ctg	883	
Ala	Ile	Val	Ala	Gly	Asp	Val	Ala	Ser	Asp	Gly	Gly	Glu	Asn	Val	Leu		
				250					255					260			
gtt	cga	gtc	cac	tct	gag	tgc	ttg	act	ggg	gat	gtt	ttt	gga	tcc	cgg	931	
Val	Arg	Val	His	Ser	Glu	Cys	Leu	Thr	Gly	Asp	Val	Phe	Gly	Ser	Arg		
			265					270					275				
cgc	tgc	gac	tgt	gga	cag	cag	ctg	cac	gag	tct	ttg	cgc	ctg	atc	cag	979	
Arg	Cys	Asp	Cys	Gly	Gln	Gln	Leu	His	Glu	Ser	Leu	Arg	Leu	Ile	Gln		
		280					285					290					
gaa	gct	ggg	cgg	gga	gta	gtg	gtg	tac	atg	cgt	ggg	cat	gag	gga	cga		
1027																	
Glu	Ala	Gly	Arg	Gly	Val	Val	Val	Tyr	Met	Arg	Gly	His	Glu	Gly	Arg		
	295					300					305						
ggc	att	ggg	ctg	ctc	gcc	aag	cta	cgc	gcc	tac	caa	ctc	cag	gat	gaa		
1075																	
Gly	Ile	Gly	Leu	Leu	Ala	Lys	Leu	Arg	Ala	Tyr	Gln	Leu	Gln	Asp	Glu		
310					315					320					325		
ggg	gcc	gac	acc	gtc	gat	gcc	aac	ctc	gca	ctt	ggg	ctt	cca	gcc	gat		
1123																	
Gly	Ala	Asp	Thr	Val	Asp	Ala	Asn	Leu	Ala	Leu	Gly	Leu	Pro	Ala	Asp		
				330					335					340			
gcc	cgc	gaa	ttt	ggc	acc	agc	gcc	cag	att	ctc	tac	gac	ttg	ggg	gtg		
1171																	
Ala	Arg	Glu	Phe	Gly	Thr	Ser	Ala	Gln	Ile	Leu	Tyr	Asp	Leu	Gly	Val		
			345					350					355				
cgc	tcg	ctc	aac	ttg	atc	agc	aac	aac	cca	gcc	aag	aag	gtg	gga	ctt		
1219																	
Arg	Ser	Leu	Asn	Leu	Ile	Ser	Asn	Asn	Pro	Ala	Lys	Lys	Val	Gly	Leu		
		360					365					370					
gaa	ggc	cac	ggc	att	tcc	att	gcc	agc	cga	acc	ccc	atc	cct	gtt	gct		
1267																	
Glu	Gly	His	Gly	Ile	Ser	Ile	Ala	Ser	Arg	Thr	Pro	Ile	Pro	Val	Ala		
	375					380					385						
gtt	cat	gaa	gac	aat	gtt	cga	tac	ctg	aaa	acc	aag	cgt	gac	cgc	atg		
1315																	
Val	His	Glu	Asp	Asn	Val	Arg	Tyr	Leu	Lys	Thr	Lys	Arg	Asp	Arg	Met		
390					395					400					405		
gga	cat	gac	ctc	cca	gat	gtc	gca	ctg	tgg	gaa	caa	gag	cac	cca	gaa		
1363																	
Gly	His	Asp	Leu	Pro	Asp	Val	Ala	Leu	Trp	Glu	Gln	Glu	His	Pro	Glu		

410

415

420

aac taaggagcac aacaatggct aaa
1389
Asn

<210> 562

<211> 422

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 562

Val Ser Glu His Glu Gln Ala His Ser Gln Leu Asp Ser Val Glu Glu
1 5 10 15

Ala Ile Ala Asp Ile Ala Ala Gly Lys Ala Val Val Val Val Asp Asp
20 25 30

Glu Asp Arg Glu Asn Glu Gly Asp Ile Ile Phe Ala Ala Glu Leu Ala
35 40 45

Thr Pro Glu Leu Val Ala Phe Met Val Arg Tyr Ser Ser Gly Tyr Ile
50 55 60

Cys Ala Pro Leu Thr Ala Lys Asp Ala Asp Arg Leu Asp Leu Pro Pro
65 70 75 80

Met Thr Ala His Asn Gln Asp Ala Arg Gly Thr Ala Tyr Thr Val Thr
85 90 95

Val Asp Ala Asn Thr Gly Thr Thr Gly Ile Ser Ala Thr Asp Arg Ala
100 105 110

His Thr Leu Arg Leu Leu Ala Asp Pro Glu Ala Asp Arg Thr Asp Phe
115 120 125

Thr Arg Pro Gly His Val Val Pro Leu Arg Ala Arg Glu Gly Gly Val
130 135 140

Leu Val Arg Ala Gly His Thr Glu Ala Ala Val Asp Leu Ala Arg Ala
145 150 155 160

Ala Gly Leu Arg Pro Ala Gly Val Ile Cys Glu Val Val Ser Glu Glu
165 170 175

Asp Pro Thr Gly Met Ala Arg Val Pro Glu Leu Arg Arg Phe Cys Asp
180 185 190

Glu His Asp Leu Lys Leu Ile Ser Ile Glu Gln Leu Ile Glu Trp Arg
195 200 205

Arg Lys Asn Glu Ile Leu Val Glu Arg Gln Val Glu Thr Val Leu Pro
210 215 220

Thr Asp Phe Gly Thr Phe Lys Ala Val Gly Tyr Arg Ser Ile Ile Asp
225 230 235 240

Gly Thr Glu Leu Val Ala Ile Val Ala Gly Asp Val Ala Ser Asp Gly
245 250 255

Gly Glu Asn Val Leu Val Arg Val His Ser Glu Cys Leu Thr Gly Asp
 260 265 270
 Val Phe Gly Ser Arg Arg Cys Asp Cys Gly Gln Gln Leu His Glu Ser
 275 280 285
 Leu Arg Leu Ile Gln Glu Ala Gly Arg Gly Val Val Val Tyr Met Arg
 290 295 300
 Gly His Glu Gly Arg Gly Ile Gly Leu Leu Ala Lys Leu Arg Ala Tyr
 305 310 315 320
 Gln Leu Gln Asp Glu Gly Ala Asp Thr Val Asp Ala Asn Leu Ala Leu
 325 330 335
 Gly Leu Pro Ala Asp Ala Arg Glu Phe Gly Thr Ser Ala Gln Ile Leu
 340 345 350
 Tyr Asp Leu Gly Val Arg Ser Leu Asn Leu Ile Ser Asn Asn Pro Ala
 355 360 365
 Lys Lys Val Gly Leu Glu Gly His Gly Ile Ser Ile Ala Ser Arg Thr
 370 375 380
 Pro Ile Pro Val Ala Val His Glu Asp Asn Val Arg Tyr Leu Lys Thr
 385 390 395 400
 Lys Arg Asp Arg Met Gly His Asp Leu Pro Asp Val Ala Leu Trp Glu
 405 410 415
 Gln Glu His Pro Glu Asn
 420

<210> 563
 <211> 600
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(577)
 <223> RXN02249

<400> 563
 atgttcgata cctgaaaacc aagcgtgacc gcatgggaca tgacctcca gatgtcgac 60
 tgtgggaaca agagcaccca gaaaactaag gagcacaaca atg gct aaa gaa gga 115
 Met Ala Lys Glu Gly
 1 5
 ttg ccg gca gtc gaa ctc ccc gac gcc agc gga tta aaa gtc gcc gta 163
 Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly Leu Lys Val Ala Val
 10 15 20
 gtc acc gca cgg tgg aac gca gaa atc tgc gac cgc ctg cac aag cac 211
 Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp Arg Leu His Lys His
 25 30 35
 gca gta gat gcg gga cgt gca gca gga gca acg gtg agc gaa tac cgc 259

Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr Val Ser Glu Tyr Arg
40 45 50

gtc atc ggc gcc ctg gaa ctt cca gtc gta gtg caa gaa ctg gca cgc 307
Val Ile Gly Ala Leu Glu Leu Pro Val Val Val Gln Glu Leu Ala Arg
55 60 65

acc cat gac gca gta gtt gcc ttg ggc tgt gtc gtt cgt ggc ggc acc 355
Thr His Asp Ala Val Val Ala Leu Gly Cys Val Val Arg Gly Gly Thr
70 75 80 85

cca cac ttt gat tac gtg tgc gac tct gtc acc gaa ggc ctc acc cgc 403
Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr Glu Gly Leu Thr Arg
90 95 100

att gct ctt gat act tcc acc cca atc ggc aac ggt gtg ttg act acc 451
Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn Gly Val Leu Thr Thr
105 110 115

aac acc gaa gag caa gcc gtg gaa cgc tcc ggt gga gaa ggc tct gta 499
Asn Thr Glu Glu Gln Ala Val Glu Arg Ser Gly Gly Glu Gly Ser Val
120 125 130

gag gac aaa ggc gca gag gca atg gtc gct gca ctc gat act gcc ctc 547
Glu Asp Lys Gly Ala Glu Ala Met Val Ala Ala Leu Asp Thr Ala Leu
135 140 145

gtg ctt tct caa att cgt gca act gag ggt tagactgttc tttaaaaggt 597
Val Leu Ser Gln Ile Arg Ala Thr Glu Gly
150 155

ttg 600

<210> 564

<211> 159

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 564

Met Ala Lys Glu Gly Leu Pro Ala Val Glu Leu Pro Asp Ala Ser Gly
1 5 10 15

Leu Lys Val Ala Val Val Thr Ala Arg Trp Asn Ala Glu Ile Cys Asp
20 25 30

Arg Leu His Lys His Ala Val Asp Ala Gly Arg Ala Ala Gly Ala Thr
35 40 45

Val Ser Glu Tyr Arg Val Ile Gly Ala Leu Glu Leu Pro Val Val Val
50 55 60

Gln Glu Leu Ala Arg Thr His Asp Ala Val Val Ala Leu Gly Cys Val
65 70 75 80

Val Arg Gly Gly Thr Pro His Phe Asp Tyr Val Cys Asp Ser Val Thr
85 90 95

Glu Gly Leu Thr Arg Ile Ala Leu Asp Thr Ser Thr Pro Ile Gly Asn
100 105 110